

AA

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	5
---	---	---	---	---	---	---	---	---	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	---

**(10) International Publication Number**  
**WO 01/77168 A2**

*[Continued on next page]*

**BEST AVAILABLE COPY**



CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

(84) Designated States (regional): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

**Published:**

- without international search report and to be republished upon receipt of that report
- with sequence listing part of description published separately in electronic form and available upon request from the International Bureau

*For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.*

## COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS OF LUNG CANCER

### TECHNICAL FIELD OF THE INVENTION

The present invention relates generally to therapy and diagnosis of  
5 cancer, such as lung cancer. the invention is more specifically related to polypeptides,  
comprising at least a portion of a lung tumor protein, and to polynucleotides encoding  
such polypeptides. such polypeptides and polynucleotides are useful in pharmaceutical  
compositions, *e.g.*, vaccines, and other compositions for the diagnosis and treatment of  
lung cancer.

### 10 BACKGROUND OF THE INVENTION

Lung cancer is the primary cause of cancer death among both men and  
women in the U.S., with an estimated 172,000 new cases being reported in 1994. The  
five-year survival rate among all lung cancer patients, regardless of the stage of disease  
at diagnosis, is only 13%. This contrasts with a five-year survival rate of 46% among  
15 cases detected while the disease is still localized. However, only 16% of lung cancers  
are discovered before the disease has spread.

Early detection is difficult since clinical symptoms are often not seen  
until the disease has reached an advanced stage. Currently, diagnosis is aided by the use  
of chest x-rays, analysis of the type of cells contained in sputum and fiberoptic  
20 examination of the bronchial passages. Treatment regimens are determined by the type  
and stage of the cancer, and include surgery, radiation therapy and/or chemotherapy. In  
spite of considerable research into therapies for the disease, lung cancer remains  
difficult to treat.

Accordingly, there remains a need in the art for improved vaccines,  
25 treatment methods and diagnostic techniques for lung cancer.

### SUMMARY OF THE INVENTION

In one aspect, the present invention provides polynucleotide  
compositions comprising a sequence selected from the group consisting of:

(a) sequences provided in SEQ ID NO:1-232, 243-396, 398-412, 414-424 and 437-440;

(b) complements of the sequences provided in SEQ ID NO:1-232, 243-396, 398-412, 414-424 and 437-440;

5 (c) sequences consisting of at least 20 contiguous residues of a sequence provided in SEQ ID NO:1-232, 243-396, 398-412, 414-424 and 437-440;

(d) sequences that hybridize to a sequence provided in SEQ ID NO:1-232, 243-396, 398-412, 414-424 and 437-440, under moderately stringent conditions;

10 (e) sequences having at least 75% identity to a sequence of SEQ ID NO:1-232, 243-396, 398-412, 414-424 and 437-440;

(f) sequences having at least 90% identity to a sequence of SEQ ID NO:1-232, 243-396, 398-412, 414-424 and 437-440; and

(g) degenerate variants of a sequence provided in SEQ ID NO:1-232,  
15 243-396, 398-412, 414-424 and 437-440.

In one preferred embodiment, the polynucleotide compositions of the invention are expressed in at least about 20%, more preferably in at least about 30%, and most preferably in at least about 50% of lung tumor samples tested, at a level that is  
20 at least about 2-fold, preferably at least about 5-fold, and most preferably at least about 10-fold higher than that for normal tissues.

The present invention, in another aspect, provides polypeptide compositions comprising an amino acid sequence that is encoded by a polynucleotide sequence described above. In certain specific embodiments, the present invention  
25 provides polypeptide compositions comprising an amino acid sequence selected from the group consisting of sequences recited in SEQ ID NO:229-232, 237-242, 397, 413 and 425-436.

In certain preferred embodiments, the polypeptides and/or polynucleotides of the present invention are immunogenic, *i.e.*, they are capable of  
30 eliciting an immune response, particularly a humoral and/or cellular immune response, as further described herein.



The present invention further provides fragments, variants and/or derivatives of the disclosed polypeptide and/or polynucleotide sequences, wherein the fragments, variants and/or derivatives preferably have a level of immunogenic activity of at least about 50%, preferably at least about 70% and more preferably at least about 90% of the level of immunogenic activity of a polypeptide sequence set forth in SEQ ID NOs: 229-232, 237-242, 397, 413 and 425-436, or a polypeptide sequence encoded by a polynucleotide sequence set forth in SEQ ID NOs: 1-232, 243-396, 398-412, 414-424 and 437-440.

The present invention further provides polynucleotides that encode a polypeptide described above, expression vectors comprising such polynucleotides and host cells transformed or transfected with such expression vectors.

Within other aspects, the present invention provides pharmaceutical compositions comprising a polypeptide or polynucleotide as described above and a physiologically acceptable carrier.

Within a related aspect of the present invention, the pharmaceutical compositions, *e.g.*, vaccine compositions, are provided for prophylactic or therapeutic applications. Such compositions generally comprise an immunogenic polypeptide or polynucleotide of the invention and an immunostimulant, such as an adjuvant.

The present invention further provides pharmaceutical compositions that comprise: (a) an antibody or antigen-binding fragment thereof that specifically binds to a polypeptide of the present invention, or a fragment thereof; and (b) a physiologically acceptable carrier.

Within further aspects, the present invention provides pharmaceutical compositions comprising: (a) an antigen presenting cell that expresses a polypeptide as described above and (b) a pharmaceutically acceptable carrier or excipient. Illustrative antigen presenting cells include dendritic cells, macrophages, monocytes, fibroblasts and B cells.

Within related aspects, pharmaceutical compositions are provided that comprise: (a) an antigen presenting cell that expresses a polypeptide as described above and (b) an immunostimulant.

The present invention further provides, in other aspects, fusion proteins that comprise at least one polypeptide as described above, as well as polynucleotides

encoding such fusion proteins, typically in the form of pharmaceutical compositions, *e.g.*, vaccine compositions, comprising a physiologically acceptable carrier and/or an immunostimulant. The fusions proteins may comprise multiple immunogenic polypeptides or portions/variants thereof, as described herein, and may further comprise  
5 one or more polypeptide segments for facilitating the expression, purification and/or immunogenicity of the polypeptide(s).

Within further aspects, the present invention provides methods for stimulating an immune response in a patient, preferably a T cell response in a human patient, comprising administering a pharmaceutical composition described herein. The  
10 patient may be afflicted with lung cancer, in which case the methods provide treatment for the disease, or patient considered at risk for such a disease may be treated prophylactically.

Within further aspects, the present invention provides methods for inhibiting the development of a cancer in a patient, comprising administering to a  
15 patient a pharmaceutical composition as recited above. The patient may be afflicted with lung cancer, in which case the methods provide treatment for the disease, or patient considered at risk for such a disease may be treated prophylactically.

The present invention further provides, within other aspects, methods for removing tumor cells from a biological sample, comprising contacting a biological  
20 sample with T cells that specifically react with a polypeptide of the present invention, wherein the step of contacting is performed under conditions and for a time sufficient to permit the removal of cells expressing the protein from the sample.

Within related aspects, methods are provided for inhibiting the development of a cancer in a patient, comprising administering to a patient a biological  
25 sample treated as described above.

Methods are further provided, within other aspects, for stimulating and/or expanding T cells specific for a polypeptide of the present invention, comprising contacting T cells with one or more of: (i) a polypeptide as described above; (ii) a polynucleotide encoding such a polypeptide; and/or (iii) an antigen presenting cell that  
30 expresses such a polypeptide; under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells. Isolated T cell populations comprising T cells prepared as described above are also provided.

Within further aspects, the present invention provides methods for inhibiting the development of a cancer in a patient, comprising administering to a patient an effective amount of a T cell population as described above.

The present invention further provides methods for inhibiting the development of a cancer in a patient, comprising the steps of: (a) incubating CD4<sup>+</sup> and/or CD8<sup>+</sup> T cells isolated from a patient with one or more of: (i) a polypeptide comprising at least an immunogenic portion of polypeptide disclosed herein; (ii) a polynucleotide encoding such a polypeptide; and (iii) an antigen-presenting cell that expressed such a polypeptide; and (b) administering to the patient an effective amount of the proliferated T cells, and thereby inhibiting the development of a cancer in the patient. Proliferated cells may, but need not, be cloned prior to administration to the patient.

Within further aspects, the present invention provides methods for determining the presence or absence of a cancer, preferably a lung cancer, in a patient comprising: (a) contacting a biological sample obtained from a patient with a binding agent that binds to a polypeptide as recited above; (b) detecting in the sample an amount of polypeptide that binds to the binding agent; and (c) comparing the amount of polypeptide with a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient. Within preferred embodiments, the binding agent is an antibody, more preferably a monoclonal antibody.

The present invention also provides, within other aspects, methods for monitoring the progression of a cancer in a patient. Such methods comprise the steps of: (a) contacting a biological sample obtained from a patient at a first point in time with a binding agent that binds to a polypeptide as recited above; (b) detecting in the sample an amount of polypeptide that binds to the binding agent; (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and (d) comparing the amount of polypeptide detected in step (c) with the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

The present invention further provides, within other aspects, methods for determining the presence or absence of a cancer in a patient, comprising the steps of: (a) contacting a biological sample obtained from a patient with an oligonucleotide that

hybridizes to a polynucleotide that encodes a polypeptide of the present invention; (b) detecting in the sample a level of a polynucleotide, preferably mRNA, that hybridizes to the oligonucleotide; and (c) comparing the level of polynucleotide that hybridizes to the oligonucleotide with a predetermined cut-off value, and therefrom determining the presence or absence of a cancer in the patient. Within certain embodiments, the amount of mRNA is detected via polymerase chain reaction using, for example, at least one oligonucleotide primer that hybridizes to a polynucleotide encoding a polypeptide as recited above, or a complement of such a polynucleotide. Within other embodiments, the amount of mRNA is detected using a hybridization technique, employing an oligonucleotide probe that hybridizes to a polynucleotide that encodes a polypeptide as recited above, or a complement of such a polynucleotide.

In related aspects, methods are provided for monitoring the progression of a cancer in a patient, comprising the steps of: (a) contacting a biological sample obtained from a patient with an oligonucleotide that hybridizes to a polynucleotide that encodes a polypeptide of the present invention; (b) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide; (c) repeating steps (a) and (b) using a biological sample obtained from the patient at a subsequent point in time; and (d) comparing the amount of polynucleotide detected in step (c) with the amount detected in step (b) and therefrom monitoring the progression of the cancer in the patient.

Within further aspects, the present invention provides antibodies, such as monoclonal antibodies, that bind to a polypeptide as described above, as well as diagnostic kits comprising such antibodies. Diagnostic kits comprising one or more oligonucleotide probes or primers as described above are also provided.

These and other aspects of the present invention will become apparent upon reference to the following detailed description and attached drawings. All references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

#### BRIEF DESCRIPTION OF THE DRAWINGS AND SEQUENCE IDENTIFIERS

Figure 1 is a bar graph showing expression of clone SCC2-51 in normal tissues and tumor tissues.

SEQ ID NO:1 is the determined cDNA sequence for LSC-1.

SEQ ID NO:2 is the determined cDNA sequence for LSC-2.

SEQ ID NO:3 is the determined cDNA sequence for LSC-3.

SEQ ID NO:4 is the determined cDNA sequence for LSC-5.

5 SEQ ID NO:5 is the determined cDNA sequence for LSC-6.

SEQ ID NO:6 is the determined cDNA sequence for LSC-7.

SEQ ID NO:7 is the determined cDNA sequence for LSC-9.

SEQ ID NO:8 is the determined cDNA sequence for LSC-10.

SEQ ID NO:9 is the determined cDNA sequence for LSC-11.

10 SEQ ID NO:10 is the determined cDNA sequence for LSC-13.

SEQ ID NO:11 is the determined cDNA sequence for LSC-15.

SEQ ID NO:12 is the determined cDNA sequence for LSC-20.

SEQ ID NO:13 is the determined cDNA sequence for LSC-23.

SEQ ID NO:14 is the determined cDNA sequence for LSC-24.

15 SEQ ID NO:15 is the determined cDNA sequence for LSC-25.

SEQ ID NO:16 is the determined cDNA sequence for LSC-26.

SEQ ID NO:17 is the determined cDNA sequence for LSC-27.

SEQ ID NO:18 is the determined cDNA sequence for LSC-28.

SEQ ID NO:19 is the determined cDNA sequence for LSC-29.

20 SEQ ID NO:20 is the determined cDNA sequence for LSC-30.

SEQ ID NO:21 is the determined cDNA sequence for LSC-31.

SEQ ID NO:22 is the determined cDNA sequence for LSC-33.

SEQ ID NO:23 is the determined cDNA sequence for LSC-34.

SEQ ID NO:24 is the determined cDNA sequence for LSC-35.

25 SEQ ID NO:25 is the determined cDNA sequence for LSC-37.

SEQ ID NO:26 is the determined cDNA sequence for LSC-39.

SEQ ID NO:27 is the determined cDNA sequence for LSC-43.

SEQ ID NO:28 is the determined cDNA sequence for LSC-46.

SEQ ID NO:29 is the determined cDNA sequence for LSC-49.

30 SEQ ID NO:30 is the determined cDNA sequence for LSC-51.

SEQ ID NO:31 is the determined cDNA sequence for LSC-53.

SEQ ID NO:32 is the determined cDNA sequence for LSC-55.

SEQ ID NO:33 is the determined cDNA sequence for LSC-60.  
SEQ ID NO:34 is the determined cDNA sequence for LSC-62.  
SEQ ID NO:35 is the determined cDNA sequence for LSC-64.  
SEQ ID NO:36 is the determined cDNA sequence for LSC-65.  
5 SEQ ID NO:37 is the determined cDNA sequence for LSC-71.  
SEQ ID NO:38 is the determined cDNA sequence for LSC-72.  
SEQ ID NO:39 is the determined cDNA sequence for LSC-74.  
SEQ ID NO:40 is the determined cDNA sequence for LSC-76.  
SEQ ID NO:41 is the determined cDNA sequence for LSC-77.  
10 SEQ ID NO:42 is the determined cDNA sequence for LSC-78.  
SEQ ID NO:43 is the determined cDNA sequence for LSC-81.  
SEQ ID NO:44 is the determined cDNA sequence for LSC-93.  
SEQ ID NO:45 is the determined cDNA sequence for LSC-101.  
SEQ ID NO:46 is the determined cDNA sequence for LSC-102.  
15 SEQ ID NO:47 is the determined cDNA sequence for LSC-103.  
SEQ ID NO:48 is the determined cDNA sequence for LSC-105.  
SEQ ID NO:49 is the determined cDNA sequence for LSC-110.  
SEQ ID NO:50 is the determined cDNA sequence for LSC-125.  
SEQ ID NO:51 is the determined cDNA sequence for LSC-134.  
20 SEQ ID NO:52 is the determined cDNA sequence for LSC-142.  
SEQ ID NO:53 is the determined cDNA sequence for LSC-144.  
SEQ ID NO:54 is the determined cDNA sequence for LSC-148.  
SEQ ID NO:55 is the determined cDNA sequence for LSC-149.  
SEQ ID NO:56 is the determined cDNA sequence for LSC-153.  
25 SEQ ID NO:57 is the determined cDNA sequence for LSC-163.  
SEQ ID NO:58 is the determined cDNA sequence for LSC-170.  
SEQ ID NO:59 is the determined cDNA sequence for LSC-171.  
SEQ ID NO:60 is the determined cDNA sequence for LSC-172.  
SEQ ID NO:61 is the determined cDNA sequence for LSC-175.  
30 SEQ ID NO:62 is the determined cDNA sequence for LSC-177.  
SEQ ID NO:63 is the determined cDNA sequence for LSC-182.  
SEQ ID NO:64 is the determined cDNA sequence for LSC-184.

SEQ ID NO:65 is the determined cDNA sequence for LSC-189.

SEQ ID NO:66 is the determined cDNA sequence for LSC-194.

SEQ ID NO:67 is the determined cDNA sequence for LSC-195.

SEQ ID NO:68 is the determined cDNA sequence for LSC-196.

5 SEQ ID NO:69 is the determined cDNA sequence for LSC-199.

SEQ ID NO:70 is the determined cDNA sequence for LSC-202.

SEQ ID NO:71 is the determined cDNA sequence for LSC-203.

SEQ ID NO:72 is the determined cDNA sequence for LSC-205.

SEQ ID NO:73 is the determined cDNA sequence for LSC-206.

10 SEQ ID NO:74 is the determined cDNA sequence for LSC-210.

SEQ ID NO:75 is the determined cDNA sequence for LSC-215.

SEQ ID NO:76 is the determined cDNA sequence for LSC-218.

SEQ ID NO:77 is the determined cDNA sequence for clone 48060.

SEQ ID NO:78 is the determined cDNA sequence for clone 48069.

15 SEQ ID NO:79 is the determined cDNA sequence for clone 48071.

SEQ ID NO:80 is the determined cDNA sequence for clone 48080.

SEQ ID NO:81 is the determined cDNA sequence for clone 48090.

SEQ ID NO:82 is the determined cDNA sequence for clone 48102.

SEQ ID NO:83 is the determined cDNA sequence for clone 48112.

20 SEQ ID NO:84 is the determined cDNA sequence for clone 48118.

SEQ ID NO:85 is the determined cDNA sequence for clone 48125.

SEQ ID NO:86 is the determined cDNA sequence for clone 48129.

SEQ ID NO:87 is the determined cDNA sequence for clone 48134.

SEQ ID NO:88 is the determined cDNA sequence for clone 48135.

25 SEQ ID NO:89 is the determined cDNA sequence for clone 48137.

SEQ ID NO:90 is the determined cDNA sequence for clone 48138.

SEQ ID NO:91 is the determined cDNA sequence for clone 48142.

SEQ ID NO:92 is the determined cDNA sequence for clone 48143.

SEQ ID NO:93 is the determined cDNA sequence for clone 48149.

30 SEQ ID NO:94 is the determined cDNA sequence for clone 48150.

SEQ ID NO:95 is the determined cDNA sequence for clone 48179.

SEQ ID NO:96 is the determined cDNA sequence for clone 48183.

SEQ ID NO:97 is the determined cDNA sequence for clone 48193.

SEQ ID NO:98 is the determined cDNA sequence for clone 48196.

SEQ ID NO:99 is the determined cDNA sequence for clone 48202.

SEQ ID NO:100 is the determined cDNA sequence for clone 48204.

5 SEQ ID NO:101 is the determined cDNA sequence for clone 48205.

SEQ ID NO:102 is the determined cDNA sequence for clone 48206.

SEQ ID NO:103 is the determined cDNA sequence for clone 48211.

SEQ ID NO:104 is the determined cDNA sequence for clone 48216.

SEQ ID NO:105 is the determined cDNA sequence for clone 48219.

10 SEQ ID NO:106 is the determined cDNA sequence for clone 48223.

SEQ ID NO:107 is the determined cDNA sequence for clone 48224.

SEQ ID NO:108 is the determined cDNA sequence for clone 48225.

SEQ ID NO:109 is the determined cDNA sequence for clone 48228.

SEQ ID NO:110 is the determined cDNA sequence for clone 48236.

15 SEQ ID NO:111 is the determined cDNA sequence for clone lcl/15745.

SEQ ID NO:112 is the determined cDNA sequence for clone lcl/16256.

SEQ ID NO:113 is the determined cDNA sequence for clone lcl/21736.

SEQ ID NO:114 is the determined cDNA sequence for clone lcl/22291.

SEQ ID NO:115 is the determined cDNA sequence for clone lcl/24845.

20 SEQ ID NO:116 is the determined cDNA sequence for clone lcl/24847.

SEQ ID NO:117 is the determined cDNA sequence for clone lcl/24848.

SEQ ID NO:118 is the determined cDNA sequence for clone lcl/24849.

SEQ ID NO:119 is the determined cDNA sequence for clone lcl/24851.

SEQ ID NO:120 is the determined cDNA sequence for clone lcl/24852.

25 SEQ ID NO:121 is the determined cDNA sequence for clone lcl/24854.

SEQ ID NO:122 is the determined cDNA sequence for clone lcl/24855.

SEQ ID NO:123 is the determined cDNA sequence for clone lcl/24857.

SEQ ID NO:124 is the determined cDNA sequence for clone lcl/24859.

SEQ ID NO:125 is the determined cDNA sequence for clone lcl/24864.

30 SEQ ID NO:126 is the determined cDNA sequence for clone lcl/24865.

SEQ ID NO:127 is the determined cDNA sequence for clone lcl/24866.

SEQ ID NO:128 is the determined cDNA sequence for clone lcl/24867.



SEQ ID NO:129 is the determined cDNA sequence for clone lcl/24869.  
SEQ ID NO:130 is the determined cDNA sequence for clone lcl/24871.  
SEQ ID NO:131 is the determined cDNA sequence for clone lcl/24873.  
SEQ ID NO:132 is the determined cDNA sequence for clone lcl/24874.  
5 SEQ ID NO:133 is the determined cDNA sequence for clone lcl/26008.  
SEQ ID NO:134 is the determined cDNA sequence for clone lcl/56871.  
SEQ ID NO:135 is the determined cDNA sequence for clone lcl/57480.  
SEQ ID NO:136 is the determined cDNA sequence for clone lcl/57499.  
SEQ ID NO:137 is the determined cDNA sequence for clone lcl/16785.  
10 SEQ ID NO:138 is the determined cDNA sequence for clone lcl/16787.  
SEQ ID NO:139 is the determined cDNA sequence for clone lcl/22175.  
SEQ ID NO:140 is the determined cDNA sequence for clone lcl/29484.  
SEQ ID NO:141 is the determined cDNA sequence for clone lcl/30354.  
SEQ ID NO:142 is the determined cDNA sequence for clone lcl/56868.  
15 SEQ ID NO:143 is the determined cDNA sequence for clone SCC2-1.  
SEQ ID NO:144 is the determined cDNA sequence for clone SCC2-2.  
SEQ ID NO:145 is the determined cDNA sequence for clone SCC2-4.  
SEQ ID NO:146 is the determined cDNA sequence for clone SCC2-5.  
SEQ ID NO:147 is the determined cDNA sequence for clone SCC2-7.  
20 SEQ ID NO:148 is the determined cDNA sequence for clone SCC2-9.  
SEQ ID NO:149 is the determined cDNA sequence for clone SCC2-10.  
SEQ ID NO:150 is the determined cDNA sequence for clone SCC2-11.  
SEQ ID NO:151 is the determined cDNA sequence for clone SCC2-12.  
SEQ ID NO:152 is the determined cDNA sequence for clone SCC2-13.  
25 SEQ ID NO:153 is the determined cDNA sequence for clone SCC2-14.  
SEQ ID NO:154 is the determined cDNA sequence for clone SCC2-17.  
SEQ ID NO:155 is the determined cDNA sequence for clone SCC2-18.  
SEQ ID NO:156 is the determined cDNA sequence for clone SCC2-20.  
SEQ ID NO:157 is the determined cDNA sequence for clone SCC2-23.  
30 SEQ ID NO:158 is the determined cDNA sequence for clone SCC2-24.  
SEQ ID NO:159 is the determined cDNA sequence for clone SCC2-27.  
SEQ ID NO:160 is the determined cDNA sequence for clone SCC2-29.

SEQ ID NO:161 is the determined cDNA sequence for clone SCC2-30.  
SEQ ID NO:162 is the determined cDNA sequence for clone SCC2-31.  
SEQ ID NO:163 is the determined cDNA sequence for clone SCC2-33.  
SEQ ID NO:164 is the determined cDNA sequence for clone SCC2-35.  
5 SEQ ID NO:165 is the determined cDNA sequence for clone SCC2-36.  
SEQ ID NO:166 is the determined cDNA sequence for clone SCC2-37.  
SEQ ID NO:167 is the determined cDNA sequence for clone SCC2-38.  
SEQ ID NO:168 is the determined cDNA sequence for clone SCC2-39.  
SEQ ID NO:169 is the determined cDNA sequence for clone SCC2-40.  
10 SEQ ID NO:170 is the determined cDNA sequence for clone SCC2-43.  
SEQ ID NO:171 is the determined cDNA sequence for clone SCC2-44.  
SEQ ID NO:172 is the determined cDNA sequence for clone SCC2-46.  
SEQ ID NO:173 is the determined cDNA sequence for clone SCC2-47.  
SEQ ID NO:174 is the determined cDNA sequence for clone SCC2-48.  
15 SEQ ID NO:175 is the determined cDNA sequence for clone SCC2-51.  
SEQ ID NO:176 is the determined cDNA sequence for clone SCC2-52.  
SEQ ID NO:177 is the determined cDNA sequence for clone SCC2-53.  
SEQ ID NO:178 is the determined cDNA sequence for clone SCC2-54.  
SEQ ID NO:179 is the determined cDNA sequence for clone SCC2-57.  
20 SEQ ID NO:180 is the determined cDNA sequence for clone SCC2-58.  
SEQ ID NO:181 is the determined cDNA sequence for clone SCC2-60.  
SEQ ID NO:182 is the determined cDNA sequence for clone SCC2-64.  
SEQ ID NO:183 is the determined cDNA sequence for clone SCC2-66.  
SEQ ID NO:184 is the determined cDNA sequence for clone SCC2-68.  
25 SEQ ID NO:185 is the determined cDNA sequence for clone SCC2-69.  
SEQ ID NO:186 is the determined cDNA sequence for clone SCC2-70.  
SEQ ID NO:187 is the determined cDNA sequence for clone SCC2-75.  
SEQ ID NO:188 is the determined cDNA sequence for clone SCC2-77.  
SEQ ID NO:189 is the determined cDNA sequence for clone SCC2-78.  
30 SEQ ID NO:190 is the determined cDNA sequence for clone SCC2-79.  
SEQ ID NO:191 is the determined cDNA sequence for clone SCC2-80.  
SEQ ID NO:192 is the determined cDNA sequence for clone SCC2-84.

SEQ ID NO:193 is the determined cDNA sequence for clone SCC2-85.  
SEQ ID NO:194 is the determined cDNA sequence for clone SCC2-91.  
SEQ ID NO:195 is the determined cDNA sequence for clone SCC2-92.  
SEQ ID NO:196 is the determined cDNA sequence for clone SCC2-95.  
5 SEQ ID NO:197 is the determined cDNA sequence for clone SCC2-96.  
SEQ ID NO:198 is the determined cDNA sequence for clone SCC2-97.  
SEQ ID NO:199 is the determined cDNA sequence for clone SCC2-98.  
SEQ ID NO:200 is the determined cDNA sequence for clone SCC2-100.  
SEQ ID NO:201 is the determined cDNA sequence for clone SCC2-101.  
10 SEQ ID NO:202 is the determined cDNA sequence for clone SCC2-102.  
SEQ ID NO:203 is the determined cDNA sequence for clone SCC2-103.  
SEQ ID NO:204 is the determined cDNA sequence for clone SCC2-104.  
SEQ ID NO:205 is the determined cDNA sequence for clone SCC2-107.  
SEQ ID NO:206 is the determined cDNA sequence for clone SCC2-108.  
15 SEQ ID NO:207 is the determined cDNA sequence for clone SCC2-110.  
SEQ ID NO:208 is the determined cDNA sequence for clone SCC2-112.  
SEQ ID NO:209 is the determined cDNA sequence for clone SCC2-116.  
SEQ ID NO:210 is the determined cDNA sequence for clone SCC2-124.  
SEQ ID NO:211 is the determined cDNA sequence for clone SCC2-125.  
20 SEQ ID NO:212 is the determined cDNA sequence for clone SCC2-131.  
SEQ ID NO:213 is the determined cDNA sequence for clone SCC2-137.  
SEQ ID NO:214 is the determined cDNA sequence for clone SCC2-143.  
SEQ ID NO:215 is the determined cDNA sequence for clone SCC2-146.  
SEQ ID NO:216 is the determined cDNA sequence for clone SCC2-154.  
25 SEQ ID NO:217 is the determined cDNA sequence for clone SCC2-164.  
SEQ ID NO:218 is the determined cDNA sequence for clone SCC2-179.  
SEQ ID NO:219 is the determined cDNA sequence for clone SCC2-183.  
SEQ ID NO:220 is the determined cDNA sequence for clone SCC2-187.  
SEQ ID NO:221 is the determined cDNA sequence for clone SCC2-188.  
30 SEQ ID NO:222 is the determined cDNA sequence for clone SCC2-232.  
SEQ ID NO:223 is the determined cDNA sequence for clone SCC2-236.  
SEQ ID NO:224 is the determined cDNA sequence for clone SCC2-260.

SEQ ID NO:225 is the determined cDNA sequence for clone SCC2-261.

SEQ ID NO:226 is the determined cDNA sequence for clone SCC2-266.

SEQ ID NO:227 is the determined cDNA sequence for clone SCC2-275.

SEQ ID NO:228 is the determined cDNA sequence for clone SCC2-283.

5       SEQ ID NO:229 is the determined cDNA extended sequence for clone  
SCC2-5, which relates to SEQ ID NO:146.

SEQ ID NO:230 is the determined cDNA extended sequence for clone  
SCC2-14, which relates to SEQ ID NO:153.

SEQ ID NO:231 is the determined cDNA sequence for clone SCC2-50.

10       SEQ ID NO:232 is the determined cDNA extended sequence for clone  
SCC2-51, which relates to SEQ ID NO:175.

SEQ ID NO:233 is the amino acid sequence encoded by SEQ ID  
NO:229.

15       SEQ ID NO:234 is the amino acid sequence encoded by SEQ ID  
NO:230.

SEQ ID NO:235 is the amino acid sequence encoded by SEQ ID  
NO:231.

SEQ ID NO:236 is the amino acid sequence encoded by SEQ ID  
NO:232.

20       SEQ ID NO:237 is GenBank Accession No. CAA58926

SEQ ID NO:238 is GenBank Accession No. BAA91327

SEQ ID NO:239 is GenBank Accession No. BAA22955

SEQ ID NO:240 is GenBank Accession No. NP\_004258

SEQ ID NO:241 is GenBank Accession No. AAF61208

25       SEQ ID NO:242 is GenBank Accession No. CAA26370

SEQ ID NO:243 is the determined cDNA sequence for '56908.1

SEQ ID NO:244 is the determined cDNA sequence for '56909.1

SEQ ID NO:245 is the determined cDNA sequence for '56911.1

SEQ ID NO:246 is GenBank Accession No. AK000700

30       SEQ ID NO:247 is the determined cDNA sequence for '56912.1

SEQ ID NO:248 is GenBank Accession No. AB006624

SEQ ID NO:249 is the determined cDNA sequence for '56913.1

SEQ ID NO:250 is GenBank Accession No. NM\_004267

SEQ ID NO:251 is the determined cDNA sequence for '56916.1

SEQ ID NO:252 is the determined cDNA sequence for '56917.1

SEQ ID NO:253 is the determined cDNA sequence for '56921.1

5 SEQ ID NO:254 is GenBank Accession No. AF216751

SEQ ID NO:255 is the determined cDNA sequence for '56922.1

SEQ ID NO:256 is GenBank Accession No. X02530

SEQ ID NO:257 is the determined cDNA sequence for '56923.1

SEQ ID NO:258 is the determined cDNA sequence for 54533.1

10 SEQ ID NO:259 is the determined cDNA sequence for 54534.1

SEQ ID NO:260 is the determined cDNA sequence for 54536.1

SEQ ID NO:261 is the determined cDNA sequence for 54538.1

SEQ ID NO:262 is the determined cDNA sequence for 54540.1

SEQ ID NO:263 is the determined cDNA sequence for 55084.1

15 SEQ ID NO:264 is the determined cDNA sequence for 55086.1

SEQ ID NO:265 is the determined cDNA sequence for 54555.1

SEQ ID NO:266 is the determined cDNA sequence for 54557.1

SEQ ID NO:267 is the determined cDNA sequence for 54564.1

SEQ ID NO:268 is the determined cDNA sequence for 55098.1

20 SEQ ID NO:269 is the determined cDNA sequence for 55473.1

SEQ ID NO:270 is the determined cDNA sequence for 55104.1

SEQ ID NO:271 is the determined cDNA sequence for 55105.1

SEQ ID NO:272 is the determined cDNA sequence for 55107.1

SEQ ID NO:273 is the determined cDNA sequence for 55108.1

25 SEQ ID NO:274 is the determined cDNA sequence for 55114.1

SEQ ID NO:275 is the determined cDNA sequence for 55477.1

SEQ ID NO:276 is the determined cDNA sequence for 55482.1

SEQ ID NO:277 is the determined cDNA sequence for 55483.1

SEQ ID NO:278 is the determined cDNA sequence for 55485.1

30 SEQ ID NO:279 is the determined cDNA sequence for 55487.1

SEQ ID NO:280 is the determined cDNA sequence for 55488.1

SEQ ID NO:281 is the determined cDNA sequence for 55087.1

SEQ ID NO:282 is the determined cDNA sequence for 55089.1  
SEQ ID NO:283 is the determined cDNA sequence for 55092.1  
SEQ ID NO:284 is the determined cDNA sequence for 55093.1  
SEQ ID NO:285 is the determined cDNA sequence for 56926.1  
5 SEQ ID NO:286 is the determined cDNA sequence for 56930.1  
SEQ ID NO:287 is the determined cDNA sequence for 56944.1  
SEQ ID NO:288 is the determined cDNA sequence for 56945.1  
SEQ ID NO:289 is the determined cDNA sequence for 55490.1  
SEQ ID NO:290 is the determined cDNA sequence for 55495.1  
10 SEQ ID NO:291 is the determined cDNA sequence for 55504.1  
SEQ ID NO:292 is the determined cDNA sequence for 55506.1  
SEQ ID NO:293 is the determined cDNA sequence for 56480.1  
SEQ ID NO:294 is the determined cDNA sequence for 56482.1  
SEQ ID NO:295 is the determined cDNA sequence for 56484.1  
15 SEQ ID NO:296 is the determined cDNA sequence for 56487.1  
SEQ ID NO:297 is the determined cDNA sequence for 56488.1  
SEQ ID NO:298 is the determined cDNA sequence for 56490.1  
SEQ ID NO:299 is the determined cDNA sequence for 56493.1  
SEQ ID NO:300 is the determined cDNA sequence for 56494.1  
20 SEQ ID NO:301 is the determined cDNA sequence for 56495.1  
SEQ ID NO:302 is the determined cDNA sequence for 56499.1  
SEQ ID NO:303 is the determined cDNA sequence for 56517.1  
SEQ ID NO:304 is the determined cDNA sequence for 56952.1  
SEQ ID NO:305 is the determined cDNA sequence for 56953.1  
25 SEQ ID NO:306 is the determined cDNA sequence for 56959.1  
SEQ ID NO:307 is the determined cDNA sequence for 57139.1  
SEQ ID NO:308 is the determined cDNA sequence for 57078.1  
SEQ ID NO:309 is the determined cDNA sequence for 57092.1  
SEQ ID NO:310 is the determined cDNA sequence for 57099.1  
30 SEQ ID NO:311 is the determined cDNA sequence for 57100.1  
SEQ ID NO:312 is the determined cDNA sequence for 57105.1  
SEQ ID NO:313 is the determined cDNA sequence for 57111.1

SEQ ID NO:314 is the determined cDNA sequence for 57117.1  
SEQ ID NO:315 is the determined cDNA sequence for 57121.1  
SEQ ID NO:316 is the determined cDNA sequence for 57124.1  
SEQ ID NO:317 is the determined cDNA sequence for 57125.1  
5 SEQ ID NO:318 is the determined cDNA sequence for 54800.2  
SEQ ID NO:319 is the determined cDNA sequence for 54802.2  
SEQ ID NO:320 is the determined cDNA sequence for 54803.2  
SEQ ID NO:321 is the determined cDNA sequence for 54805.2  
SEQ ID NO:322 is the determined cDNA sequence for 54806.2  
10 SEQ ID NO:323 is the determined cDNA sequence for 54809.2  
SEQ ID NO:324 is the determined cDNA sequence for 54810.2  
SEQ ID NO:325 is the determined cDNA sequence for 54813.2  
SEQ ID NO:326 is the determined cDNA sequence for 54814.2  
SEQ ID NO:327 is the determined cDNA sequence for 54816.2  
15 SEQ ID NO:328 is the determined cDNA sequence for 54817.2  
SEQ ID NO:329 is the determined cDNA sequence for 54819.2  
SEQ ID NO:330 is the determined cDNA sequence for 54821.2  
SEQ ID NO:331 is the determined cDNA sequence for 54823.2  
SEQ ID NO:332 is the determined cDNA sequence for 54824.2  
20 SEQ ID NO:333 is the determined cDNA sequence for 54825.2  
SEQ ID NO:334 is the determined cDNA sequence for 54826.2  
SEQ ID NO:335 is the determined cDNA sequence for 54827.2  
SEQ ID NO:336 is the determined cDNA sequence for 54829.2  
SEQ ID NO:337 is the determined cDNA sequence for 54830.2  
25 SEQ ID NO:338 is the determined cDNA sequence for 54832.2  
SEQ ID NO:339 is the determined cDNA sequence for 55800.2  
SEQ ID NO:340 is the determined cDNA sequence for 55801.2  
SEQ ID NO:341 is the determined cDNA sequence for 55803.2  
SEQ ID NO:342 is the determined cDNA sequence for 55804.2  
30 SEQ ID NO:343 is the determined cDNA sequence for 55805.2  
SEQ ID NO:344 is the determined cDNA sequence for 55806.2  
SEQ ID NO:345 is the determined cDNA sequence for 55808.2

SEQ ID NO:346 is the determined cDNA sequence for 55810.2

SEQ ID NO:347 is the determined cDNA sequence for 55811.2

SEQ ID NO:348 is the determined cDNA sequence for 55812.2

SEQ ID NO:349 is the determined cDNA sequence for 55814.2

5 SEQ ID NO:350 is the determined cDNA sequence for 55816.2

SEQ ID NO:351 is the determined cDNA sequence for 55817.2

SEQ ID NO:352 is the determined cDNA sequence for 55819.2

SEQ ID NO:353 is the determined cDNA sequence for 55820.2

SEQ ID NO:354 is the determined cDNA sequence for 55823.2

10 SEQ ID NO:355 is the determined cDNA sequence for 55824.2

SEQ ID NO:356 is the determined cDNA sequence for 55826.2

SEQ ID NO:357 is the determined cDNA sequence for 55828.2

SEQ ID NO:358 is the determined cDNA sequence for 55829.2

SEQ ID NO:359 is the determined cDNA sequence for 55831.2

15 SEQ ID NO:360 is the determined cDNA sequence for 55832.2

SEQ ID NO:361 is the determined cDNA sequence for 55833.2

SEQ ID NO:362 is the determined cDNA sequence for 55834.2

SEQ ID NO:363 is the determined cDNA sequence for 55835.2

SEQ ID NO:364 is the determined cDNA sequence for 55838.2

20 SEQ ID NO:365 is a predicted extended cDNA sequence for clone  
48137 (L578S) having the isolated sequence of SEQ ID NO:89)

SEQ ID NO:366 is the predicted amino acid encoded by SEQ ID  
NO:365

SEQ ID NO:367 is the determined cDNA sequence for 49949.5

25 SEQ ID NO:368 is the determined cDNA sequence for 49952.1

SEQ ID NO:369 is the determined cDNA sequence for 49956;contig 29

SEQ ID NO:370 is the determined cDNA sequence for 49960.4

SEQ ID NO:371 is the determined cDNA sequence for 49961;contig 21

SEQ ID NO:372 is the determined cDNA sequence for 49962.4

30 SEQ ID NO:373 is the determined cDNA sequence for 49962.5

SEQ ID NO:374 is the determined cDNA sequence for 49965.1

SEQ ID NO:375 is the determined cDNA sequence for 49966.1



SEQ ID NO:376 is the determined cDNA sequence for 49971.1

SEQ ID NO:377 is the determined cDNA sequence for 49975.1

SEQ ID NO:378 is the determined cDNA sequence for 49982.1

SEQ ID NO:379 is the determined cDNA sequence for 49986.1

5 SEQ ID NO:380 is the determined cDNA sequence for 49988.1

SEQ ID NO:381 is the determined cDNA sequence for 49993.1

SEQ ID NO:382 is the determined cDNA sequence for 49995.1

SEQ ID NO:383 is the determined cDNA sequence for 49996;contig 22

SEQ ID NO:384 is the determined cDNA sequence for 49999.1

10 SEQ ID NO:385 is the determined cDNA sequence for 50006;contig 23

SEQ ID NO:386 is the determined cDNA sequence for 50007.1

SEQ ID NO:387 is the determined cDNA sequence for 50009.3

SEQ ID NO:388 is the determined cDNA sequence for 50014.1

SEQ ID NO:389 is the determined cDNA sequence for 50016;contig 24

15 SEQ ID NO:390 is the determined cDNA sequence for 50017.1

SEQ ID NO:391 is the determined cDNA sequence for 50019.1

SEQ ID NO:392 is the determined cDNA sequence for 50022.1

SEQ ID NO:393 is the determined cDNA sequence for 50023.1

SEQ ID NO:394 is the determined cDNA sequence for 50024.1

20 SEQ ID NO:395 is the determined cDNA sequence for 50033.1

SEQ ID NO:396 is an extended cDNA sequence for SCC2-54 (SEQ ID

NO:178)

SEQ ID NO:397 is the amino acid sequence encoded by SEQ ID NO:396

SEQ ID NO:398 is the determined cDNA sequence for 56908.1

25 SEQ ID NO:399 is the determined cDNA sequence for 56911.1

SEQ ID NO:400 is the determined cDNA sequence for 56912.1

SEQ ID NO:401 is the determined cDNA sequence for 56913.1

SEQ ID NO:402 is the determined cDNA sequence for 56916.1

SEQ ID NO:403 is the determined cDNA sequence for 56917.1

30 SEQ ID NO:404 is the determined cDNA sequence for 56921.1

SEQ ID NO:405 is the determined cDNA sequence for 56922.1

SEQ ID NO:406 is the determined cDNA sequence for 56923.1

SEQ ID NO:407 is the determined cDNA sequence for 60974.1

SEQ ID NO:408 is the determined cDNA sequence for 60976.1

SEQ ID NO:409 is the determined cDNA sequence for 60977.1

SEQ ID NO:410 is the determined cDNA sequence for 60978.1

5 SEQ ID NO:411 is the determined cDNA sequence for 60980.1

SEQ ID NO:412 is an extended cDNA sequence for LSC-49 (SEQ ID  
NO:29)

SEQ ID NO:413 is the amino acid sequence encoded by SEQ ID NO:412

10 SEQ ID NO:414 is an extended cDNA sequence for LSC-39 (SEQ ID  
NO:26)

SEQ ID NO:415 is an extended cDNA sequence for LSC-46 (SEQ ID  
NO:28)

SEQ ID NO:416 is an extended cDNA sequence for LSC-49 (SEQ ID  
NO:29)

15 SEQ ID NO:417 is an extended cDNA sequence for LSC-51 (SEQ ID  
NO:30)

SEQ ID NO:418 is an extended cDNA sequence for LSC-55 (SEQ ID  
NO:32)

20 SEQ ID NO:419 is an extended cDNA sequence for LSC-64 (SEQ ID  
NO:35)

SEQ ID NO:420 is an extended cDNA sequence for LSC-78 (SEQ ID  
NO:42)

SEQ ID NO:421 is an extended cDNA sequence for LSC-103 (SEQ ID  
NO:47)

25 SEQ ID NO:422 is an extended cDNA sequence for LSC-144 (SEQ ID  
NO:53)

SEQ ID NO:423 is an extended cDNA sequence for LSC-148 (SEQ ID  
NO:54)

30 SEQ ID NO:424 is an extended cDNA sequence for LSC-210 (SEQ ID  
NO:74)

SEQ ID NO:425 is the amino acid sequence encoded by SEQ ID NO:414

SEQ ID NO:426 is the amino acid sequence encoded by SEQ ID NO:415

SEQ ID NO:427 is the amino acid sequence encoded by SEQ ID NO:416  
SEQ ID NO:428 is the amino acid sequence encoded by SEQ ID NO:417  
SEQ ID NO:429 is the amino acid sequence encoded by SEQ ID NO:418  
SEQ ID NO:430 is the amino acid sequence encoded by SEQ ID NO:419  
5 SEQ ID NO:431 is the amino acid sequence encoded by SEQ ID NO:420  
SEQ ID NO:432 is the amino acid sequence encoded by SEQ ID NO:421  
SEQ ID NO:433 is the amino acid sequence encoded by SEQ ID NO:422  
SEQ ID NO:434 is the amino acid sequence encoded by SEQ ID NO:423  
SEQ ID NO:435 is the amino acid sequence encoded by SEQ ID NO:424  
10 SEQ ID NO:436 is the amino acid sequence encoded by a second open  
reading frame (ORF-2) of clone SCC2-51, SEQ ID NO:175  
SEQ ID NO:437 is the determined cDNA sequence for SCC2-16.  
SEQ ID NO:438 is the determined cDNA sequence for SCC2-28.  
SEQ ID NO:439 is the determined cDNA sequence for SCC2-62.  
15 SEQ ID NO:440 is the determined cDNA sequence for SCC3-90.

## DETAILED DESCRIPTION OF THE INVENTION

The present invention is directed generally to compositions and their use  
20 in the therapy and diagnosis of cancer, particularly lung cancer. As described further  
below, illustrative compositions of the present invention include, but are not restricted  
to, polypeptides, particularly immunogenic polypeptides, polynucleotides encoding such  
polypeptides, antibodies and other binding agents, antigen presenting cells (APCs) and  
immune system cells (*e.g.*, T cells).

25 The practice of the present invention will employ, unless indicated  
specifically to the contrary, conventional methods of virology, immunology,  
microbiology, molecular biology and recombinant DNA techniques within the skill of  
the art, many of which are described below for the purpose of illustration. Such  
techniques are explained fully in the literature. See, *e.g.*, Sambrook, et al. Molecular  
30 Cloning: A Laboratory Manual (2nd Edition, 1989); Maniatis et al. Molecular Cloning:

A Laboratory Manual (1982); DNA Cloning: A Practical Approach, vol. I & II (D. Glover, ed.); Oligonucleotide Synthesis (N. Gait, ed., 1984); Nucleic Acid Hybridization (B. Hames & S. Higgins, eds., 1985); Transcription and Translation (B. Hames & S. Higgins, eds., 1984); Animal Cell Culture (R. Freshney, ed., 1986); Perbal,  
5 A Practical Guide to Molecular Cloning (1984).

All publications, patents and patent applications cited herein, whether supra or infra, are hereby incorporated by reference in their entirety.

As used in this specification and the appended claims, the singular forms "a," "an" and "the" include plural references unless the content clearly dictates  
10 otherwise.

#### Polypeptide Compositions

As used herein, the term "polypeptide" is used in its conventional meaning, *i.e.*, as a sequence of amino acids. The polypeptides are not limited to a specific length of the product; thus, peptides, oligopeptides, and proteins are included  
15 within the definition of polypeptide, and such terms may be used interchangeably herein unless specifically indicated otherwise. This term also does not refer to or exclude post-expression modifications of the polypeptide, for example, glycosylations, acetylations, phosphorylations and the like, as well as other modifications known in the art, both naturally occurring and non-naturally occurring. A polypeptide may be an entire  
20 protein, or a subsequence thereof. Particular polypeptides of interest in the context of this invention are amino acid subsequences comprising epitopes, *i.e.*, antigenic determinants substantially responsible for the immunogenic properties of a polypeptide and being capable of evoking an immune response.

Particularly illustrative polypeptides of the present invention comprise  
25 those encoded by a polynucleotide sequence set forth in any one of SEQ ID NOs: 1-232, 243-396, 398-412, 414-424 and 437-440, or a sequence that hybridizes under moderately stringent conditions, or, alternatively, under highly stringent conditions, to a polynucleotide sequence set forth in any one of SEQ ID NOs: 1-232, 243-396, 398-412, 414-424 and 437-440. Certain illustrative polypeptides of the invention comprise  
30 amino acid sequences as set forth in any one of SEQ ID NOs: 229-232, 237-242, 397, 413 and 425-436.

The polypeptides of the present invention are sometimes herein referred to as lung tumor proteins or lung tumor polypeptides, as an indication that their identification has been based at least in part upon their increased levels of expression in lung tumor samples. Thus, a "lung tumor polypeptide" or "lung tumor protein," refers generally to a polypeptide sequence of the present invention, or a polynucleotide sequence encoding such a polypeptide, that is expressed in a substantial proportion of lung tumor samples, for example preferably greater than about 20%, more preferably greater than about 30%, and most preferably greater than about 50% or more of lung tumor samples tested, at a level that is at least two fold, and preferably at least five fold, greater than the level of expression in normal tissues, as determined using a representative assay provided herein. A lung tumor polypeptide sequence of the invention, based upon its increased level of expression in tumor cells, has particular utility both as a diagnostic marker as well as a therapeutic target, as further described below.

In certain preferred embodiments, the polypeptides of the invention are immunogenic, *i.e.*, they react detectably within an immunoassay (such as an ELISA or T-cell stimulation assay) with antisera and/or T-cells from a patient with lung cancer. Screening for immunogenic activity can be performed using techniques well known to the skilled artisan. For example, such screens can be performed using methods such as those described in Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In one illustrative example, a polypeptide may be immobilized on a solid support and contacted with patient sera to allow binding of antibodies within the sera to the immobilized polypeptide. Unbound sera may then be removed and bound antibodies detected using, for example, <sup>125</sup>I-labeled Protein A.

As would be recognized by the skilled artisan, immunogenic portions of the polypeptides disclosed herein are also encompassed by the present invention. An "immunogenic portion," as used herein, is a fragment of an immunogenic polypeptide of the invention that itself is immunologically reactive (*i.e.*, specifically binds) with the B-cells and/or T-cell surface antigen receptors that recognize the polypeptide. Immunogenic portions may generally be identified using well known techniques, such as those summarized in Paul, *Fundamental Immunology*, 3rd ed., 243-247 (Raven Press, 1993) and references cited therein. Such techniques include screening polypeptides for

the ability to react with antigen-specific antibodies, antisera and/or T-cell lines or clones. As used herein, antisera and antibodies are "antigen-specific" if they specifically bind to an antigen (*i.e.*, they react with the protein in an ELISA or other immunoassay, and do not react detectably with unrelated proteins). Such antisera and  
5 antibodies may be prepared as described herein, and using well-known techniques.

In one preferred embodiment, an immunogenic portion of a polypeptide of the present invention is a portion that reacts with antisera and/or T-cells at a level that is not substantially less than the reactivity of the full-length polypeptide (*e.g.*, in an ELISA and/or T-cell reactivity assay). Preferably, the level of immunogenic activity of  
10 the immunogenic portion is at least about 50%, preferably at least about 70% and most preferably greater than about 90% of the immunogenicity for the full-length polypeptide. In some instances, preferred immunogenic portions will be identified that have a level of immunogenic activity greater than that of the corresponding full-length polypeptide, *e.g.*, having greater than about 100% or 150% or more immunogenic  
15 activity.

In certain other embodiments, illustrative immunogenic portions may include peptides in which an N-terminal leader sequence and/or transmembrane domain have been deleted. Other illustrative immunogenic portions will contain a small N- and/or C-terminal deletion (*e.g.*, 1-30 amino acids, preferably 5-15 amino acids),  
20 relative to the mature protein.

In another embodiment, a polypeptide composition of the invention may also comprise one or more polypeptides that are immunologically reactive with T cells and/or antibodies generated against a polypeptide of the invention, particularly a polypeptide having an amino acid sequence disclosed herein, or to an immunogenic  
25 fragment or variant thereof.

In another embodiment of the invention, polypeptides are provided that comprise one or more polypeptides that are capable of eliciting T cells and/or antibodies that are immunologically reactive with one or more polypeptides described herein, or one or more polypeptides encoded by contiguous nucleic acid sequences contained in  
30 the polynucleotide sequences disclosed herein, or immunogenic fragments or variants thereof, or to one or more nucleic acid sequences which hybridize to one or more of these sequences under conditions of moderate to high stringency.

The present invention, in another aspect, provides polypeptide fragments comprising at least about 5, 10, 15, 20, 25, 50, or 100 contiguous amino acids, or more, including all intermediate lengths, of a polypeptide compositions set forth herein, such as those set forth in SEQ ID NOs: 229-232, 237-242, 397, 413 and 425-436, or those  
5 encoded by a polynucleotide sequence set forth in a sequence of SEQ ID NOs: 1-232, 243-396, 398-412, 414-424 and 437-440.

In another aspect, the present invention provides variants of the polypeptide compositions described herein. Polypeptide variants generally encompassed by the present invention will typically exhibit at least about 70%, 75%,  
10 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% or more identity (determined as described below), along its length, to a polypeptide sequences set forth herein.

In one preferred embodiment, the polypeptide fragments and variants provide by the present invention are immunologically reactive with an antibody and/or  
15 T-cell that reacts with a full-length polypeptide specifically set forth herein.

In another preferred embodiment, the polypeptide fragments and variants provided by the present invention exhibit a level of immunogenic activity of at least about 50%, preferably at least about 70%, and most preferably at least about 90% or more of that exhibited by a full-length polypeptide sequence specifically set forth  
20 herein.

A polypeptide "variant," as the term is used herein, is a polypeptide that typically differs from a polypeptide specifically disclosed herein in one or more substitutions, deletions, additions and/or insertions. Such variants may be naturally occurring or may be synthetically generated, for example, by modifying one or more of  
25 the above polypeptide sequences of the invention and evaluating their immunogenic activity as described herein and/or using any of a number of techniques well known in the art.

For example, certain illustrative variants of the polypeptides of the invention include those in which one or more portions, such as an N-terminal leader  
30 sequence or transmembrane domain, have been removed. Other illustrative variants include variants in which a small portion (*e.g.*, 1-30 amino acids, preferably 5-15 amino acids) has been removed from the N- and/or C-terminal of the mature protein.

In many instances, a variant will contain conservative substitutions. A "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydrophobic nature of the polypeptide to be substantially unchanged. As described above, modifications may be made in the structure of the polynucleotides and polypeptides of the present invention and still obtain a functional molecule that encodes a variant or derivative polypeptide with desirable characteristics, *e.g.*, with immunogenic characteristics. When it is desired to alter the amino acid sequence of a polypeptide to create an equivalent, or even an improved, immunogenic variant or portion of a polypeptide of the invention, one skilled in the art will typically change one or more of the codons of the encoding DNA sequence according to Table 1.

For example, certain amino acids may be substituted for other amino acids in a protein structure without appreciable loss of interactive binding capacity with structures such as, for example, antigen-binding regions of antibodies or binding sites on substrate molecules. Since it is the interactive capacity and nature of a protein that defines that protein's biological functional activity, certain amino acid sequence substitutions can be made in a protein sequence, and, of course, its underlying DNA coding sequence, and nevertheless obtain a protein with like properties. It is thus contemplated that various changes may be made in the peptide sequences of the disclosed compositions, or corresponding DNA sequences which encode said peptides without appreciable loss of their biological utility or activity.



TABLE 1

Amino Acids			Codons						
Alanine	Ala	A	GCA	GCC	GCG	GCU			
Cysteine	Cys	C	UGC	UGU					
Aspartic acid	Asp	D	GAC	GAU					
Glutamic acid	Glu	E	GAA	GAG					
Phenylalanine	Phe	F	UUC	UUU					
Glycine	Gly	G	GGA	GGC	GGG	GGU			
Histidine	His	H	CAC	CAU					
Isoleucine	Ile	I	AUA	AUC	AUU				
Lysine	Lys	K	AAA	AAG					
Leucine	Leu	L	UUA	UUG	CUA	CUC	CUG	CUU	
Methionine	Met	M	AUG						
Asparagine	Asn	N	AAC	AAU					
Proline	Pro	P	CCA	CCC	CCG	CCU			
Glutamine	Gln	Q	CAA	CAG					
Arginine	Arg	R	AGA	AGG	CGA	CGC	CGG	CGU	
Serine	Ser	S	AGC	AGU	UCA	UCC	UCG	UCU	
Threonine	Thr	T	ACA	ACC	ACG	ACU			
Valine	Val	V	GUA	GUC	GUG	GUU			
Tryptophan	Trp	W	UGG						
Tyrosine	Tyr	Y	UAC	UAU					

In making such changes, the hydropathic index of amino acids may be considered. The importance of the hydropathic amino acid index in conferring interactive biologic function on a protein is generally understood in the art (Kyte and Doolittle, 1982, incorporated herein by reference). It is accepted that the relative hydropathic character of the amino acid contributes to the secondary structure of the resultant protein, which in turn defines the interaction of the protein with other molecules, for example, enzymes, substrates, receptors, DNA, antibodies, antigens, and the like. Each amino acid has been assigned a hydropathic index on the basis of its hydrophobicity and charge characteristics (Kyte and Doolittle, 1982). These values are:

isoleucine (+4.5); valine (+4.2); leucine (+3.8); phenylalanine (+2.8); cysteine/cystine (+2.5); methionine (+1.9); alanine (+1.8); glycine (−0.4); threonine (−0.7); serine (−0.8); tryptophan (−0.9); tyrosine (−1.3); proline (−1.6); histidine (−3.2); glutamate (−3.5); glutamine (−3.5); aspartate (−3.5); asparagine (−3.5); lysine (−3.9); and arginine (−4.5).

5           It is known in the art that certain amino acids may be substituted by other amino acids having a similar hydropathic index or score and still result in a protein with similar biological activity, *i.e.* still obtain a biological functionally equivalent protein. In making such changes, the substitution of amino acids whose hydropathic indices are within  $\pm 2$  is preferred, those within  $\pm 1$  are particularly preferred, and those within  $\pm 0.5$   
10 are even more particularly preferred. It is also understood in the art that the substitution of like amino acids can be made effectively on the basis of hydrophilicity. U. S. Patent 4,554,101 (specifically incorporated herein by reference in its entirety), states that the greatest local average hydrophilicity of a protein, as governed by the hydrophilicity of its adjacent amino acids, correlates with a biological property of the protein.

15           As detailed in U. S. Patent 4,554,101, the following hydrophilicity values have been assigned to amino acid residues: arginine (+3.0); lysine (+3.0); aspartate (+3.0  $\pm$  1); glutamate (+3.0  $\pm$  1); serine (+0.3); asparagine (+0.2); glutamine (+0.2); glycine (0); threonine (−0.4); proline (−0.5  $\pm$  1); alanine (−0.5); histidine (−0.5); cysteine (−1.0); methionine (−1.3); valine (−1.5); leucine (−1.8); isoleucine (−1.8); tyrosine (−  
20 2.3); phenylalanine (−2.5); tryptophan (−3.4). It is understood that an amino acid can be substituted for another having a similar hydrophilicity value and still obtain a biologically equivalent, and in particular, an immunologically equivalent protein. In such changes, the substitution of amino acids whose hydrophilicity values are within  $\pm 2$  is preferred, those within  $\pm 1$  are particularly preferred, and those within  $\pm 0.5$  are even  
25 more particularly preferred.

          As outlined above, amino acid substitutions are generally therefore based on the relative similarity of the amino acid side-chain substituents, for example, their hydrophobicity, hydrophilicity, charge, size, and the like. Exemplary substitutions that take various of the foregoing characteristics into consideration are well known to those  
30 of skill in the art and include: arginine and lysine; glutamate and aspartate; serine and threonine; glutamine and asparagine; and valine, leucine and isoleucine.

In addition, any polynucleotide may be further modified to increase stability *in vivo*. Possible modifications include, but are not limited to, the addition of flanking sequences at the 5' and/or 3' ends; the use of phosphorothioate or 2' O-methyl rather than phosphodiesterase linkages in the backbone; and/or the inclusion of  
5 nontraditional bases such as inosine, queosine and wybutosine, as well as acetyl-methyl-, thio- and other modified forms of adenine, cytidine, guanine, thymine and uridine.

Amino acid substitutions may further be made on the basis of similarity in polarity, charge, solubility, hydrophobicity, hydrophilicity and/or the amphipathic  
10 nature of the residues. For example, negatively charged amino acids include aspartic acid and glutamic acid; positively charged amino acids include lysine and arginine; and amino acids with uncharged polar head groups having similar hydrophilicity values include leucine, isoleucine and valine; glycine and alanine; asparagine and glutamine; and serine, threonine, phenylalanine and tyrosine. Other groups of amino acids that may  
15 represent conservative changes include: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his. A variant may also, or alternatively, contain nonconservative changes. In a preferred embodiment, variant polypeptides differ from a native sequence by substitution, deletion or addition of five amino acids or fewer. Variants may also (or  
20 alternatively) be modified by, for example, the deletion or addition of amino acids that have minimal influence on the immunogenicity, secondary structure and hydrophobic nature of the polypeptide.

As noted above, polypeptides may comprise a signal (or leader) sequence at the N-terminal end of the protein, which co-translationally or post-translationally  
25 directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (e.g., poly-His), or to enhance binding of the polypeptide to a solid support. For example, a polypeptide may be conjugated to an immunoglobulin Fc region.

When comparing polypeptide sequences, two sequences are said to be  
30 "identical" if the sequence of amino acids in the two sequences is the same when aligned for maximum correspondence, as described below. Comparisons between two sequences are typically performed by comparing the sequences over a comparison

window to identify and compare local regions of sequence similarity. A "comparison window" as used herein, refers to a segment of at least about 20 contiguous positions, usually 30 to about 75, 40 to about 50, in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned.

Optimal alignment of sequences for comparison may be conducted using the Megalign program in the Lasergene suite of bioinformatics software (DNASTAR, Inc., Madison, WI), using default parameters. This program embodies several alignment schemes described in the following references: Dayhoff, M.O. (1978) A model of evolutionary change in proteins – Matrices for detecting distant relationships. In Dayhoff, M.O. (ed.) *Atlas of Protein Sequence and Structure*, National Biomedical Research Foundation, Washington DC Vol. 5, Suppl. 3, pp. 345-358; Hein J. (1990) Unified Approach to Alignment and Phylogenies pp. 626-645 *Methods in Enzymology* vol. 183, Academic Press, Inc., San Diego, CA; Higgins, D.G. and Sharp, P.M. (1989) *CABIOS* 5:151-153; Myers, E.W. and Muller W. (1988) *CABIOS* 4:11-17; Robinson, E.D. (1971) *Comb. Theor* 11:105; Santou, N. Nes, M. (1987) *Mol. Biol. Evol.* 4:406-425; Sneath, P.H.A. and Sokal, R.R. (1973) *Numerical Taxonomy – the Principles and Practice of Numerical Taxonomy*, Freeman Press, San Francisco, CA; Wilbur, W.J. and Lipman, D.J. (1983) *Proc. Natl. Acad. Sci. USA* 80:726-730.

Alternatively, optimal alignment of sequences for comparison may be conducted by the local identity algorithm of Smith and Waterman (1981) *Add. APL Math* 2:482, by the identity alignment algorithm of Needleman and Wunsch (1970) *J. Mol. Biol.* 48:443, by the search for similarity methods of Pearson and Lipman (1988) *Proc. Natl. Acad. Sci. USA* 85: 2444, by computerized implementations of these algorithms (GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group (GCG), 575 Science Dr., Madison, WI), or by inspection.

One preferred example of algorithms that are suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul et al. (1977) *Nucl. Acids Res.* 25:3389-3402 and Altschul et al. (1990) *J. Mol. Biol.* 215:403-410, respectively. BLAST and BLAST 2.0 can be used, for example with the parameters described herein, to determine percent

sequence identity for the polynucleotides and polypeptides of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information. For amino acid sequences, a scoring matrix can be used to calculate the cumulative score. Extension of the word hits in each direction are halted  
5 when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T and X determine the sensitivity and speed of the alignment.

10 In one preferred approach, the "percentage of sequence identity" is determined by comparing two optimally aligned sequences over a window of comparison of at least 20 positions, wherein the portion of the polypeptide sequence in the comparison window may comprise additions or deletions (*i.e.*, gaps) of 20 percent or less, usually 5 to 15 percent, or 10 to 12 percent, as compared to the reference  
15 sequences (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical amino acid residue occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the reference sequence (*i.e.*, the window size) and multiplying the results by  
20 100 to yield the percentage of sequence identity.

Within other illustrative embodiments, a polypeptide may be a fusion polypeptide that comprises multiple polypeptides as described herein, or that comprises at least one polypeptide as described herein and an unrelated sequence, such as a known tumor protein. A fusion partner may, for example, assist in providing T helper epitopes  
25 (an immunological fusion partner), preferably T helper epitopes recognized by humans, or may assist in expressing the protein (an expression enhancer) at higher yields than the native recombinant protein. Certain preferred fusion partners are both immunological and expression enhancing fusion partners. Other fusion partners may be selected so as to increase the solubility of the polypeptide or to enable the polypeptide to be targeted to  
30 desired intracellular compartments. Still further fusion partners include affinity tags, which facilitate purification of the polypeptide.

Fusion polypeptides may generally be prepared using standard techniques, including chemical conjugation. Preferably, a fusion polypeptide is expressed as a recombinant polypeptide, allowing the production of increased levels, relative to a non-fused polypeptide, in an expression system. Briefly, DNA sequences encoding the polypeptide components may be assembled separately, and ligated into an appropriate expression vector. The 3' end of the DNA sequence encoding one polypeptide component is ligated, with or without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide component so that the reading frames of the sequences are in phase. This permits translation into a single fusion polypeptide that retains the biological activity of both component polypeptides.

A peptide linker sequence may be employed to separate the first and second polypeptide components by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into the fusion polypeptide using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as linkers include those disclosed in Maratea et al., *Gene* 40:39-46, 1985; Murphy et al., *Proc. Natl. Acad. Sci. USA* 83:8258-8262, 1986; U.S. Patent No. 4,935,233 and U.S. Patent No. 4,751,180. The linker sequence may generally be from 1 to about 50 amino acids in length. Linker sequences are not required when the first and second polypeptides have non-essential N-terminal amino acid regions that can be used to separate the functional domains and prevent steric interference.

The ligated DNA sequences are operably linked to suitable transcriptional or translational regulatory elements. The regulatory elements responsible for expression of DNA are located only 5' to the DNA sequence encoding the first polypeptides. Similarly, stop codons required to end translation and

transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

The fusion polypeptide can comprise a polypeptide as described herein together with an unrelated immunogenic protein, such as an immunogenic protein  
5 capable of eliciting a recall response. Examples of such proteins include tetanus, tuberculosis and hepatitis proteins (*see, for example, Stoute et al. New Engl. J. Med., 336:86-91, 1997*).

In one preferred embodiment, the immunological fusion partner is derived from a *Mycobacterium* sp., such as a *Mycobacterium tuberculosis*-derived Ra12  
10 fragment. Ra12 compositions and methods for their use in enhancing the expression and/or immunogenicity of heterologous polynucleotide/polypeptide sequences is described in U.S. Patent Application 60/158,585, the disclosure of which is incorporated herein by reference in its entirety. Briefly, Ra12 refers to a polynucleotide region that is a subsequence of a *Mycobacterium tuberculosis* MTB32A nucleic acid.  
15 MTB32A is a serine protease of 32 KD molecular weight encoded by a gene in virulent and avirulent strains of *M. tuberculosis*. The nucleotide sequence and amino acid sequence of MTB32A have been described (for example, U.S. Patent Application 60/158,585; *see also, Skeiky et al., Infection and Immunity* (1999) 67:3998-4007, incorporated herein by reference). C-terminal fragments of the MTB32A coding  
20 sequence express at high levels and remain as a soluble polypeptides throughout the purification process. Moreover, Ra12 may enhance the immunogenicity of heterologous immunogenic polypeptides with which it is fused. One preferred Ra12 fusion polypeptide comprises a 14 KD C-terminal fragment corresponding to amino acid residues 192 to 323 of MTB32A. Other preferred Ra12 polynucleotides generally  
25 comprise at least about 15 consecutive nucleotides, at least about 30 nucleotides, at least about 60 nucleotides, at least about 100 nucleotides, at least about 200 nucleotides, or at least about 300 nucleotides that encode a portion of a Ra12 polypeptide. Ra12 polynucleotides may comprise a native sequence (*i.e.*, an endogenous sequence that encodes a Ra12 polypeptide or a portion thereof) or may comprise a variant of such a  
30 sequence. Ra12 polynucleotide variants may contain one or more substitutions, additions, deletions and/or insertions such that the biological activity of the encoded fusion polypeptide is not substantially diminished, relative to a fusion polypeptide

comprising a native Ra12 polypeptide. Variants preferably exhibit at least about 70% identity, more preferably at least about 80% identity and most preferably at least about 90% identity to a polynucleotide sequence that encodes a native Ra12 polypeptide or a portion thereof.

5           Within other preferred embodiments, an immunological fusion partner is derived from protein D, a surface protein of the gram-negative bacterium *Haemophilus influenza B* (WO 91/18926). Preferably, a protein D derivative comprises approximately the first third of the protein (*e.g.*, the first N-terminal 100-110 amino acids), and a protein D derivative may be lipidated. Within certain preferred  
10   embodiments, the first 109 residues of a Lipoprotein D fusion partner is included on the N-terminus to provide the polypeptide with additional exogenous T-cell epitopes and to increase the expression level in *E. coli* (thus functioning as an expression enhancer). The lipid tail ensures optimal presentation of the antigen to antigen presenting cells. Other fusion partners include the non-structural protein from influenzae virus, NS1  
15   (hemagglutinin). Typically, the N-terminal 81 amino acids are used, although different fragments that include T-helper epitopes may be used.

          In another embodiment, the immunological fusion partner is the protein known as LYTA, or a portion thereof (preferably a C-terminal portion). LYTA is derived from *Streptococcus pneumoniae*, which synthesizes an N-acetyl-L-alanine  
20   amidase known as amidase LYTA (encoded by the *LytA* gene; *Gene* 43:265-292, 1986). LYTA is an autolysin that specifically degrades certain bonds in the peptidoglycan backbone. The C-terminal domain of the LYTA protein is responsible for the affinity to the choline or to some choline analogues such as DEAE. This property has been exploited for the development of *E. coli* C-LYTA expressing plasmids useful for  
25   expression of fusion proteins. Purification of hybrid proteins containing the C-LYTA fragment at the amino terminus has been described (*see Biotechnology* 10:795-798, 1992). Within a preferred embodiment, a repeat portion of LYTA may be incorporated into a fusion polypeptide. A repeat portion is found in the C-terminal region starting at residue 178. A particularly preferred repeat portion incorporates residues 188-305.

30           Yet another illustrative embodiment involves fusion polypeptides, and the polynucleotides encoding them, wherein the fusion partner comprises a targeting signal capable of directing a polypeptide to the endosomal/lysosomal compartment, as



described in U.S. Patent No. 5,633,234. An immunogenic polypeptide of the invention, when fused with this targeting signal, will associate more efficiently with MHC class II molecules and thereby provide enhanced in vivo stimulation of CD4<sup>+</sup> T-cells specific for the polypeptide.

5 Polypeptides of the invention are prepared using any of a variety of well known synthetic and/or recombinant techniques, the latter of which are further described below. Polypeptides, portions and other variants generally less than about 150 amino acids can be generated by synthetic means, using techniques well known to those of ordinary skill in the art. In one illustrative example, such polypeptides are  
10 synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain. See Merrifield, *J. Am. Chem. Soc.* 85:2149-2146, 1963. Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied BioSystems Division (Foster City, CA), and  
15 may be operated according to the manufacturer's instructions.

In general, polypeptide compositions (including fusion polypeptides) of the invention are isolated. An "isolated" polypeptide is one that is removed from its original environment. For example, a naturally-occurring protein or polypeptide is isolated if it is separated from some or all of the coexisting materials in the natural  
20 system. Preferably, such polypeptides are also purified, *e.g.*, are at least about 90% pure, more preferably at least about 95% pure and most preferably at least about 99% pure.

#### Polynucleotide Compositions

The present invention, in other aspects, provides polynucleotide  
25 compositions. The terms "DNA" and "polynucleotide" are used essentially interchangeably herein to refer to a DNA molecule that has been isolated free of total genomic DNA of a particular species. "Isolated," as used herein, means that a polynucleotide is substantially away from other coding sequences, and that the DNA molecule does not contain large portions of unrelated coding DNA, such as large  
30 chromosomal fragments or other functional genes or polypeptide coding regions. Of

course, this refers to the DNA molecule as originally isolated, and does not exclude genes or coding regions later added to the segment by the hand of man.

As will be understood by those skilled in the art, the polynucleotide compositions of this invention can include genomic sequences, extra-genomic and plasmid-encoded sequences and smaller engineered gene segments that express, or may  
5 be adapted to express, proteins, polypeptides, peptides and the like. Such segments may be naturally isolated, or modified synthetically by the hand of man.

As will be also recognized by the skilled artisan, polynucleotides of the invention may be single-stranded (coding or antisense) or double-stranded, and may be  
10 DNA (genomic, cDNA or synthetic) or RNA molecules. RNA molecules may include HnRNA molecules, which contain introns and correspond to a DNA molecule in a one-to-one manner, and mRNA molecules, which do not contain introns. Additional coding or non-coding sequences may, but need not, be present within a polynucleotide of the present invention, and a polynucleotide may, but need not, be linked to other molecules  
15 and/or support materials.

Polynucleotides may comprise a native sequence (*i.e.*, an endogenous sequence that encodes a polypeptide/protein of the invention or a portion thereof) or may comprise a sequence that encodes a variant or derivative, preferably and immunogenic variant or derivative, of such a sequence.

20 Therefore, according to another aspect of the present invention, polynucleotide compositions are provided that comprise some or all of a polynucleotide sequence set forth in any one of SEQ ID NOs: 1-232, 243-396, 398-412, 414-424 and 437-440, complements of a polynucleotide sequence set forth in any one of SEQ ID NOs: 1-232, 243-396, 398-412, 414-424 and 437-440, and degenerate variants of a  
25 polynucleotide sequence set forth in any one of SEQ ID NOs: 1-232, 243-396, 398-412, 414-424 and 437-440. In certain preferred embodiments, the polynucleotide sequences set forth herein encode immunogenic polypeptides, as described above.

In other related embodiments, the present invention provides polynucleotide variants having substantial identity to the sequences disclosed herein in  
30 SEQ ID NOs: 1-232, 243-396, 398-412, 414-424 and 437-440, for example those comprising at least 70% sequence identity, preferably at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% or higher, sequence identity compared to a

polynucleotide sequence of this invention using the methods described herein, (e.g., BLAST analysis using standard parameters, as described below). One skilled in this art will recognize that these values can be appropriately adjusted to determine corresponding identity of proteins encoded by two nucleotide sequences by taking into  
5 account codon degeneracy, amino acid similarity, reading frame positioning and the like.

Typically, polynucleotide variants will contain one or more substitutions, additions, deletions and/or insertions, preferably such that the immunogenicity of the polypeptide encoded by the variant polynucleotide is not substantially diminished  
10 relative to a polypeptide encoded by a polynucleotide sequence specifically set forth herein). The term "variants" should also be understood to encompass homologous genes of xenogenic origin.

In additional embodiments, the present invention provides polynucleotide fragments comprising various lengths of contiguous stretches of  
15 sequence identical to or complementary to one or more of the sequences disclosed herein. For example, polynucleotides are provided by this invention that comprise at least about 10, 15, 20, 30, 40, 50, 75, 100, 150, 200, 300, 400, 500 or 1000 or more contiguous nucleotides of one or more of the sequences disclosed herein as well as all intermediate lengths there between. It will be readily understood that "intermediate  
20 lengths", in this context, means any length between the quoted values, such as 16, 17, 18, 19, *etc.*; 21, 22, 23, *etc.*; 30, 31, 32, *etc.*; 50, 51, 52, 53, *etc.*; 100, 101, 102, 103, *etc.*; 150, 151, 152, 153, *etc.*; including all integers through 200-500; 500-1,000, and the like.

In another embodiment of the invention, polynucleotide compositions are  
25 provided that are capable of hybridizing under moderate to high stringency conditions to a polynucleotide sequence provided herein, or a fragment thereof, or a complementary sequence thereof. Hybridization techniques are well known in the art of molecular biology. For purposes of illustration, suitable moderately stringent conditions for testing the hybridization of a polynucleotide of this invention with other polynucleotides  
30 include prewashing in a solution of 5 X SSC, 0.5% SDS, 1.0 mM EDTA (pH 8.0); hybridizing at 50°C-60°C, 5 X SSC, overnight; followed by washing twice at 65°C for 20 minutes with each of 2X, 0.5X and 0.2X SSC containing 0.1% SDS. One skilled in

the art will understand that the stringency of hybridization can be readily manipulated, such as by altering the salt content of the hybridization solution and/or the temperature at which the hybridization is performed. For example, in another embodiment, suitable highly stringent hybridization conditions include those described above, with the  
5 exception that the temperature of hybridization is increased, *e.g.*, to 60-65°C or 65-70°C.

In certain preferred embodiments, the polynucleotides described above, *e.g.*, polynucleotide variants, fragments and hybridizing sequences, encode polypeptides that are immunologically cross-reactive with a polypeptide sequence specifically set  
10 forth herein. In other preferred embodiments, such polynucleotides encode polypeptides that have a level of immunogenic activity of at least about 50%, preferably at least about 70%, and more preferably at least about 90% of that for a polypeptide sequence specifically set forth herein.

The polynucleotides of the present invention, or fragments thereof,  
15 regardless of the length of the coding sequence itself, may be combined with other DNA sequences, such as promoters, polyadenylation signals, additional restriction enzyme sites, multiple cloning sites, other coding segments, and the like, such that their overall length may vary considerably. It is therefore contemplated that a nucleic acid fragment of almost any length may be employed, with the total length preferably being limited by  
20 the ease of preparation and use in the intended recombinant DNA protocol. For example, illustrative polynucleotide segments with total lengths of about 10,000, about 5000, about 3000, about 2,000, about 1,000, about 500, about 200, about 100, about 50 base pairs in length, and the like, (including all intermediate lengths) are contemplated to be useful in many implementations of this invention.

25 When comparing polynucleotide sequences, two sequences are said to be "identical" if the sequence of nucleotides in the two sequences is the same when aligned for maximum correspondence, as described below. Comparisons between two sequences are typically performed by comparing the sequences over a comparison window to identify and compare local regions of sequence similarity. A "comparison  
30 window" as used herein, refers to a segment of at least about 20 contiguous positions, usually 30 to about 75, 40 to about 50, in which a sequence may be compared to a

reference sequence of the same number of contiguous positions after the two sequences are optimally aligned.

- Optimal alignment of sequences for comparison may be conducted using the Megalign program in the Lasergene suite of bioinformatics software (DNASTAR, Inc., Madison, WI), using default parameters. This program embodies several alignment schemes described in the following references: Dayhoff, M.O. (1978) A model of evolutionary change in proteins – Matrices for detecting distant relationships. In Dayhoff, M.O. (ed.) *Atlas of Protein Sequence and Structure*, National Biomedical Research Foundation, Washington DC Vol. 5, Suppl. 3, pp. 345-358; Hein J. (1990) Unified Approach to Alignment and Phylogenies pp. 626-645 *Methods in Enzymology* vol. 183, Academic Press, Inc., San Diego, CA; Higgins, D.G. and Sharp, P.M. (1989) *CABIOS* 5:151-153; Myers, E.W. and Muller W. (1988) *CABIOS* 4:11-17; Robinson, E.D. (1971) *Comb. Theor* 11:105; Santou, N. Nes, M. (1987) *Mol. Biol. Evol.* 4:406-425; Sneath, P.H.A. and Sokal, R.R. (1973) *Numerical Taxonomy – the Principles and Practice of Numerical Taxonomy*, Freeman Press, San Francisco, CA; Wilbur, W.J. and Lipman, D.J. (1983) *Proc. Natl. Acad. Sci. USA* 80:726-730.

- Alternatively, optimal alignment of sequences for comparison may be conducted by the local identity algorithm of Smith and Waterman (1981) *Add. APL. Math* 2:482, by the identity alignment algorithm of Needleman and Wunsch (1970) *J. Mol. Biol.* 48:443, by the search for similarity methods of Pearson and Lipman (1988) *Proc. Natl. Acad. Sci. USA* 85: 2444, by computerized implementations of these algorithms (GAP, BESTFIT, BLAST, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group (GCG), 575 Science Dr., Madison, WI), or by inspection.

- One preferred example of algorithms that are suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul et al. (1977) *Nucl. Acids Res.* 25:3389-3402 and Altschul et al. (1990) *J. Mol. Biol.* 215:403-410, respectively. BLAST and BLAST 2.0 can be used, for example with the parameters described herein, to determine percent sequence identity for the polynucleotides of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information. In one illustrative example, cumulative scores can be calculated using, for

nucleotide sequences, the parameters M (reward score for a pair of matching residues; always >0) and N (penalty score for mismatching residues; always <0). Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff and Henikoff (1989) *Proc. Natl. Acad. Sci. USA* 89:10915) alignments, (B) of 50, expectation (E) of 10, M=5, N=-4 and a comparison of both strands.

Preferably, the "percentage of sequence identity" is determined by comparing two optimally aligned sequences over a window of comparison of at least 20 positions, wherein the portion of the polynucleotide sequence in the comparison window may comprise additions or deletions (*i.e.*, gaps) of 20 percent or less, usually 5 to 15 percent, or 10 to 12 percent, as compared to the reference sequences (which does not comprise additions or deletions) for optimal alignment of the two sequences. The percentage is calculated by determining the number of positions at which the identical nucleic acid bases occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the reference sequence (*i.e.*, the window size) and multiplying the results by 100 to yield the percentage of sequence identity.

It will be appreciated by those of ordinary skill in the art that, as a result of the degeneracy of the genetic code, there are many nucleotide sequences that encode a polypeptide as described herein. Some of these polynucleotides bear minimal homology to the nucleotide sequence of any native gene. Nonetheless, polynucleotides that vary due to differences in codon usage are specifically contemplated by the present invention. Further, alleles of the genes comprising the polynucleotide sequences provided herein are within the scope of the present invention. Alleles are endogenous genes that are altered as a result of one or more mutations, such as deletions, additions and/or substitutions of nucleotides. The resulting mRNA and protein may, but need not,

have an altered structure or function. Alleles may be identified using standard techniques (such as hybridization, amplification and/or database sequence comparison).

Therefore, in another embodiment of the invention, a mutagenesis approach, such as site-specific mutagenesis, is employed for the preparation of immunogenic variants and/or derivatives of the polypeptides described herein. By this approach, specific modifications in a polypeptide sequence can be made through mutagenesis of the underlying polynucleotides that encode them. These techniques provides a straightforward approach to prepare and test sequence variants, for example, incorporating one or more of the foregoing considerations, by introducing one or more nucleotide sequence changes into the polynucleotide.

Site-specific mutagenesis allows the production of mutants through the use of specific oligonucleotide sequences which encode the DNA sequence of the desired mutation, as well as a sufficient number of adjacent nucleotides, to provide a primer sequence of sufficient size and sequence complexity to form a stable duplex on both sides of the deletion junction being traversed. Mutations may be employed in a selected polynucleotide sequence to improve, alter, decrease, modify, or otherwise change the properties of the polynucleotide itself, and/or alter the properties, activity, composition, stability, or primary sequence of the encoded polypeptide.

In certain embodiments of the present invention, the inventors contemplate the mutagenesis of the disclosed polynucleotide sequences to alter one or more properties of the encoded polypeptide, such as the immunogenicity of a polypeptide vaccine. The techniques of site-specific mutagenesis are well-known in the art, and are widely used to create variants of both polypeptides and polynucleotides. For example, site-specific mutagenesis is often used to alter a specific portion of a DNA molecule. In such embodiments, a primer comprising typically about 14 to about 25 nucleotides or so in length is employed, with about 5 to about 10 residues on both sides of the junction of the sequence being altered.

As will be appreciated by those of skill in the art, site-specific mutagenesis techniques have often employed a phage vector that exists in both a single stranded and double stranded form. Typical vectors useful in site-directed mutagenesis include vectors such as the M13 phage. These phage are readily commercially-available and their use is generally well-known to those skilled in the art. Double-stranded

plasmids are also routinely employed in site directed mutagenesis that eliminates the step of transferring the gene of interest from a plasmid to a phage.

In general, site-directed mutagenesis in accordance herewith is performed by first obtaining a single-stranded vector or melting apart of two strands of a double-stranded vector that includes within its sequence a DNA sequence that encodes the desired peptide. An oligonucleotide primer bearing the desired mutated sequence is prepared, generally synthetically. This primer is then annealed with the single-stranded vector, and subjected to DNA polymerizing enzymes such as *E. coli* polymerase I Klenow fragment, in order to complete the synthesis of the mutation-bearing strand. Thus, a heteroduplex is formed wherein one strand encodes the original non-mutated sequence and the second strand bears the desired mutation. This heteroduplex vector is then used to transform appropriate cells, such as *E. coli* cells, and clones are selected which include recombinant vectors bearing the mutated sequence arrangement.

The preparation of sequence variants of the selected peptide-encoding DNA segments using site-directed mutagenesis provides a means of producing potentially useful species and is not meant to be limiting as there are other ways in which sequence variants of peptides and the DNA sequences encoding them may be obtained. For example, recombinant vectors encoding the desired peptide sequence may be treated with mutagenic agents, such as hydroxylamine, to obtain sequence variants. Specific details regarding these methods and protocols are found in the teachings of Maloy *et al.*, 1994; Segal, 1976; Prokop and Bajpai, 1991; Kuby, 1994; and Maniatis *et al.*, 1982, each incorporated herein by reference, for that purpose.

As used herein, the term "oligonucleotide directed mutagenesis procedure" refers to template-dependent processes and vector-mediated propagation which result in an increase in the concentration of a specific nucleic acid molecule relative to its initial concentration, or in an increase in the concentration of a detectable signal, such as amplification. As used herein, the term "oligonucleotide directed mutagenesis procedure" is intended to refer to a process that involves the template-dependent extension of a primer molecule. The term template dependent process refers to nucleic acid synthesis of an RNA or a DNA molecule wherein the sequence of the newly synthesized strand of nucleic acid is dictated by the well-known rules of complementary base pairing (see, for example, Watson, 1987). Typically,



vector mediated methodologies involve the introduction of the nucleic acid fragment into a DNA or RNA vector, the clonal amplification of the vector, and the recovery of the amplified nucleic acid fragment. Examples of such methodologies are provided by U. S. Patent No. 4,237,224, specifically incorporated herein by reference in its entirety.

5 In another approach for the production of polypeptide variants of the present invention, recursive sequence recombination, as described in U.S. Patent No. 5,837,458, may be employed. In this approach, iterative cycles of recombination and screening or selection are performed to "evolve" individual polynucleotide variants of the invention having, for example, enhanced immunogenic activity.

10 In other embodiments of the present invention, the polynucleotide sequences provided herein can be advantageously used as probes or primers for nucleic acid hybridization. As such, it is contemplated that nucleic acid segments that comprise a sequence region of at least about 15 nucleotide long contiguous sequence that has the same sequence as, or is complementary to, a 15 nucleotide long contiguous sequence  
15 disclosed herein will find particular utility. Longer contiguous identical or complementary sequences, *e.g.*, those of about 20, 30, 40, 50, 100, 200, 500, 1000 (including all intermediate lengths) and even up to full length sequences will also be of use in certain embodiments.

20 The ability of such nucleic acid probes to specifically hybridize to a sequence of interest will enable them to be of use in detecting the presence of complementary sequences in a given sample. However, other uses are also envisioned, such as the use of the sequence information for the preparation of mutant species primers, or primers for use in preparing other genetic constructions.

25 Polynucleotide molecules having sequence regions consisting of contiguous nucleotide stretches of 10-14, 15-20, 30, 50, or even of 100-200 nucleotides or so (including intermediate lengths as well), identical or complementary to a polynucleotide sequence disclosed herein, are particularly contemplated as hybridization probes for use in, *e.g.*, Southern and Northern blotting. This would allow a gene product, or fragment thereof, to be analyzed, both in diverse cell types and also in  
30 various bacterial cells. The total size of fragment, as well as the size of the complementary stretch(es), will ultimately depend on the intended use or application of the particular nucleic acid segment. Smaller fragments will generally find use in

hybridization embodiments, wherein the length of the contiguous complementary region may be varied, such as between about 15 and about 100 nucleotides, but larger contiguous complementarity stretches may be used, according to the length complementary sequences one wishes to detect.

5           The use of a hybridization probe of about 15-25 nucleotides in length allows the formation of a duplex molecule that is both stable and selective. Molecules having contiguous complementary sequences over stretches greater than 15 bases in length are generally preferred, though, in order to increase stability and selectivity of the hybrid, and thereby improve the quality and degree of specific hybrid molecules  
10       obtained. One will generally prefer to design nucleic acid molecules having gene-complementary stretches of 15 to 25 contiguous nucleotides, or even longer where desired.

          Hybridization probes may be selected from any portion of any of the sequences disclosed herein. All that is required is to review the sequences set forth  
15       herein, or to any continuous portion of the sequences, from about 15-25 nucleotides in length up to and including the full length sequence, that one wishes to utilize as a probe or primer. The choice of probe and primer sequences may be governed by various factors. For example, one may wish to employ primers from towards the termini of the total sequence.

20           Small polynucleotide segments or fragments may be readily prepared by, for example, directly synthesizing the fragment by chemical means, as is commonly practiced using an automated oligonucleotide synthesizer. Also, fragments may be obtained by application of nucleic acid reproduction technology, such as the PCR™  
25       technology of U. S. Patent 4,683,202 (incorporated herein by reference), by introducing selected sequences into recombinant vectors for recombinant production, and by other recombinant DNA techniques generally known to those of skill in the art of molecular biology.

          The nucleotide sequences of the invention may be used for their ability to selectively form duplex molecules with complementary stretches of the entire gene or  
30       gene fragments of interest. Depending on the application envisioned, one will typically desire to employ varying conditions of hybridization to achieve varying degrees of selectivity of probe towards target sequence. For applications requiring high selectivity,

one will typically desire to employ relatively stringent conditions to form the hybrids, *e.g.*, one will select relatively low salt and/or high temperature conditions, such as provided by a salt concentration of from about 0.02 M to about 0.15 M salt at temperatures of from about 50°C to about 70°C. Such selective conditions tolerate  
5 little, if any, mismatch between the probe and the template or target strand, and would be particularly suitable for isolating related sequences.

Of course, for some applications, for example, where one desires to prepare mutants employing a mutant primer strand hybridized to an underlying template, less stringent (reduced stringency) hybridization conditions will typically be  
10 needed in order to allow formation of the heteroduplex. In these circumstances, one may desire to employ salt conditions such as those of from about 0.15 M to about 0.9 M salt, at temperatures ranging from about 20°C to about 55°C. Cross-hybridizing species can thereby be readily identified as positively hybridizing signals with respect to control hybridizations. In any case, it is generally appreciated that conditions can be rendered  
15 more stringent by the addition of increasing amounts of formamide, which serves to destabilize the hybrid duplex in the same manner as increased temperature. Thus, hybridization conditions can be readily manipulated, and thus will generally be a method of choice depending on the desired results.

According to another embodiment of the present invention,  
20 polynucleotide compositions comprising antisense oligonucleotides are provided. Antisense oligonucleotides have been demonstrated to be effective and targeted inhibitors of protein synthesis, and, consequently, provide a therapeutic approach by which a disease can be treated by inhibiting the synthesis of proteins that contribute to the disease. The efficacy of antisense oligonucleotides for inhibiting protein synthesis  
25 is well established. For example, the synthesis of polygalacturonase and the muscarine type 2 acetylcholine receptor are inhibited by antisense oligonucleotides directed to their respective mRNA sequences (U. S. Patent 5,739,119 and U. S. Patent 5,759,829). Further, examples of antisense inhibition have been demonstrated with the nuclear protein cyclin, the multiple drug resistance gene (MDG1), ICAM-1, E-selectin, STK-1,  
30 striatal GABA<sub>A</sub> receptor and human EGF (Jaskulski *et al.*, Science. 1988 Jun 10;240(4858):1544-6; Vasanthakumar and Ahmed, Cancer Commun. 1989;1(4):225-32; Peris *et al.*, Brain Res Mol Brain Res. 1998 Jun 15;57(2):310-20; U. S. Patent

5,801,154; U.S. Patent 5,789,573; U. S. Patent 5,718,709 and U.S. Patent 5,610,288). Antisense constructs have also been described that inhibit and can be used to treat a variety of abnormal cellular proliferations, *e.g.* cancer (U. S. Patent 5,747,470; U. S. Patent 5,591,317 and U. S. Patent 5,783,683).

5 Therefore, in certain embodiments, the present invention provides oligonucleotide sequences that comprise all, or a portion of, any sequence that is capable of specifically binding to polynucleotide sequence described herein, or a complement thereof. In one embodiment, the antisense oligonucleotides comprise DNA or derivatives thereof. In another embodiment, the oligonucleotides comprise RNA or  
10 derivatives thereof. In a third embodiment, the oligonucleotides are modified DNAs comprising a phosphorothioated modified backbone. In a fourth embodiment, the oligonucleotide sequences comprise peptide nucleic acids or derivatives thereof. In each case, preferred compositions comprise a sequence region that is complementary, and more preferably substantially-complementary, and even more preferably,  
15 completely complementary to one or more portions of polynucleotides disclosed herein. Selection of antisense compositions specific for a given gene sequence is based upon analysis of the chosen target sequence and determination of secondary structure,  $T_m$ , binding energy, and relative stability. Antisense compositions may be selected based upon their relative inability to form dimers, hairpins, or other secondary structures that  
20 would reduce or prohibit specific binding to the target mRNA in a host cell. Highly preferred target regions of the mRNA, are those which are at or near the AUG translation initiation codon, and those sequences which are substantially complementary to 5' regions of the mRNA. These secondary structure analyses and target site selection considerations can be performed, for example, using v.4 of the OLIGO primer analysis  
25 software and/or the BLASTN 2.0.5 algorithm software (Altschul *et al.*, Nucleic Acids Res. 1997, 25(17):3389-402).

The use of an antisense delivery method employing a short peptide vector, termed MPG (27 residues), is also contemplated. The MPG peptide contains a hydrophobic domain derived from the fusion sequence of HIV gp41 and a hydrophilic  
30 domain from the nuclear localization sequence of SV40 T-antigen (Morris *et al.*, Nucleic Acids Res. 1997 Jul 15;25(14):2730-6). It has been demonstrated that several molecules of the MPG peptide coat the antisense oligonucleotides and can be delivered

into cultured mammalian cells in less than 1 hour with relatively high efficiency (90%). Further, the interaction with MPG strongly increases both the stability of the oligonucleotide to nuclease and the ability to cross the plasma membrane.

According to another embodiment of the invention, the polynucleotide compositions described herein are used in the design and preparation of ribozyme molecules for inhibiting expression of the tumor polypeptides and proteins of the present invention in tumor cells. Ribozymes are RNA-protein complexes that cleave nucleic acids in a site-specific fashion. Ribozymes have specific catalytic domains that possess endonuclease activity (Kim and Cech, Proc Natl Acad Sci U S A. 1987 Dec;84(24):8788-92; Forster and Symons, Cell. 1987 Apr 24;49(2):211-20). For example, a large number of ribozymes accelerate phosphoester transfer reactions with a high degree of specificity, often cleaving only one of several phosphoesters in an oligonucleotide substrate (Cech *et al.*, Cell. 1981 Dec;27(3 Pt 2):487-96; Michel and Westhof, J Mol Biol. 1990 Dec 5;216(3):585-610; Reinhold-Hurek and Shub, Nature. 1992 May 14;357(6374):173-6). This specificity has been attributed to the requirement that the substrate bind via specific base-pairing interactions to the internal guide sequence ("IGS") of the ribozyme prior to chemical reaction.

Six basic varieties of naturally-occurring enzymatic RNAs are known presently. Each can catalyze the hydrolysis of RNA phosphodiester bonds *in trans* (and thus can cleave other RNA molecules) under physiological conditions. In general, enzymatic nucleic acids act by first binding to a target RNA. Such binding occurs through the target binding portion of a enzymatic nucleic acid which is held in close proximity to an enzymatic portion of the molecule that acts to cleave the target RNA. Thus, the enzymatic nucleic acid first recognizes and then binds a target RNA through complementary base-pairing, and once bound to the correct site, acts enzymatically to cut the target RNA. Strategic cleavage of such a target RNA will destroy its ability to direct synthesis of an encoded protein. After an enzymatic nucleic acid has bound and cleaved its RNA target, it is released from that RNA to search for another target and can repeatedly bind and cleave new targets.

The enzymatic nature of a ribozyme is advantageous over many technologies, such as antisense technology (where a nucleic acid molecule simply binds to a nucleic acid target to block its translation) since the concentration of ribozyme

necessary to affect a therapeutic treatment is lower than that of an antisense oligonucleotide. This advantage reflects the ability of the ribozyme to act enzymatically. Thus, a single ribozyme molecule is able to cleave many molecules of target RNA. In addition, the ribozyme is a highly specific inhibitor, with the specificity  
5 of inhibition depending not only on the base pairing mechanism of binding to the target RNA, but also on the mechanism of target RNA cleavage. Single mismatches, or base-substitutions, near the site of cleavage can completely eliminate catalytic activity of a ribozyme. Similar mismatches in antisense molecules do not prevent their action (Woolf *et al.*, Proc Natl Acad Sci U S A. 1992 Aug 15;89(16):7305-9). Thus, the  
10 specificity of action of a ribozyme is greater than that of an antisense oligonucleotide binding the same RNA site.

The enzymatic nucleic acid molecule may be formed in a hammerhead, hairpin, a hepatitis  $\delta$  virus, group I intron or RNaseP RNA (in association with an RNA guide sequence) or Neurospora VS RNA motif. Examples of hammerhead motifs are  
15 described by Rossi *et al.* Nucleic Acids Res. 1992 Sep 11;20(17):4559-65. Examples of hairpin motifs are described by Hampel *et al.* (Eur. Pat. Appl. Publ. No. EP 0360257), Hampel and Tritz, Biochemistry 1989 Jun 13;28(12):4929-33; Hampel *et al.*, Nucleic Acids Res. 1990 Jan 25;18(2):299-304 and U. S. Patent 5,631,359. An example of the hepatitis  $\delta$  virus motif is described by Perrotta and Been, Biochemistry. 1992 Dec  
20 1;31(47):11843-52; an example of the RNaseP motif is described by Guerrier-Takada *et al.*, Cell. 1983 Dec;35(3 Pt 2):849-57; Neurospora VS RNA ribozyme motif is described by Collins (Saville and Collins, Cell. 1990 May 18;61(4):685-96; Saville and Collins, Proc Natl Acad Sci U S A. 1991 Oct 1;88(19):8826-30; Collins and Olive, Biochemistry. 1993 Mar 23;32(11):2795-9); and an example of the Group I intron is  
25 described in (U. S. Patent 4,987,071). All that is important in an enzymatic nucleic acid molecule of this invention is that it has a specific substrate binding site which is complementary to one or more of the target gene RNA regions, and that it have nucleotide sequences within or surrounding that substrate binding site which impart an RNA cleaving activity to the molecule. Thus the ribozyme constructs need not be  
30 limited to specific motifs mentioned herein.

Ribozymes may be designed as described in Int. Pat. Appl. Publ. No. WO 93/23569 and Int. Pat. Appl. Publ. No. WO 94/02595, each specifically

incorporated herein by reference) and synthesized to be tested *in vitro* and *in vivo*, as described. Such ribozymes can also be optimized for delivery. While specific examples are provided, those in the art will recognize that equivalent RNA targets in other species can be utilized when necessary.

- 5 Ribozyme activity can be optimized by altering the length of the ribozyme binding arms, or chemically synthesizing ribozymes with modifications that prevent their degradation by serum ribonucleases (see *e.g.*, Int. Pat. Appl. Publ. No. WO 92/07065; Int. Pat. Appl. Publ. No. WO 93/15187; Int. Pat. Appl. Publ. No. WO 91/03162; Eur. Pat. Appl. Publ. No. 92110298.4; U. S. Patent 5,334,711; and Int. Pat. Appl. Publ. No. WO 94/13688, which describe various chemical modifications that can be made to the sugar moieties of enzymatic RNA molecules), modifications which enhance their efficacy in cells, and removal of stem II bases to shorten RNA synthesis times and reduce chemical requirements.

- Sullivan *et al.* (Int. Pat. Appl. Publ. No. WO 94/02595) describes the  
15 general methods for delivery of enzymatic RNA molecules. Ribozymes may be administered to cells by a variety of methods known to those familiar to the art, including, but not restricted to, encapsulation in liposomes, by iontophoresis, or by incorporation into other vehicles, such as hydrogels, cyclodextrins, biodegradable nanocapsules, and bioadhesive microspheres. For some indications, ribozymes may be  
20 directly delivered *ex vivo* to cells or tissues with or without the aforementioned vehicles. Alternatively, the RNA/vehicle combination may be locally delivered by direct inhalation, by direct injection or by use of a catheter, infusion pump or stent. Other routes of delivery include, but are not limited to, intravascular, intramuscular, subcutaneous or joint injection, aerosol inhalation, oral (tablet or pill form), topical,  
25 systemic, ocular, intraperitoneal and/or intrathecal delivery. More detailed descriptions of ribozyme delivery and administration are provided in Int. Pat. Appl. Publ. No. WO 94/02595 and Int. Pat. Appl. Publ. No. WO 93/23569, each specifically incorporated herein by reference.

- Another means of accumulating high concentrations of a ribozyme(s)  
30 within cells is to incorporate the ribozyme-encoding sequences into a DNA expression vector. Transcription of the ribozyme sequences are driven from a promoter for eukaryotic RNA polymerase I (pol I), RNA polymerase II (pol II), or RNA polymerase

III (pol III). Transcripts from pol II or pol III promoters will be expressed at high levels in all cells; the levels of a given pol II promoter in a given cell type will depend on the nature of the gene regulatory sequences (enhancers, silencers, *etc.*) present nearby. Prokaryotic RNA polymerase promoters may also be used, providing that the prokaryotic RNA polymerase enzyme is expressed in the appropriate cells. Ribozymes expressed from such promoters have been shown to function in mammalian cells. Such transcription units can be incorporated into a variety of vectors for introduction into mammalian cells, including but not restricted to, plasmid DNA vectors, viral DNA vectors (such as adenovirus or adeno-associated vectors), or viral RNA vectors (such as retroviral, semliki forest virus, sindbis virus vectors).

In another embodiment of the invention, peptide nucleic acids (PNAs) compositions are provided. PNA is a DNA mimic in which the nucleobases are attached to a pseudopeptide backbone (Good and Nielsen, *Antisense Nucleic Acid Drug Dev.* 1997 7(4) 431-37). PNA is able to be utilized in a number methods that traditionally have used RNA or DNA. Often PNA sequences perform better in techniques than the corresponding RNA or DNA sequences and have utilities that are not inherent to RNA or DNA. A review of PNA including methods of making, characteristics of, and methods of using, is provided by Corey (*Trends Biotechnol* 1997 Jun;15(6):224-9). As such, in certain embodiments, one may prepare PNA sequences that are complementary to one or more portions of the ACE mRNA sequence, and such PNA compositions may be used to regulate, alter, decrease, or reduce the translation of ACE-specific mRNA, and thereby alter the level of ACE activity in a host cell to which such PNA compositions have been administered.

PNAs have 2-aminoethyl-glycine linkages replacing the normal phosphodiester backbone of DNA (Nielsen *et al.*, *Science* 1991 Dec 6;254(5037):1497-500; Hanvey *et al.*, *Science*. 1992 Nov 27;258(5087):1481-5; Hyrup and Nielsen, *Bioorg Med Chem.* 1996 Jan;4(1):5-23). This chemistry has three important consequences: firstly, in contrast to DNA or phosphorothioate oligonucleotides, PNAs are neutral molecules; secondly, PNAs are achiral, which avoids the need to develop a stereoselective synthesis; and thirdly, PNA synthesis uses standard Boc or Fmoc protocols for solid-phase peptide synthesis, although other methods, including a modified Merrifield method, have been used.



PNA monomers or ready-made oligomers are commercially available from PerSeptive Biosystems (Framingham, MA). PNA syntheses by either Boc or Fmoc protocols are straightforward using manual or automated protocols (Norton *et al.*, Bioorg Med Chem. 1995 Apr;3(4):437-45). The manual protocol lends itself to the  
5 production of chemically modified PNAs or the simultaneous synthesis of families of closely related PNAs.

As with peptide synthesis, the success of a particular PNA synthesis will depend on the properties of the chosen sequence. For example, while in theory PNAs can incorporate any combination of nucleotide bases, the presence of adjacent purines  
10 can lead to deletions of one or more residues in the product. In expectation of this difficulty, it is suggested that, in producing PNAs with adjacent purines, one should repeat the coupling of residues likely to be added inefficiently. This should be followed by the purification of PNAs by reverse-phase high-pressure liquid chromatography, providing yields and purity of product similar to those observed during the synthesis of  
15 peptides.

Modifications of PNAs for a given application may be accomplished by coupling amino acids during solid-phase synthesis or by attaching compounds that contain a carboxylic acid group to the exposed N-terminal amine. Alternatively, PNAs can be modified after synthesis by coupling to an introduced lysine or cysteine. The  
20 ease with which PNAs can be modified facilitates optimization for better solubility or for specific functional requirements. Once synthesized, the identity of PNAs and their derivatives can be confirmed by mass spectrometry. Several studies have made and utilized modifications of PNAs (for example, Norton *et al.*, Bioorg Med Chem. 1995 Apr;3(4):437-45; Petersen *et al.*, J Pept Sci. 1995 May-Jun;1(3):175-83; Orum *et al.*,  
25 Biotechniques. 1995 Sep;19(3):472-80; Footer *et al.*, Biochemistry. 1996 Aug 20;35(33):10673-9; Griffith *et al.*, Nucleic Acids Res. 1995 Aug 11;23(15):3003-8; Pardridge *et al.*, Proc Natl Acad Sci U S A. 1995 Jun 6;92(12):5592-6; Boffa *et al.*, Proc Natl Acad Sci U S A. 1995 Mar 14;92(6):1901-5; Gambacorti-Passerini *et al.*, Blood. 1996 Aug 15;88(4):1411-7; Armitage *et al.*, Proc Natl Acad Sci U S A. 1997  
30 Nov 11;94(23):12320-5; Seeger *et al.*, Biotechniques. 1997 Sep;23(3):512-7). U.S. Patent No. 5,700,922 discusses PNA-DNA-PNA chimeric molecules and their uses in

diagnostics, modulating protein in organisms, and treatment of conditions susceptible to therapeutics.

Methods of characterizing the antisense binding properties of PNAs are discussed in Rose (Anal Chem. 1993 Dec 15;65(24):3545-9) and Jensen *et al.* (Biochemistry. 1997 Apr 22;36(16):5072-7). Rose uses capillary gel electrophoresis to determine binding of PNAs to their complementary oligonucleotide, measuring the relative binding kinetics and stoichiometry. Similar types of measurements were made by Jensen *et al.* using BIAcore™ technology.

Other applications of PNAs that have been described and will be apparent to the skilled artisan include use in DNA strand invasion, antisense inhibition, mutational analysis, enhancers of transcription, nucleic acid purification, isolation of transcriptionally active genes, blocking of transcription factor binding, genome cleavage, biosensors, *in situ* hybridization, and the like.

#### Polynucleotide Identification, Characterization and Expression

Polynucleotides compositions of the present invention may be identified, prepared and/or manipulated using any of a variety of well established techniques (see generally, Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989, and other like references). For example, a polynucleotide may be identified, as described in more detail below, by screening a microarray of cDNAs for tumor-associated expression (*i.e.*, expression that is at least two fold greater in a tumor than in normal tissue, as determined using a representative assay provided herein). Such screens may be performed, for example, using the microarray technology of Affymetrix, Inc. (Santa Clara, CA) according to the manufacturer's instructions (and essentially as described by Schena et al., *Proc. Natl. Acad. Sci. USA* 93:10614-10619, 1996 and Heller et al., *Proc. Natl. Acad. Sci. USA* 94:2150-2155, 1997). Alternatively, polynucleotides may be amplified from cDNA prepared from cells expressing the proteins described herein, such as tumor cells.

Many template dependent processes are available to amplify a target sequences of interest present in a sample. One of the best known amplification methods is the polymerase chain reaction (PCR™) which is described in detail in U.S. Patent Nos. 4,683,195, 4,683,202 and 4,800,159, each of which is incorporated herein by

reference in its entirety. Briefly, in PCR<sup>TM</sup>, two primer sequences are prepared which are complementary to regions on opposite complementary strands of the target sequence. An excess of deoxynucleoside triphosphates is added to a reaction mixture along with a DNA polymerase (*e.g.*, *Taq* polymerase). If the target sequence is present  
5 in a sample, the primers will bind to the target and the polymerase will cause the primers to be extended along the target sequence by adding on nucleotides. By raising and lowering the temperature of the reaction mixture, the extended primers will dissociate from the target to form reaction products, excess primers will bind to the target and to the reaction product and the process is repeated. Preferably reverse  
10 transcription and PCR<sup>TM</sup> amplification procedure may be performed in order to quantify the amount of mRNA amplified. Polymerase chain reaction methodologies are well known in the art.

Any of a number of other template dependent processes, many of which are variations of the PCR<sup>TM</sup> amplification technique, are readily known and available in  
15 the art. Illustratively, some such methods include the ligase chain reaction (referred to as LCR), described, for example, in Eur. Pat. Appl. Publ. No. 320,308 and U.S. Patent No. 4,883,750; Qbeta Replicase, described in PCT Intl. Pat. Appl. Publ. No. PCT/US87/00880; Strand Displacement Amplification (SDA) and Repair Chain Reaction (RCR). Still other amplification methods are described in Great Britain Pat.  
20 Appl. No. 2 202 328, and in PCT Intl. Pat. Appl. Publ. No. PCT/US89/01025. Other nucleic acid amplification procedures include transcription-based amplification systems (TAS) (PCT Intl. Pat. Appl. Publ. No. WO 88/10315), including nucleic acid sequence based amplification (NASBA) and 3SR. Eur. Pat. Appl. Publ. No. 329,822 describes a nucleic acid amplification process involving cyclically synthesizing single-stranded  
25 RNA ("ssRNA"), ssDNA, and double-stranded DNA (dsDNA). PCT Intl. Pat. Appl. Publ. No. WO 89/06700 describes a nucleic acid sequence amplification scheme based on the hybridization of a promoter/primer sequence to a target single-stranded DNA ("ssDNA") followed by transcription of many RNA copies of the sequence. Other amplification methods such as "RACE" (Frohman, 1990), and "one-sided PCR" (Ohara,  
30 1989) are also well-known to those of skill in the art.

An amplified portion of a polynucleotide of the present invention may be used to isolate a full length gene from a suitable library (*e.g.*, a tumor cDNA library)

using well known techniques. Within such techniques, a library (cDNA or genomic) is screened using one or more polynucleotide probes or primers suitable for amplification. Preferably, a library is size-selected to include larger molecules. Random primed libraries may also be preferred for identifying 5' and upstream regions of genes.

- 5 Genomic libraries are preferred for obtaining introns and extending 5' sequences.

For hybridization techniques, a partial sequence may be labeled (*e.g.*, by nick-translation or end-labeling with  $^{32}\text{P}$ ) using well known techniques. A bacterial or bacteriophage library is then generally screened by hybridizing filters containing denatured bacterial colonies (or lawns containing phage plaques) with the labeled probe  
10 (*see* Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989). Hybridizing colonies or plaques are selected and expanded, and the DNA is isolated for further analysis. cDNA clones may be analyzed to determine the amount of additional sequence by, for example, PCR using a primer from the partial sequence and a primer from the vector. Restriction maps and  
15 partial sequences may be generated to identify one or more overlapping clones. The complete sequence may then be determined using standard techniques, which may involve generating a series of deletion clones. The resulting overlapping sequences can then be assembled into a single contiguous sequence. A full length cDNA molecule can be generated by ligating suitable fragments, using well known techniques.

- 20 Alternatively, amplification techniques, such as those described above, can be useful for obtaining a full length coding sequence from a partial cDNA sequence. One such amplification technique is inverse PCR (*see* Triglia et al., *Nucl. Acids Res.* 16:8186, 1988), which uses restriction enzymes to generate a fragment in the known region of the gene. The fragment is then circularized by intramolecular ligation and  
25 used as a template for PCR with divergent primers derived from the known region. Within an alternative approach, sequences adjacent to a partial sequence may be retrieved by amplification with a primer to a linker sequence and a primer specific to a known region. The amplified sequences are typically subjected to a second round of amplification with the same linker primer and a second primer specific to the known  
30 region. A variation on this procedure, which employs two primers that initiate extension in opposite directions from the known sequence, is described in WO 96/38591. Another such technique is known as "rapid amplification of cDNA ends" or

RACE. This technique involves the use of an internal primer and an external primer, which hybridizes to a polyA region or vector sequence, to identify sequences that are 5' and 3' of a known sequence. Additional techniques include capture PCR (Lagerstrom et al., *PCR Methods Applic. 1*:111-19, 1991) and walking PCR (Parker et al., *Nucl. Acids. Res. 19*:3055-60, 1991). Other methods employing amplification may also be employed to obtain a full length cDNA sequence.

In certain instances, it is possible to obtain a full length cDNA sequence by analysis of sequences provided in an expressed sequence tag (EST) database, such as that available from GenBank. Searches for overlapping ESTs may generally be performed using well known programs (e.g., NCBI BLAST searches), and such ESTs may be used to generate a contiguous full length sequence. Full length DNA sequences may also be obtained by analysis of genomic fragments.

In other embodiments of the invention, polynucleotide sequences or fragments thereof which encode polypeptides of the invention, or fusion proteins or functional equivalents thereof, may be used in recombinant DNA molecules to direct expression of a polypeptide in appropriate host cells. Due to the inherent degeneracy of the genetic code, other DNA sequences that encode substantially the same or a functionally equivalent amino acid sequence may be produced and these sequences may be used to clone and express a given polypeptide.

As will be understood by those of skill in the art, it may be advantageous in some instances to produce polypeptide-encoding nucleotide sequences possessing non-naturally occurring codons. For example, codons preferred by a particular prokaryotic or eukaryotic host can be selected to increase the rate of protein expression or to produce a recombinant RNA transcript having desirable properties, such as a half-life which is longer than that of a transcript generated from the naturally occurring sequence.

Moreover, the polynucleotide sequences of the present invention can be engineered using methods generally known in the art in order to alter polypeptide encoding sequences for a variety of reasons, including but not limited to, alterations which modify the cloning, processing, and/or expression of the gene product. For example, DNA shuffling by random fragmentation and PCR reassembly of gene fragments and synthetic oligonucleotides may be used to engineer the nucleotide

sequences. In addition, site-directed mutagenesis may be used to insert new restriction sites, alter glycosylation patterns, change codon preference, produce splice variants, or introduce mutations, and so forth.

In another embodiment of the invention, natural, modified, or  
5 recombinant nucleic acid sequences may be ligated to a heterologous sequence to encode a fusion protein. For example, to screen peptide libraries for inhibitors of polypeptide activity, it may be useful to encode a chimeric protein that can be recognized by a commercially available antibody. A fusion protein may also be engineered to contain a cleavage site located between the polypeptide-encoding  
10 sequence and the heterologous protein sequence, so that the polypeptide may be cleaved and purified away from the heterologous moiety.

Sequences encoding a desired polypeptide may be synthesized, in whole or in part, using chemical methods well known in the art (see Caruthers, M. H. et al. (1980) *Nucl. Acids Res. Symp. Ser.* 215-223, Horn, T. et al. (1980) *Nucl. Acids Res. Symp. Ser.* 225-232). Alternatively, the protein itself may be produced using chemical  
15 methods to synthesize the amino acid sequence of a polypeptide, or a portion thereof. For example, peptide synthesis can be performed using various solid-phase techniques (Roberge, J. Y. et al. (1995) *Science* 269:202-204) and automated synthesis may be achieved, for example, using the ABI 431A Peptide Synthesizer (Perkin Elmer, Palo  
20 Alto, CA).

A newly synthesized peptide may be substantially purified by preparative high performance liquid chromatography (e.g., Creighton, T. (1983) *Proteins, Structures and Molecular Principles*, WH Freeman and Co., New York, N.Y.) or other comparable techniques available in the art. The composition of the synthetic peptides may be  
25 confirmed by amino acid analysis or sequencing (e.g., the Edman degradation procedure). Additionally, the amino acid sequence of a polypeptide, or any part thereof, may be altered during direct synthesis and/or combined using chemical methods with sequences from other proteins, or any part thereof, to produce a variant polypeptide.

In order to express a desired polypeptide, the nucleotide sequences  
30 encoding the polypeptide, or functional equivalents, may be inserted into appropriate expression vector, i.e., a vector which contains the necessary elements for the transcription and translation of the inserted coding sequence. Methods which are well

known to those skilled in the art may be used to construct expression vectors containing sequences encoding a polypeptide of interest and appropriate transcriptional and translational control elements. These methods include *in vitro* recombinant DNA techniques, synthetic techniques, and *in vivo* genetic recombination. Such techniques  
5 are described, for example, in Sambrook, J. et al. (1989) *Molecular Cloning, A Laboratory Manual*, Cold Spring Harbor Press, Plainview, N.Y., and Ausubel, F. M. et al. (1989) *Current Protocols in Molecular Biology*, John Wiley & Sons, New York, N.Y.

A variety of expression vector/host systems may be utilized to contain  
10 and express polynucleotide sequences. These include, but are not limited to, microorganisms such as bacteria transformed with recombinant bacteriophage, plasmid, or cosmid DNA expression vectors; yeast transformed with yeast expression vectors; insect cell systems infected with virus expression vectors (*e.g.*, baculovirus); plant cell systems transformed with virus expression vectors (*e.g.*, cauliflower mosaic virus,  
15 CaMV; tobacco mosaic virus, TMV) or with bacterial expression vectors (*e.g.*, Ti or pBR322 plasmids); or animal cell systems.

The "control elements" or "regulatory sequences" present in an expression vector are those non-translated regions of the vector—enhancers, promoters, 5' and 3' untranslated regions—which interact with host cellular proteins to carry out  
20 transcription and translation. Such elements may vary in their strength and specificity. Depending on the vector system and host utilized, any number of suitable transcription and translation elements, including constitutive and inducible promoters, may be used. For example, when cloning in bacterial systems, inducible promoters such as the hybrid lacZ promoter of the PBLUESCRIPT phagemid (Stratagene, La Jolla, Calif.) or  
25 PSPT1 plasmid (Gibco BRL, Gaithersburg, MD) and the like may be used. In mammalian cell systems, promoters from mammalian genes or from mammalian viruses are generally preferred. If it is necessary to generate a cell line that contains multiple copies of the sequence encoding a polypeptide, vectors based on SV40 or EBV may be advantageously used with an appropriate selectable marker.

30 In bacterial systems, any of a number of expression vectors may be selected depending upon the use intended for the expressed polypeptide. For example, when large quantities are needed, for example for the induction of antibodies, vectors

which direct high level expression of fusion proteins that are readily purified may be used. Such vectors include, but are not limited to, the multifunctional *E. coli* cloning and expression vectors such as BLUESCRIPT (Stratagene), in which the sequence encoding the polypeptide of interest may be ligated into the vector in frame with sequences for the amino-terminal Met and the subsequent 7 residues of .beta.-galactosidase so that a hybrid protein is produced; pIN vectors (Van Heeke, G. and S. M. Schuster (1989) *J. Biol. Chem.* 264:5503-5509); and the like. pGEX Vectors (Promega, Madison, Wis.) may also be used to express foreign polypeptides as fusion proteins with glutathione S-transferase (GST). In general, such fusion proteins are soluble and can easily be purified from lysed cells by adsorption to glutathione-agarose beads followed by elution in the presence of free glutathione. Proteins made in such systems may be designed to include heparin, thrombin, or factor XA protease cleavage sites so that the cloned polypeptide of interest can be released from the GST moiety at will.

In the yeast, *Saccharomyces cerevisiae*, a number of vectors containing constitutive or inducible promoters such as alpha factor, alcohol oxidase, and PGH may be used. For reviews, see Ausubel et al. (supra) and Grant et al. (1987) *Methods Enzymol.* 153:516-544.

In cases where plant expression vectors are used, the expression of sequences encoding polypeptides may be driven by any of a number of promoters. For example, viral promoters such as the 35S and 19S promoters of CaMV may be used alone or in combination with the omega leader sequence from TMV (Takamatsu, N. (1987) *EMBO J.* 6:307-311. Alternatively, plant promoters such as the small subunit of RUBISCO or heat shock promoters may be used (Coruzzi, G. et al. (1984) *EMBO J.* 3:1671-1680; Broglie, R. et al. (1984) *Science* 224:838-843; and Winter, J. et al. (1991) *Results Probl. Cell Differ.* 17:85-105). These constructs can be introduced into plant cells by direct DNA transformation or pathogen-mediated transfection. Such techniques are described in a number of generally available reviews (see, for example, Hobbs, S. or Murry, L. E. in McGraw Hill Yearbook of Science and Technology (1992) McGraw Hill, New York, N.Y.; pp. 191-196).

An insect system may also be used to express a polypeptide of interest. For example, in one such system, *Autographa californica* nuclear polyhedrosis virus



(AcNPV) is used as a vector to express foreign genes in *Spodoptera frugiperda* cells or in *Trichoplusia* larvae. The sequences encoding the polypeptide may be cloned into a non-essential region of the virus, such as the polyhedrin gene, and placed under control of the polyhedrin promoter. Successful insertion of the polypeptide-encoding sequence will render the polyhedrin gene inactive and produce recombinant virus lacking coat protein. The recombinant viruses may then be used to infect, for example, *S. frugiperda* cells or *Trichoplusia* larvae in which the polypeptide of interest may be expressed (Engelhard, E. K. et al. (1994) *Proc. Natl. Acad. Sci.* 91 :3224-3227).

In mammalian host cells, a number of viral-based expression systems are generally available. For example, in cases where an adenovirus is used as an expression vector, sequences encoding a polypeptide of interest may be ligated into an adenovirus transcription/translation complex consisting of the late promoter and tripartite leader sequence. Insertion in a non-essential E1 or E3 region of the viral genome may be used to obtain a viable virus which is capable of expressing the polypeptide in infected host cells (Logan, J. and Shenk, T. (1984) *Proc. Natl. Acad. Sci.* 81:3655-3659). In addition, transcription enhancers, such as the Rous sarcoma virus (RSV) enhancer, may be used to increase expression in mammalian host cells.

Specific initiation signals may also be used to achieve more efficient translation of sequences encoding a polypeptide of interest. Such signals include the ATG initiation codon and adjacent sequences. In cases where sequences encoding the polypeptide, its initiation codon, and upstream sequences are inserted into the appropriate expression vector, no additional transcriptional or translational control signals may be needed. However, in cases where only coding sequence, or a portion thereof, is inserted, exogenous translational control signals including the ATG initiation codon should be provided. Furthermore, the initiation codon should be in the correct reading frame to ensure translation of the entire insert. Exogenous translational elements and initiation codons may be of various origins, both natural and synthetic. The efficiency of expression may be enhanced by the inclusion of enhancers which are appropriate for the particular cell system which is used, such as those described in the literature (Scharf, D. et al. (1994) *Results Probl. Cell Differ.* 20:125-162).

In addition, a host cell strain may be chosen for its ability to modulate the expression of the inserted sequences or to process the expressed protein in the

desired fashion. Such modifications of the polypeptide include, but are not limited to, acetylation, carboxylation, glycosylation, phosphorylation, lipidation, and acylation. Post-translational processing which cleaves a "prepro" form of the protein may also be used to facilitate correct insertion, folding and/or function. Different host cells such as  
5 CHO, COS, HeLa, MDCK, HEK293, and WI38, which have specific cellular machinery and characteristic mechanisms for such post-translational activities, may be chosen to ensure the correct modification and processing of the foreign protein.

For long-term, high-yield production of recombinant proteins, stable expression is generally preferred. For example, cell lines which stably express a  
10 polynucleotide of interest may be transformed using expression vectors which may contain viral origins of replication and/or endogenous expression elements and a selectable marker gene on the same or on a separate vector. Following the introduction of the vector, cells may be allowed to grow for 1-2 days in an enriched media before they are switched to selective media. The purpose of the selectable marker is to confer  
15 resistance to selection, and its presence allows growth and recovery of cells which successfully express the introduced sequences. Resistant clones of stably transformed cells may be proliferated using tissue culture techniques appropriate to the cell type.

Any number of selection systems may be used to recover transformed cell lines. These include, but are not limited to, the herpes simplex virus thymidine  
20 kinase (Wigler, M. et al. (1977) *Cell* 11:223-32) and adenine phosphoribosyltransferase (Lowy, I. et al. (1990) *Cell* 22:817-23) genes which can be employed in tk.sup.- or apt.sup.- cells, respectively. Also, antimetabolite, antibiotic or herbicide resistance can be used as the basis for selection; for example, dhfr which confers resistance to methotrexate (Wigler, M. et al. (1980) *Proc. Natl. Acad. Sci.* 77:3567-70); npt, which  
25 confers resistance to the aminoglycosides, neomycin and G-418 (Colbere-Garapin, F. et al (1981) *J. Mol. Biol.* 150:1-14); and als or pat, which confer resistance to chlorsulfuron and phosphinotricin acetyltransferase, respectively (Murry, *supra*). Additional selectable genes have been described, for example, trpB, which allows cells to utilize indole in place of tryptophan, or hisD, which allows cells to utilize histinol in  
30 place of histidine (Hartman, S. C. and R. C. Mulligan (1988) *Proc. Natl. Acad. Sci.* 85:8047-51). The use of visible markers has gained popularity with such markers as anthocyanins, beta-glucuronidase and its substrate GUS, and luciferase and its substrate

luciferin, being widely used not only to identify transformants, but also to quantify the amount of transient or stable protein expression attributable to a specific vector system (Rhodes, C. A. et al. (1995) *Methods Mol. Biol.* 55:121-131).

Although the presence/absence of marker gene expression suggests that  
5 the gene of interest is also present, its presence and expression may need to be confirmed. For example, if the sequence encoding a polypeptide is inserted within a marker gene sequence, recombinant cells containing sequences can be identified by the absence of marker gene function. Alternatively, a marker gene can be placed in tandem with a polypeptide-encoding sequence under the control of a single promoter.  
10 Expression of the marker gene in response to induction or selection usually indicates expression of the tandem gene as well.

Alternatively, host cells that contain and express a desired polynucleotide sequence may be identified by a variety of procedures known to those of skill in the art. These procedures include, but are not limited to, DNA-DNA or DNA-  
15 RNA hybridizations and protein bioassay or immunoassay techniques which include, for example, membrane, solution, or chip based technologies for the detection and/or quantification of nucleic acid or protein.

A variety of protocols for detecting and measuring the expression of polynucleotide-encoded products, using either polyclonal or monoclonal antibodies  
20 specific for the product are known in the art. Examples include enzyme-linked immunosorbent assay (ELISA), radioimmunoassay (RIA), and fluorescence activated cell sorting (FACS). A two-site, monoclonal-based immunoassay utilizing monoclonal antibodies reactive to two non-interfering epitopes on a given polypeptide may be preferred for some applications, but a competitive binding assay may also be employed.  
25 These and other assays are described, among other places, in Hampton, R. et al. (1990; *Serological Methods, a Laboratory Manual*, APS Press, St Paul, Minn.) and Maddox, D. E. et al. (1983; *J. Exp. Med.* 158:1211-1216).

A wide variety of labels and conjugation techniques are known by those skilled in the art and may be used in various nucleic acid and amino acid assays. Means  
30 for producing labeled hybridization or PCR probes for detecting sequences related to polynucleotides include oligolabeling, nick translation, end-labeling or PCR amplification using a labeled nucleotide. Alternatively, the sequences, or any portions

thereof may be cloned into a vector for the production of an mRNA probe. Such vectors are known in the art, are commercially available, and may be used to synthesize RNA probes in vitro by addition of an appropriate RNA polymerase such as T7, T3, or SP6 and labeled nucleotides. These procedures may be conducted using a variety of  
5 commercially available kits. Suitable reporter molecules or labels, which may be used include radionuclides, enzymes, fluorescent, chemiluminescent, or chromogenic agents as well as substrates, cofactors, inhibitors, magnetic particles, and the like.

Host cells transformed with a polynucleotide sequence of interest may be cultured under conditions suitable for the expression and recovery of the protein from  
10 cell culture. The protein produced by a recombinant cell may be secreted or contained intracellularly depending on the sequence and/or the vector used. As will be understood by those of skill in the art, expression vectors containing polynucleotides of the invention may be designed to contain signal sequences which direct secretion of the encoded polypeptide through a prokaryotic or eukaryotic cell membrane. Other  
15 recombinant constructions may be used to join sequences encoding a polypeptide of interest to nucleotide sequence encoding a polypeptide domain which will facilitate purification of soluble proteins. Such purification facilitating domains include, but are not limited to, metal chelating peptides such as histidine-tryptophan modules that allow purification on immobilized metals, protein A domains that allow purification on  
20 immobilized immunoglobulin, and the domain utilized in the FLAGS extension/affinity purification system (Immunex Corp., Seattle, Wash.). The inclusion of cleavable linker sequences such as those specific for Factor XA or enterokinase (Invitrogen, San Diego, Calif.) between the purification domain and the encoded polypeptide may be used to facilitate purification. One such expression vector provides for expression of a fusion  
25 protein containing a polypeptide of interest and a nucleic acid encoding 6 histidine residues preceding a thioredoxin or an enterokinase cleavage site. The histidine residues facilitate purification on IMIAC (immobilized metal ion affinity chromatography) as described in Porath, J. et al. (1992, *Prot. Exp. Purif.* 3:263-281) while the enterokinase cleavage site provides a means for purifying the desired polypeptide from the fusion  
30 protein. A discussion of vectors which contain fusion proteins is provided in Kroll, D. J. et al. (1993; *DNA Cell Biol.* 12:441-453).

In addition to recombinant production methods, polypeptides of the invention, and fragments thereof, may be produced by direct peptide synthesis using solid-phase techniques (Merrifield J. (1963) *J. Am. Chem. Soc.* 85:2149-2154). Protein synthesis may be performed using manual techniques or by automation. Automated  
5 synthesis may be achieved, for example, using Applied Biosystems 431A Peptide Synthesizer (Perkin Elmer). Alternatively, various fragments may be chemically synthesized separately and combined using chemical methods to produce the full length molecule.

#### Antibody Compositions, Fragments Thereof and Other Binding Agents

10 According to another aspect, the present invention further provides binding agents, such as antibodies and antigen-binding fragments thereof, that exhibit immunological binding to a tumor polypeptide disclosed herein, or to a portion, variant or derivative thereof. An antibody, or antigen-binding fragment thereof, is said to "specifically bind," "immunologically bind," and/or is "immunologically reactive" to a  
15 polypeptide of the invention if it reacts at a detectable level (within, for example, an ELISA assay) with the polypeptide, and does not react detectably with unrelated polypeptides under similar conditions.

Immunological binding, as used in this context, generally refers to the non-covalent interactions of the type which occur between an immunoglobulin  
20 molecule and an antigen for which the immunoglobulin is specific. The strength, or affinity of immunological binding interactions can be expressed in terms of the dissociation constant ( $K_d$ ) of the interaction, wherein a smaller  $K_d$  represents a greater affinity. Immunological binding properties of selected polypeptides can be quantified using methods well known in the art. One such method entails measuring the rates of  
25 antigen-binding site/antigen complex formation and dissociation, wherein those rates depend on the concentrations of the complex partners, the affinity of the interaction, and on geometric parameters that equally influence the rate in both directions. Thus, both the "on rate constant" ( $K_{on}$ ) and the "off rate constant" ( $K_{off}$ ) can be determined by calculation of the concentrations and the actual rates of association and dissociation.  
30 The ratio of  $K_{off}/K_{on}$  enables cancellation of all parameters not related to affinity, and is

thus equal to the dissociation constant  $K_d$ . See, generally, Davies et al. (1990) Annual Rev. Biochem. 59:439-473.

An "antigen-binding site," or "binding portion" of an antibody refers to the part of the immunoglobulin molecule that participates in antigen binding. The antigen binding site is formed by amino acid residues of the N-terminal variable ("V") regions of the heavy ("H") and light ("L") chains. Three highly divergent stretches within the V regions of the heavy and light chains are referred to as "hypervariable regions" which are interposed between more conserved flanking stretches known as "framework regions," or "FRs". Thus the term "FR" refers to amino acid sequences which are naturally found between and adjacent to hypervariable regions in immunoglobulins. In an antibody molecule, the three hypervariable regions of a light chain and the three hypervariable regions of a heavy chain are disposed relative to each other in three dimensional space to form an antigen-binding surface. The antigen-binding surface is complementary to the three-dimensional surface of a bound antigen, and the three hypervariable regions of each of the heavy and light chains are referred to as "complementarity-determining regions," or "CDRs."

Binding agents may be further capable of differentiating between patients with and without a cancer, such as lung cancer, using the representative assays provided herein. For example, antibodies or other binding agents that bind to a tumor protein will preferably generate a signal indicating the presence of a cancer in at least about 20% of patients with the disease, more preferably at least about 30% of patients. Alternatively, or in addition, the antibody will generate a negative signal indicating the absence of the disease in at least about 90% of individuals without the cancer. To determine whether a binding agent satisfies this requirement, biological samples (*e.g.*, blood, sera, sputum, urine and/or tumor biopsies) from patients with and without a cancer (as determined using standard clinical tests) may be assayed as described herein for the presence of polypeptides that bind to the binding agent. Preferably, a statistically significant number of samples with and without the disease will be assayed. Each binding agent should satisfy the above criteria; however, those of ordinary skill in the art will recognize that binding agents may be used in combination to improve sensitivity.

Any agent that satisfies the above requirements may be a binding agent. For example, a binding agent may be a ribosome, with or without a peptide component, an RNA molecule or a polypeptide. In a preferred embodiment, a binding agent is an antibody or an antigen-binding fragment thereof. Antibodies may be prepared by any of  
5 a variety of techniques known to those of ordinary skill in the art. *See, e.g., Harlow and Lane, Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, antibodies can be produced by cell culture techniques, including the generation of monoclonal antibodies as described herein, or via transfection of antibody genes into suitable bacterial or mammalian cell hosts, in order to allow for the production of  
10 recombinant antibodies. In one technique, an immunogen comprising the polypeptide is initially injected into any of a wide variety of mammals (*e.g., mice, rats, rabbits, sheep or goats*). In this step, the polypeptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier  
15 protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically. Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a  
20 suitable solid support.

Monoclonal antibodies specific for an antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol.* 6:511-519, 1976, and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the  
25 desired specificity (*i.e., reactivity with the polypeptide of interest*). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells  
30 and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine,

aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and their culture supernatants tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

5 Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield, such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by  
10 conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process in, for example, an affinity chromatography step.

A number of therapeutically useful molecules are known in the art which comprise antigen-binding sites that are capable of exhibiting immunological binding  
15 properties of an antibody molecule. The proteolytic enzyme papain preferentially cleaves IgG molecules to yield several fragments, two of which (the "F(ab)" fragments) each comprise a covalent heterodimer that includes an intact antigen-binding site. The enzyme pepsin is able to cleave IgG molecules to provide several fragments, including the "F(ab)<sub>2</sub>" fragment which comprises both antigen-binding sites. An "Fv" fragment  
20 can be produced by preferential proteolytic cleavage of an IgM, and on rare occasions IgG or IgA immunoglobulin molecule. Fv fragments are, however, more commonly derived using recombinant techniques known in the art. The Fv fragment includes a non-covalent V<sub>H</sub>::V<sub>L</sub> heterodimer including an antigen-binding site which retains much of the antigen recognition and binding capabilities of the native antibody molecule.  
25 Inbar et al. (1972) Proc. Nat. Acad. Sci. USA 69:2659-2662; Hochman et al. (1976) Biochem 15:2706-2710; and Ehrlich et al. (1980) Biochem 19:4091-4096.

A single chain Fv ("sFv") polypeptide is a covalently linked V<sub>H</sub>::V<sub>L</sub> heterodimer which is expressed from a gene fusion including V<sub>H</sub>- and V<sub>L</sub>-encoding genes linked by a peptide-encoding linker. Huston et al. (1988) Proc. Nat. Acad. Sci.  
30 USA 85(16):5879-5883. A number of methods have been described to discern chemical structures for converting the naturally aggregated—but chemically separated—light and heavy polypeptide chains from an antibody V region into an sFv molecule which will



fold into a three dimensional structure substantially similar to the structure of an antigen-binding site. See, *e.g.*, U.S. Pat. Nos. 5,091,513 and 5,132,405, to Huston et al.; and U.S. Pat. No. 4,946,778, to Ladner et al.

Each of the above-described molecules includes a heavy chain and a light chain CDR set, respectively interposed between a heavy chain and a light chain FR set which provide support to the CDRs and define the spatial relationship of the CDRs relative to each other. As used herein, the term "CDR set" refers to the three hypervariable regions of a heavy or light chain V region. Proceeding from the N-terminus of a heavy or light chain, these regions are denoted as "CDR1," "CDR2," and "CDR3" respectively. An antigen-binding site, therefore, includes six CDRs, comprising the CDR set from each of a heavy and a light chain V region. A polypeptide comprising a single CDR, (*e.g.*, a CDR1, CDR2 or CDR3) is referred to herein as a "molecular recognition unit." Crystallographic analysis of a number of antigen-antibody complexes has demonstrated that the amino acid residues of CDRs form extensive contact with bound antigen, wherein the most extensive antigen contact is with the heavy chain CDR3. Thus, the molecular recognition units are primarily responsible for the specificity of an antigen-binding site.

As used herein, the term "FR set" refers to the four flanking amino acid sequences which frame the CDRs of a CDR set of a heavy or light chain V region. Some FR residues may contact bound antigen; however, FRs are primarily responsible for folding the V region into the antigen-binding site, particularly the FR residues directly adjacent to the CDRs. Within FRs, certain amino residues and certain structural features are very highly conserved. In this regard, all V region sequences contain an internal disulfide loop of around 90 amino acid residues. When the V regions fold into a binding-site, the CDRs are displayed as projecting loop motifs which form an antigen-binding surface. It is generally recognized that there are conserved structural regions of FRs which influence the folded shape of the CDR loops into certain "canonical" structures—regardless of the precise CDR amino acid sequence. Further, certain FR residues are known to participate in non-covalent interdomain contacts which stabilize the interaction of the antibody heavy and light chains.

A number of "humanized" antibody molecules comprising an antigen-binding site derived from a non-human immunoglobulin have been described, including

chimeric antibodies having rodent V regions and their associated CDRs fused to human constant domains (Winter et al. (1991) Nature 349:293-299; Lobuglio et al. (1989) Proc. Nat. Acad. Sci. USA 86:4220-4224; Shaw et al. (1987) J Immunol. 138:4534-4538; and Brown et al. (1987) Cancer Res. 47:3577-3583), rodent CDRs grafted into a human supporting FR prior to fusion with an appropriate human antibody constant domain (Riechmann et al. (1988) Nature 332:323-327; Verhoeyen et al. (1988) Science 239:1534-1536; and Jones et al. (1986) Nature 321:522-525), and rodent CDRs supported by recombinantly veneered rodent FRs (European Patent Publication No. 519,596, published Dec. 23, 1992). These "humanized" molecules are designed to minimize unwanted immunological response toward rodent antihuman antibody molecules which limits the duration and effectiveness of therapeutic applications of those moieties in human recipients.

As used herein, the terms "veneered FRs" and "recombinantly veneered FRs" refer to the selective replacement of FR residues from, *e.g.*, a rodent heavy or light chain V region, with human FR residues in order to provide a xenogeneic molecule comprising an antigen-binding site which retains substantially all of the native FR polypeptide folding structure. Veneering techniques are based on the understanding that the ligand binding characteristics of an antigen-binding site are determined primarily by the structure and relative disposition of the heavy and light chain CDR sets within the antigen-binding surface. Davies et al. (1990) Ann. Rev. Biochem. 59:439-473. Thus, antigen binding specificity can be preserved in a humanized antibody only wherein the CDR structures, their interaction with each other, and their interaction with the rest of the V region domains are carefully maintained. By using veneering techniques, exterior (*e.g.*, solvent-accessible) FR residues which are readily encountered by the immune system are selectively replaced with human residues to provide a hybrid molecule that comprises either a weakly immunogenic, or substantially non-immunogenic veneered surface.

The process of veneering makes use of the available sequence data for human antibody variable domains compiled by Kabat et al., in Sequences of Proteins of Immunological Interest, 4th ed., (U.S. Dept. of Health and Human Services, U.S. Government Printing Office, 1987), updates to the Kabat database, and other accessible U.S. and foreign databases (both nucleic acid and protein). Solvent accessibilities of V

region amino acids can be deduced from the known three-dimensional structure for human and murine antibody fragments. There are two general steps in veneering a murine antigen-binding site. Initially, the FRs of the variable domains of an antibody molecule of interest are compared with corresponding FR sequences of human variable domains obtained from the above-identified sources. The most homologous human V regions are then compared residue by residue to corresponding murine amino acids. The residues in the murine FR which differ from the human counterpart are replaced by the residues present in the human moiety using recombinant techniques well known in the art. Residue switching is only carried out with moieties which are at least partially exposed (solvent accessible), and care is exercised in the replacement of amino acid residues which may have a significant effect on the tertiary structure of V region domains, such as proline, glycine and charged amino acids.

In this manner, the resultant "veneered" murine antigen-binding sites are thus designed to retain the murine CDR residues, the residues substantially adjacent to the CDRs, the residues identified as buried or mostly buried (solvent inaccessible), the residues believed to participate in non-covalent (*e.g.*, electrostatic and hydrophobic) contacts between heavy and light chain domains, and the residues from conserved structural regions of the FRs which are believed to influence the "canonical" tertiary structures of the CDR loops. These design criteria are then used to prepare recombinant nucleotide sequences which combine the CDRs of both the heavy and light chain of a murine antigen-binding site into human-appearing FRs that can be used to transfect mammalian cells for the expression of recombinant human antibodies which exhibit the antigen specificity of the murine antibody molecule.

In another embodiment of the invention, monoclonal antibodies of the present invention may be coupled to one or more therapeutic agents. Suitable agents in this regard include radionuclides, differentiation inducers, drugs, toxins, and derivatives thereof. Preferred radionuclides include  $^{90}\text{Y}$ ,  $^{123}\text{I}$ ,  $^{125}\text{I}$ ,  $^{131}\text{I}$ ,  $^{186}\text{Re}$ ,  $^{188}\text{Re}$ ,  $^{211}\text{At}$ , and  $^{212}\text{Bi}$ . Preferred drugs include methotrexate, and pyrimidine and purine analogs. Preferred differentiation inducers include phorbol esters and butyric acid. Preferred toxins include ricin, abrin, diphtheria toxin, cholera toxin, gelonin, *Pseudomonas* exotoxin, *Shigella* toxin, and pokeweed antiviral protein.

A therapeutic agent may be coupled (*e.g.*, covalently bonded) to a suitable monoclonal antibody either directly or indirectly (*e.g.*, via a linker group). A direct reaction between an agent and an antibody is possible when each possesses a substituent capable of reacting with the other. For example, a nucleophilic group, such as an amino or sulfhydryl group, on one may be capable of reacting with a carbonyl-containing group, such as an anhydride or an acid halide, or with an alkyl group containing a good leaving group (*e.g.*, a halide) on the other.

Alternatively, it may be desirable to couple a therapeutic agent and an antibody via a linker group. A linker group can function as a spacer to distance an antibody from an agent in order to avoid interference with binding capabilities. A linker group can also serve to increase the chemical reactivity of a substituent on an agent or an antibody, and thus increase the coupling efficiency. An increase in chemical reactivity may also facilitate the use of agents, or functional groups on agents, which otherwise would not be possible.

It will be evident to those skilled in the art that a variety of bifunctional or polyfunctional reagents, both homo- and hetero-functional (such as those described in the catalog of the Pierce Chemical Co., Rockford, IL), may be employed as the linker group. Coupling may be effected, for example, through amino groups, carboxyl groups, sulfhydryl groups or oxidized carbohydrate residues. There are numerous references describing such methodology, *e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.

Where a therapeutic agent is more potent when free from the antibody portion of the immunoconjugates of the present invention, it may be desirable to use a linker group which is cleavable during or upon internalization into a cell. A number of different cleavable linker groups have been described. The mechanisms for the intracellular release of an agent from these linker groups include cleavage by reduction of a disulfide bond (*e.g.*, U.S. Patent No. 4,489,710, to Spitler), by irradiation of a photolabile bond (*e.g.*, U.S. Patent No. 4,625,014, to Senter et al.), by hydrolysis of derivatized amino acid side chains (*e.g.*, U.S. Patent No. 4,638,045, to Kohn et al.), by serum complement-mediated hydrolysis (*e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.), and acid-catalyzed hydrolysis (*e.g.*, U.S. Patent No. 4,569,789, to Blattler et al.).

It may be desirable to couple more than one agent to an antibody. In one embodiment, multiple molecules of an agent are coupled to one antibody molecule. In

another embodiment, more than one type of agent may be coupled to one antibody. Regardless of the particular embodiment, immunoconjugates with more than one agent may be prepared in a variety of ways. For example, more than one agent may be coupled directly to an antibody molecule, or linkers that provide multiple sites for attachment can be used. Alternatively, a carrier can be used.

A carrier may bear the agents in a variety of ways, including covalent bonding either directly or via a linker group. Suitable carriers include proteins such as albumins (e.g., U.S. Patent No. 4,507,234, to Kato et al.), peptides and polysaccharides such as aminodextran (e.g., U.S. Patent No. 4,699,784, to Shih et al.). A carrier may also bear an agent by noncovalent bonding or by encapsulation, such as within a liposome vesicle (e.g., U.S. Patent Nos. 4,429,008 and 4,873,088). Carriers specific for radionuclide agents include radiohalogenated small molecules and chelating compounds. For example, U.S. Patent No. 4,735,792 discloses representative radiohalogenated small molecules and their synthesis. A radionuclide chelate may be formed from chelating compounds that include those containing nitrogen and sulfur atoms as the donor atoms for binding the metal, or metal oxide, radionuclide. For example, U.S. Patent No. 4,673,562, to Davison et al. discloses representative chelating compounds and their synthesis.

#### T Cell Compositions

The present invention, in another aspect, provides T cells specific for a tumor polypeptide disclosed herein, or for a variant or derivative thereof. Such cells may generally be prepared *in vitro* or *ex vivo*, using standard procedures. For example, T cells may be isolated from bone marrow, peripheral blood, or a fraction of bone marrow or peripheral blood of a patient, using a commercially available cell separation system, such as the Isolex™ System, available from Nexell Therapeutics, Inc. (Irvine, CA; see also U.S. Patent No. 5,240,856; U.S. Patent No. 5,215,926; WO 89/06280; WO 91/16116 and WO 92/07243). Alternatively, T cells may be derived from related or unrelated humans, non-human mammals, cell lines or cultures.

T cells may be stimulated with a polypeptide, polynucleotide encoding a polypeptide and/or an antigen presenting cell (APC) that expresses such a polypeptide. Such stimulation is performed under conditions and for a time sufficient to permit the

generation of T cells that are specific for the polypeptide of interest. Preferably, a tumor polypeptide or polynucleotide of the invention is present within a delivery vehicle, such as a microsphere, to facilitate the generation of specific T cells.

T cells are considered to be specific for a polypeptide of the present invention if the T cells specifically proliferate, secrete cytokines or kill target cells coated with the polypeptide or expressing a gene encoding the polypeptide. T cell specificity may be evaluated using any of a variety of standard techniques. For example, within a chromium release assay or proliferation assay, a stimulation index of more than two fold increase in lysis and/or proliferation, compared to negative controls, indicates T cell specificity. Such assays may be performed, for example, as described in Chen et al., *Cancer Res.* 54:1065-1070, 1994. Alternatively, detection of the proliferation of T cells may be accomplished by a variety of known techniques. For example, T cell proliferation can be detected by measuring an increased rate of DNA synthesis (e.g., by pulse-labeling cultures of T cells with tritiated thymidine and measuring the amount of tritiated thymidine incorporated into DNA). Contact with a tumor polypeptide (100 ng/ml - 100 µg/ml, preferably 200 ng/ml - 25 µg/ml) for 3 - 7 days will typically result in at least a two fold increase in proliferation of the T cells. Contact as described above for 2-3 hours should result in activation of the T cells, as measured using standard cytokine assays in which a two fold increase in the level of cytokine release (e.g., TNF or IFN-γ) is indicative of T cell activation (see Coligan et al., *Current Protocols in Immunology*, vol. 1, Wiley Interscience (Greene 1998)). T cells that have been activated in response to a tumor polypeptide, polynucleotide or polypeptide-expressing APC may be CD4<sup>+</sup> and/or CD8<sup>+</sup>. Tumor polypeptide-specific T cells may be expanded using standard techniques. Within preferred embodiments, the T cells are derived from a patient, a related donor or an unrelated donor, and are administered to the patient following stimulation and expansion.

For therapeutic purposes, CD4<sup>+</sup> or CD8<sup>+</sup> T cells that proliferate in response to a tumor polypeptide, polynucleotide or APC can be expanded in number either *in vitro* or *in vivo*. Proliferation of such T cells *in vitro* may be accomplished in a variety of ways. For example, the T cells can be re-exposed to a tumor polypeptide, or a short peptide corresponding to an immunogenic portion of such a polypeptide, with or without the addition of T cell growth factors, such as interleukin-2, and/or stimulator

cells that synthesize a tumor polypeptide. Alternatively, one or more T cells that proliferate in the presence of the tumor polypeptide can be expanded in number by cloning. Methods for cloning cells are well known in the art, and include limiting dilution.

## 5 Pharmaceutical Compositions

In additional embodiments, the present invention concerns formulation of one or more of the polynucleotide, polypeptide, T-cell and/or antibody compositions disclosed herein in pharmaceutically-acceptable carriers for administration to a cell or an animal, either alone, or in combination with one or more other modalities of therapy.

10 It will be understood that, if desired, a composition as disclosed herein may be administered in combination with other agents as well, such as, *e.g.*, other proteins or polypeptides or various pharmaceutically-active agents. In fact, there is virtually no limit to other components that may also be included, given that the additional agents do not cause a significant adverse effect upon contact with the target  
15 cells or host tissues. The compositions may thus be delivered along with various other agents as required in the particular instance. Such compositions may be purified from host cells or other biological sources, or alternatively may be chemically synthesized as described herein. Likewise, such compositions may further comprise substituted or derivatized RNA or DNA compositions.

20 Therefore, in another aspect of the present invention, pharmaceutical compositions are provided comprising one or more of the polynucleotide, polypeptide, antibody, and/or T-cell compositions described herein in combination with a physiologically acceptable carrier. In certain preferred embodiments, the pharmaceutical compositions of the invention comprise immunogenic polynucleotide  
25 and/or polypeptide compositions of the invention for use in prophylactic and therapeutic vaccine applications. Vaccine preparation is generally described in, for example, M.F. Powell and M.J. Newman, eds., "Vaccine Design (the subunit and adjuvant approach)," Plenum Press (NY, 1995). Generally, such compositions will comprise one or more polynucleotide and/or polypeptide compositions of the present invention in combination  
30 with one or more immunostimulants.

It will be apparent that any of the pharmaceutical compositions described herein can contain pharmaceutically acceptable salts of the polynucleotides and polypeptides of the invention. Such salts can be prepared, for example, from pharmaceutically acceptable non-toxic bases, including organic bases (*e.g.*, salts of  
5 primary, secondary and tertiary amines and basic amino acids) and inorganic bases (*e.g.*, sodium, potassium, lithium, ammonium, calcium and magnesium salts).

In another embodiment, illustrative immunogenic compositions, *e.g.*, vaccine compositions, of the present invention comprise DNA encoding one or more of the polypeptides as described above, such that the polypeptide is generated *in situ*. As  
10 noted above, the polynucleotide may be administered within any of a variety of delivery systems known to those of ordinary skill in the art. Indeed, numerous gene delivery techniques are well known in the art, such as those described by Rolland, *Crit. Rev. Therap. Drug Carrier Systems* 15:143-198, 1998, and references cited therein. Appropriate polynucleotide expression systems will, of course, contain the necessary  
15 regulatory DNA regulatory sequences for expression in a patient (such as a suitable promoter and terminating signal). Alternatively, bacterial delivery systems may involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an immunogenic portion of the polypeptide on its cell surface or secretes such an epitope.

Therefore, in certain embodiments, polynucleotides encoding  
20 immunogenic polypeptides described herein are introduced into suitable mammalian host cells for expression using any of a number of known viral-based systems. In one illustrative embodiment, retroviruses provide a convenient and effective platform for gene delivery systems. A selected nucleotide sequence encoding a polypeptide of the present invention can be inserted into a vector and packaged in retroviral particles using  
25 techniques known in the art. The recombinant virus can then be isolated and delivered to a subject. A number of illustrative retroviral systems have been described (*e.g.*, U.S. Pat. No. 5,219,740; Miller and Rosman (1989) *BioTechniques* 7:980-990; Miller, A. D. (1990) *Human Gene Therapy* 1:5-14; Scarpa et al. (1991) *Virology* 180:849-852; Burns et al. (1993) *Proc. Natl. Acad. Sci. USA* 90:8033-8037; and Boris-Lawrie and Temin  
30 (1993) *Cur. Opin. Genet. Develop.* 3:102-109.

In addition, a number of illustrative adenovirus-based systems have also been described. Unlike retroviruses which integrate into the host genome, adenoviruses



persist extrachromosomally thus minimizing the risks associated with insertional mutagenesis (Haj-Ahmad and Graham (1986) *J. Virol.* 57:267-274; Bett et al. (1993) *J. Virol.* 67:5911-5921; Mittereder et al. (1994) *Human Gene Therapy* 5:717-729; Seth et al. (1994) *J. Virol.* 68:933-940; Barr et al. (1994) *Gene Therapy* 1:51-58; Berkner, K. L. (1988) *BioTechniques* 6:616-629; and Rich et al. (1993) *Human Gene Therapy* 4:461-476).

Various adeno-associated virus (AAV) vector systems have also been developed for polynucleotide delivery. AAV vectors can be readily constructed using techniques well known in the art. See, e.g., U.S. Pat. Nos. 5,173,414 and 5,139,941; International Publication Nos. WO 92/01070 and WO 93/03769; Lebkowski et al. (1988) *Molec. Cell. Biol.* 8:3988-3996; Vincent et al. (1990) *Vaccines 90* (Cold Spring Harbor Laboratory Press); Carter, B. J. (1992) *Current Opinion in Biotechnology* 3:533-539; Muzyczka, N. (1992) *Current Topics in Microbiol. and Immunol.* 158:97-129; Kotin, R. M. (1994) *Human Gene Therapy* 5:793-801; Shelling and Smith (1994) *Gene Therapy* 1:165-169; and Zhou et al. (1994) *J. Exp. Med.* 179:1867-1875.

Additional viral vectors useful for delivering the polynucleotides encoding polypeptides of the present invention by gene transfer include those derived from the pox family of viruses, such as vaccinia virus and avian poxvirus. By way of example, vaccinia virus recombinants expressing the novel molecules can be constructed as follows. The DNA encoding a polypeptide is first inserted into an appropriate vector so that it is adjacent to a vaccinia promoter and flanking vaccinia DNA sequences, such as the sequence encoding thymidine kinase (TK). This vector is then used to transfect cells which are simultaneously infected with vaccinia. Homologous recombination serves to insert the vaccinia promoter plus the gene encoding the polypeptide of interest into the viral genome. The resulting TK.sup.(-) recombinant can be selected by culturing the cells in the presence of 5-bromodeoxyuridine and picking viral plaques resistant thereto.

A vaccinia-based infection/transfection system can be conveniently used to provide for inducible, transient expression or coexpression of one or more polypeptides described herein in host cells of an organism. In this particular system, cells are first infected in vitro with a vaccinia virus recombinant that encodes the bacteriophage T7 RNA polymerase. This polymerase displays exquisite specificity in

that it only transcribes templates bearing T7 promoters. Following infection, cells are transfected with the polynucleotide or polynucleotides of interest, driven by a T7 promoter. The polymerase expressed in the cytoplasm from the vaccinia virus recombinant transcribes the transfected DNA into RNA which is then translated into polypeptide by the host translational machinery. The method provides for high level, transient, cytoplasmic production of large quantities of RNA and its translation products. See, *e.g.*, Elroy-Stein and Moss, *Proc. Natl. Acad. Sci. USA* (1990) 87:6743-6747; Fuerst et al. *Proc. Natl. Acad. Sci. USA* (1986) 83:8122-8126.

Alternatively, avipoxviruses, such as the fowlpox and canarypox viruses, can also be used to deliver the coding sequences of interest. Recombinant avipox viruses, expressing immunogens from mammalian pathogens, are known to confer protective immunity when administered to non-avian species. The use of an Avipox vector is particularly desirable in human and other mammalian species since members of the Avipox genus can only productively replicate in susceptible avian species and therefore are not infective in mammalian cells. Methods for producing recombinant Avipoxviruses are known in the art and employ genetic recombination, as described above with respect to the production of vaccinia viruses. See, *e.g.*, WO 91/12882; WO 89/03429; and WO 92/03545.

Any of a number of alphavirus vectors can also be used for delivery of polynucleotide compositions of the present invention, such as those vectors described in U.S. Patent Nos. 5,843,723; 6,015,686; 6,008,035 and 6,015,694. Certain vectors based on Venezuelan Equine Encephalitis (VEE) can also be used, illustrative examples of which can be found in U.S. Patent Nos. 5,505,947 and 5,643,576.

Moreover, molecular conjugate vectors, such as the adenovirus chimeric vectors described in Michael et al. *J. Biol. Chem.* (1993) 268:6866-6869 and Wagner et al. *Proc. Natl. Acad. Sci. USA* (1992) 89:6099-6103, can also be used for gene delivery under the invention.

Additional illustrative information on these and other known viral-based delivery systems can be found, for example, in Fisher-Hoch et al., *Proc. Natl. Acad. Sci. USA* 86:317-321, 1989; Flexner et al., *Ann. N.Y. Acad. Sci.* 569:86-103, 1989; Flexner et al., *Vaccine* 8:17-21, 1990; U.S. Patent Nos. 4,603,112, 4,769,330, and 5,017,487; WO 89/01973; U.S. Patent No. 4,777,127; GB 2,200,651; EP 0,345,242;

WO 91/02805; Berkner, *Biotechniques* 6:616-627, 1988; Rosenfeld et al., *Science* 252:431-434, 1991; Kolls et al., *Proc. Natl. Acad. Sci. USA* 91:215-219, 1994; Kass-Eisler et al., *Proc. Natl. Acad. Sci. USA* 90:11498-11502, 1993; Guzman et al., *Circulation* 88:2838-2848, 1993; and Guzman et al., *Cir. Res.* 73:1202-1207, 1993.

5           In certain embodiments, a polynucleotide may be integrated into the genome of a target cell. This integration may be in the specific location and orientation via homologous recombination (gene replacement) or it may be integrated in a random, non-specific location (gene augmentation). In yet further embodiments, the polynucleotide may be stably maintained in the cell as a separate, episomal segment of  
10 DNA. Such polynucleotide segments or "episomes" encode sequences sufficient to permit maintenance and replication independent of or in synchronization with the host cell cycle. The manner in which the expression construct is delivered to a cell and where in the cell the polynucleotide remains is dependent on the type of expression construct employed.

15           In another embodiment of the invention, a polynucleotide is administered/delivered as "naked" DNA, for example as described in Ulmer et al., *Science* 259:1745-1749, 1993 and reviewed by Cohen, *Science* 259:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

20           In still another embodiment, a composition of the present invention can be delivered via a particle bombardment approach, many of which have been described. In one illustrative example, gas-driven particle acceleration can be achieved with devices such as those manufactured by Powderject Pharmaceuticals PLC (Oxford, UK) and Powderject Vaccines Inc. (Madison, WI), some examples of which are described in  
25 U.S. Patent Nos. 5,846,796; 6,010,478; 5,865,796; 5,584,807; and EP Patent No. 0500 799. This approach offers a needle-free delivery approach wherein a dry powder formulation of microscopic particles, such as polynucleotide or polypeptide particles, are accelerated to high speed within a helium gas jet generated by a hand held device, propelling the particles into a target tissue of interest.

30           In a related embodiment, other devices and methods that may be useful for gas-driven needle-less injection of compositions of the present invention include those provided by Bioject, Inc. (Portland, OR), some examples of which are described

in U.S. Patent Nos. 4,790,824; 5,064,413; 5,312,335; 5,383,851; 5,399,163; 5,520,639 and 5,993,412.

According to another embodiment, the pharmaceutical compositions described herein will comprise one or more immunostimulants in addition to the immunogenic polynucleotide, polypeptide, antibody, T-cell and/or APC compositions of this invention. An immunostimulant refers to essentially any substance that enhances or potentiates an immune response (antibody and/or cell-mediated) to an exogenous antigen. One preferred type of immunostimulant comprises an adjuvant. Many adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a stimulator of immune responses, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis* derived proteins. Certain adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI); Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ); AS-2 (SmithKline Beecham, Philadelphia, PA); aluminum salts such as aluminum hydroxide gel (alum) or aluminum phosphate; salts of calcium, iron or zinc; an insoluble suspension of acylated tyrosine; acylated sugars; cationically or anionically derivatized polysaccharides; polyphosphazenes; biodegradable microspheres; monophosphoryl lipid A and quil A. Cytokines, such as GM-CSF, interleukin-2, -7, -12, and other like growth factors, may also be used as adjuvants.

Within certain embodiments of the invention, the adjuvant composition is preferably one that induces an immune response predominantly of the Th1 type. High levels of Th1-type cytokines (e.g., IFN- $\gamma$ , TNF $\alpha$ , IL-2 and IL-12) tend to favor the induction of cell mediated immune responses to an administered antigen. In contrast, high levels of Th2-type cytokines (e.g., IL-4, IL-5, IL-6 and IL-10) tend to favor the induction of humoral immune responses. Following application of a vaccine as provided herein, a patient will support an immune response that includes Th1- and Th2-type responses. Within a preferred embodiment, in which a response is predominantly Th1-type, the level of Th1-type cytokines will increase to a greater extent than the level of Th2-type cytokines. The levels of these cytokines may be readily assessed using standard assays. For a review of the families of cytokines, see Mosmann and Coffman, *Ann. Rev. Immunol.* 7:145-173, 1989.

Certain preferred adjuvants for eliciting a predominantly Th1-type response include, for example, a combination of monophosphoryl lipid A, preferably 3-de-O-acylated monophosphoryl lipid A, together with an aluminum salt. MPL<sup>®</sup> adjuvants are available from Corixa Corporation (Seattle, WA; *see*, for example, US Patent Nos. 4,436,727; 4,877,611; 4,866,034 and 4,912,094). CpG-containing oligonucleotides (in which the CpG dinucleotide is unmethylated) also induce a predominantly Th1 response. Such oligonucleotides are well known and are described, for example, in WO 96/02555, WO 99/33488 and U.S. Patent Nos. 6,008,200 and 5,856,462. Immunostimulatory DNA sequences are also described, for example, by Sato et al., *Science* 273:352, 1996. Another preferred adjuvant comprises a saponin, such as Quil A, or derivatives thereof, including QS21 and QS7 (Aquila Biopharmaceuticals Inc., Framingham, MA); Escin; Digitonin; or *Gypsophila* or *Chenopodium quinoa* saponins. Other preferred formulations include more than one saponin in the adjuvant combinations of the present invention, for example combinations of at least two of the following group comprising QS21, QS7, Quil A,  $\beta$ -escin, or digitonin.

Alternatively the saponin formulations may be combined with vaccine vehicles composed of chitosan or other polycationic polymers, polylactide and polylactide-co-glycolide particles, poly-N-acetyl glucosamine-based polymer matrix, particles composed of polysaccharides or chemically modified polysaccharides, liposomes and lipid-based particles, particles composed of glycerol monoesters, etc. The saponins may also be formulated in the presence of cholesterol to form particulate structures such as liposomes or ISCOMs. Furthermore, the saponins may be formulated together with a polyoxyethylene ether or ester, in either a non-particulate solution or suspension, or in a particulate structure such as a paucilamellar liposome or ISCOM. The saponins may also be formulated with excipients such as Carbopol<sup>R</sup> to increase viscosity, or may be formulated in a dry powder form with a powder excipient such as lactose.

In one preferred embodiment, the adjuvant system includes the combination of a monophosphoryl lipid A and a saponin derivative, such as the combination of QS21 and 3D-MPL<sup>®</sup> adjuvant, as described in WO 94/00153, or a less reactogenic composition where the QS21 is quenched with cholesterol, as described in

WO 96/33739. Other preferred formulations comprise an oil-in-water emulsion and tocopherol. Another particularly preferred adjuvant formulation employing QS21, 3D-MPL<sup>®</sup> adjuvant and tocopherol in an oil-in-water emulsion is described in WO 95/17210.

5 Another enhanced adjuvant system involves the combination of a CpG-containing oligonucleotide and a saponin derivative particularly the combination of CpG and QS21 is disclosed in WO 00/09159. Preferably the formulation additionally comprises an oil in water emulsion and tocopherol.

Additional illustrative adjuvants for use in the pharmaceutical  
10 compositions of the invention include Montanide ISA 720 (Seppic, France), SAF (Chiron, California, United States), ISCOMS (CSL), MF-59 (Chiron), the SBAS series of adjuvants (e.g., SBAS-2 or SBAS-4, available from SmithKline Beecham, Rixensart, Belgium), Detox (Enhancyn<sup>®</sup>) (Corixa, Hamilton, MT), RC-529 (Corixa, Hamilton, MT) and other aminoalkyl glucosaminide 4-phosphates (AGPs), such as those described  
15 in pending U.S. Patent Application Serial Nos. 08/853,826 and 09/074,720, the disclosures of which are incorporated herein by reference in their entireties, and polyoxyethylene ether adjuvants such as those described in WO 99/52549A1.

Other preferred adjuvants include adjuvant molecules of the general formula

20 (I):  $\text{HO}(\text{CH}_2\text{CH}_2\text{O})_n\text{-A-R}$ ,

wherein,  $n$  is 1-50,  $A$  is a bond or  $-\text{C}(\text{O})-$ ,  $R$  is  $\text{C}_{1-50}$  alkyl or Phenyl- $\text{C}_{1-50}$  alkyl.

One embodiment of the present invention consists of a vaccine formulation comprising a polyoxyethylene ether of general formula (I), wherein  $n$  is between 1 and 50, preferably 4-24, most preferably 9; the  $R$  component is  $\text{C}_{1-50}$ ,  
25 preferably  $\text{C}_4\text{-C}_{20}$  alkyl and most preferably  $\text{C}_{12}$  alkyl, and  $A$  is a bond. The concentration of the polyoxyethylene ethers should be in the range 0.1-20%, preferably from 0.1-10%, and most preferably in the range 0.1-1%. Preferred polyoxyethylene ethers are selected from the following group: polyoxyethylene-9-lauryl ether, polyoxyethylene-9-stearyl ether, polyoxyethylene-8-stearyl ether, polyoxyethylene-4-  
30 lauryl ether, polyoxyethylene-35-lauryl ether, and polyoxyethylene-23-lauryl ether. Polyoxyethylene ethers such as polyoxyethylene lauryl ether are described in the Merck

index (12<sup>th</sup> edition: entry 7717). These adjuvant molecules are described in WO 99/52549.

The polyoxyethylene ether according to the general formula (I) above may, if desired, be combined with another adjuvant. For example, a preferred adjuvant  
5 combination is preferably with CpG as described in the pending UK patent application GB 9820956.2.

According to another embodiment of this invention, an immunogenic composition described herein is delivered to a host via antigen presenting cells (APCs), such as dendritic cells, macrophages, B cells, monocytes and other cells that may be  
10 engineered to be efficient APCs. Such cells may, but need not, be genetically modified to increase the capacity for presenting the antigen, to improve activation and/or maintenance of the T cell response, to have anti-tumor effects *per se* and/or to be immunologically compatible with the receiver (*i.e.*, matched HLA haplotype). APCs may generally be isolated from any of a variety of biological fluids and organs,  
15 including tumor and peritumoral tissues, and may be autologous, allogeneic, syngeneic or xenogeneic cells.

Certain preferred embodiments of the present invention use dendritic cells or progenitors thereof as antigen-presenting cells. Dendritic cells are highly potent APCs (Banchereau and Steinman, *Nature* 392:245-251, 1998) and have been shown to  
20 be effective as a physiological adjuvant for eliciting prophylactic or therapeutic antitumor immunity (*see* Timmerman and Levy, *Ann. Rev. Med.* 50:507-529, 1999). In general, dendritic cells may be identified based on their typical shape (stellate *in situ*, with marked cytoplasmic processes (dendrites) visible *in vitro*), their ability to take up, process and present antigens with high efficiency and their ability to activate naïve T  
25 cell responses. Dendritic cells may, of course, be engineered to express specific cell-surface receptors or ligands that are not commonly found on dendritic cells *in vivo* or *ex vivo*, and such modified dendritic cells are contemplated by the present invention. As an alternative to dendritic cells, secreted vesicles antigen-loaded dendritic cells (called exosomes) may be used within a vaccine (*see* Zitvogel et al., *Nature Med.* 4:594-600,  
30 1998).

Dendritic cells and progenitors may be obtained from peripheral blood, bone marrow, tumor-infiltrating cells, peritumoral tissues-infiltrating cells, lymph nodes, spleen, skin, umbilical cord blood or any other suitable tissue or fluid. For example, dendritic cells may be differentiated *ex vivo* by adding a combination of  
5 cytokines such as GM-CSF, IL-4, IL-13 and/or TNF $\alpha$  to cultures of monocytes harvested from peripheral blood. Alternatively, CD34 positive cells harvested from peripheral blood, umbilical cord blood or bone marrow may be differentiated into dendritic cells by adding to the culture medium combinations of GM-CSF, IL-3, TNF $\alpha$ , CD40 ligand, LPS, flt3 ligand and/or other compound(s) that induce differentiation,  
10 maturation and proliferation of dendritic cells.

Dendritic cells are conveniently categorized as "immature" and "mature" cells, which allows a simple way to discriminate between two well characterized phenotypes. However, this nomenclature should not be construed to exclude all possible intermediate stages of differentiation. Immature dendritic cells are  
15 characterized as APC with a high capacity for antigen uptake and processing, which correlates with the high expression of Fc $\gamma$  receptor and mannose receptor. The mature phenotype is typically characterized by a lower expression of these markers, but a high expression of cell surface molecules responsible for T cell activation such as class I and class II MHC, adhesion molecules (*e.g.*, CD54 and CD11) and costimulatory molecules  
20 (*e.g.*, CD40, CD80, CD86 and 4-1BB).

APCs may generally be transfected with a polynucleotide of the invention (or portion or other variant thereof) such that the encoded polypeptide, or an immunogenic portion thereof, is expressed on the cell surface. Such transfection may take place *ex vivo*, and a pharmaceutical composition comprising such transfected cells  
25 may then be used for therapeutic purposes, as described herein. Alternatively, a gene delivery vehicle that targets a dendritic or other antigen presenting cell may be administered to a patient, resulting in transfection that occurs *in vivo*. *In vivo* and *ex vivo* transfection of dendritic cells, for example, may generally be performed using any methods known in the art, such as those described in WO 97/24447, or the gene gun  
30 approach described by Mahvi et al., *Immunology and cell Biology* 75:456-460, 1997. Antigen loading of dendritic cells may be achieved by incubating dendritic cells or progenitor cells with the tumor polypeptide, DNA (naked or within a plasmid vector) or



RNA; or with antigen-expressing recombinant bacterium or viruses (*e.g.*, vaccinia, fowlpox, adenovirus or lentivirus vectors). Prior to loading, the polypeptide may be covalently conjugated to an immunological partner that provides T cell help (*e.g.*, a carrier molecule). Alternatively, a dendritic cell may be pulsed with a non-conjugated immunological partner, separately or in the presence of the polypeptide.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will typically vary depending on the mode of administration. Compositions of the present invention may be formulated for any appropriate manner of administration, including for example, topical, oral, nasal, mucosal, intravenous, intracranial, intraperitoneal, subcutaneous and intramuscular administration.

Carriers for use within such pharmaceutical compositions are biocompatible, and may also be biodegradable. In certain embodiments, the formulation preferably provides a relatively constant level of active component release. In other embodiments, however, a more rapid rate of release immediately upon administration may be desired. The formulation of such compositions is well within the level of ordinary skill in the art using known techniques. Illustrative carriers useful in this regard include microparticles of poly(lactide-co-glycolide), polyacrylate, latex, starch, cellulose, dextran and the like. Other illustrative delayed-release carriers include supramolecular biovectors, which comprise a non-liquid hydrophilic core (*e.g.*, a cross-linked polysaccharide or oligosaccharide) and, optionally, an external layer comprising an amphiphilic compound, such as a phospholipid (*see e.g.*, U.S. Patent No. 5,151,254 and PCT applications WO 94/20078, WO/94/23701 and WO 96/06638). The amount of active compound contained within a sustained release formulation depends upon the site of implantation, the rate and expected duration of release and the nature of the condition to be treated or prevented.

In another illustrative embodiment, biodegradable microspheres (*e.g.*, polylactate polyglycolate) are employed as carriers for the compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268; 5,075,109; 5,928,647; 5,811,128; 5,820,883; 5,853,763; 5,814,344, 5,407,609 and 5,942,252. Modified hepatitis B core protein carrier systems, such as described in WO/99 40934, and references cited therein, will also be useful for

many applications. Another illustrative carrier/delivery system employs a carrier comprising particulate-protein complexes, such as those described in U.S. Patent No. 5,928,647, which are capable of inducing a class I-restricted cytotoxic T lymphocyte responses in a host.

5           The pharmaceutical compositions of the invention will often further comprise one or more buffers (e.g., neutral buffered saline or phosphate buffered saline), carbohydrates (e.g., glucose, mannose, sucrose or dextrans), mannitol, proteins, polypeptides or amino acids such as glycine, antioxidants, bacteriostats, chelating agents such as EDTA or glutathione, adjuvants (e.g., aluminum hydroxide), solutes that  
10       render the formulation isotonic, hypotonic or weakly hypertonic with the blood of a recipient, suspending agents, thickening agents and/or preservatives. Alternatively, compositions of the present invention may be formulated as a lyophilizate.

          The pharmaceutical compositions described herein may be presented in unit-dose or multi-dose containers, such as sealed ampoules or vials. Such containers  
15       are typically sealed in such a way to preserve the sterility and stability of the formulation until use. In general, formulations may be stored as suspensions, solutions or emulsions in oily or aqueous vehicles. Alternatively, a pharmaceutical composition may be stored in a freeze-dried condition requiring only the addition of a sterile liquid carrier immediately prior to use.

20           The development of suitable dosing and treatment regimens for using the particular compositions described herein in a variety of treatment regimens, including e.g., oral, parenteral, intravenous, intranasal, and intramuscular administration and formulation, is well known in the art, some of which are briefly discussed below for general purposes of illustration.

25           In certain applications, the pharmaceutical compositions disclosed herein may be delivered *via* oral administration to an animal. As such, these compositions may be formulated with an inert diluent or with an assimilable edible carrier, or they may be enclosed in hard- or soft-shell gelatin capsule, or they may be compressed into tablets, or they may be incorporated directly with the food of the diet.

30           The active compounds may even be incorporated with excipients and used in the form of ingestible tablets, buccal tables, troches, capsules, elixirs, suspensions, syrups, wafers, and the like (see, for example, Mathiowitz *et al.*, Nature

1997 Mar 27;386(6623):410-4; Hwang *et al.*, Crit Rev Ther Drug Carrier Syst 1998;15(3):243-84; U. S. Patent 5,641,515; U. S. Patent 5,580,579 and U. S. Patent 5,792,451). Tablets, troches, pills, capsules and the like may also contain any of a variety of additional components, for example, a binder, such as gum tragacanth, acacia, cornstarch, or gelatin; excipients, such as dicalcium phosphate; a disintegrating agent, such as corn starch, potato starch, alginic acid and the like; a lubricant, such as magnesium stearate; and a sweetening agent, such as sucrose, lactose or saccharin may be added or a flavoring agent, such as peppermint, oil of wintergreen, or cherry flavoring. When the dosage unit form is a capsule, it may contain, in addition to materials of the above type, a liquid carrier. Various other materials may be present as coatings or to otherwise modify the physical form of the dosage unit. For instance, tablets, pills, or capsules may be coated with shellac, sugar, or both. Of course, any material used in preparing any dosage unit form should be pharmaceutically pure and substantially non-toxic in the amounts employed. In addition, the active compounds may be incorporated into sustained-release preparation and formulations.

Typically, these formulations will contain at least about 0.1% of the active compound or more, although the percentage of the active ingredient(s) may, of course, be varied and may conveniently be between about 1 or 2% and about 60% or 70% or more of the weight or volume of the total formulation. Naturally, the amount of active compound(s) in each therapeutically useful composition may be prepared in such a way that a suitable dosage will be obtained in any given unit dose of the compound. Factors such as solubility, bioavailability, biological half-life, route of administration, product shelf life, as well as other pharmacological considerations will be contemplated by one skilled in the art of preparing such pharmaceutical formulations, and as such, a variety of dosages and treatment regimens may be desirable.

For oral administration the compositions of the present invention may alternatively be incorporated with one or more excipients in the form of a mouthwash, dentifrice, buccal tablet, oral spray, or sublingual orally-administered formulation. Alternatively, the active ingredient may be incorporated into an oral solution such as one containing sodium borate, glycerin and potassium bicarbonate, or dispersed in a dentifrice, or added in a therapeutically-effective amount to a composition that may include water, binders, abrasives, flavoring agents, foaming agents, and humectants.

Alternatively the compositions may be fashioned into a tablet or solution form that may be placed under the tongue or otherwise dissolved in the mouth.

In certain circumstances it will be desirable to deliver the pharmaceutical compositions disclosed herein parenterally, intravenously, intramuscularly, or even  
5 intraperitoneally. Such approaches are well known to the skilled artisan, some of which are further described, for example, in U. S. Patent 5,543,158; U. S. Patent 5,641,515 and U. S. Patent 5,399,363. In certain embodiments, solutions of the active compounds as free base or pharmacologically acceptable salts may be prepared in water suitably mixed with a surfactant, such as hydroxypropylcellulose. Dispersions may also be  
10 prepared in glycerol, liquid polyethylene glycols, and mixtures thereof and in oils. Under ordinary conditions of storage and use, these preparations generally will contain a preservative to prevent the growth of microorganisms.

Illustrative pharmaceutical forms suitable for injectable use include sterile aqueous solutions or dispersions and sterile powders for the extemporaneous  
15 preparation of sterile injectable solutions or dispersions (for example, see U. S. Patent 5,466,468). In all cases the form must be sterile and must be fluid to the extent that easy syringability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms, such as bacteria and fungi. The carrier can be a solvent or dispersion medium  
20 containing, for example, water, ethanol, polyol (*e.g.*, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), suitable mixtures thereof, and/or vegetable oils. Proper fluidity may be maintained, for example, by the use of a coating, such as lecithin, by the maintenance of the required particle size in the case of dispersion and/or by the use of surfactants. The prevention of the action of microorganisms can be  
25 facilitated by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, sorbic acid, thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars or sodium chloride. Prolonged absorption of the injectable compositions can be brought about by the use in the compositions of agents delaying absorption, for example, aluminum monostearate  
30 and gelatin.

In one embodiment, for parenteral administration in an aqueous solution, the solution should be suitably buffered if necessary and the liquid diluent first rendered

isotonic with sufficient saline or glucose. These particular aqueous solutions are especially suitable for intravenous, intramuscular, subcutaneous and intraperitoneal administration. In this connection, a sterile aqueous medium that can be employed will be known to those of skill in the art in light of the present disclosure. For example, one  
5 dosage may be dissolved in 1 ml of isotonic NaCl solution and either added to 1000 ml of hypodermoclysis fluid or injected at the proposed site of infusion, (see for example, "Remington's Pharmaceutical Sciences" 15th Edition, pages 1035-1038 and 1570-1580). Some variation in dosage will necessarily occur depending on the condition of the subject being treated. Moreover, for human administration, preparations will of  
10 course preferably meet sterility, pyrogenicity, and the general safety and purity standards as required by FDA Office of Biologics standards.

In another embodiment of the invention, the compositions disclosed herein may be formulated in a neutral or salt form. Illustrative pharmaceutically-acceptable salts include the acid addition salts (formed with the free  
15 amino groups of the protein) and which are formed with inorganic acids such as, for example, hydrochloric or phosphoric acids, or such organic acids as acetic, oxalic, tartaric, mandelic, and the like. Salts formed with the free carboxyl groups can also be derived from inorganic bases such as, for example, sodium, potassium, ammonium, calcium, or ferric hydroxides, and such organic bases as isopropylamine,  
20 trimethylamine, histidine, procaine and the like. Upon formulation, solutions will be administered in a manner compatible with the dosage formulation and in such amount as is therapeutically effective.

The carriers can further comprise any and all solvents, dispersion media, vehicles, coatings, diluents, antibacterial and antifungal agents, isotonic and absorption  
25 delaying agents, buffers, carrier solutions, suspensions, colloids, and the like. The use of such media and agents for pharmaceutical active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active ingredient, its use in the therapeutic compositions is contemplated. Supplementary active ingredients can also be incorporated into the compositions. The phrase  
30 "pharmaceutically-acceptable" refers to molecular entities and compositions that do not produce an allergic or similar untoward reaction when administered to a human.

In certain embodiments, the pharmaceutical compositions may be delivered by intranasal sprays, inhalation, and/or other aerosol delivery vehicles. Methods for delivering genes, nucleic acids, and peptide compositions directly to the lungs *via* nasal aerosol sprays has been described, *e.g.*, in U. S. Patent 5,756,353 and U. S. Patent 5,804,212. Likewise, the delivery of drugs using intranasal microparticle resins (Takenaga *et al.*, J Controlled Release 1998 Mar 2;52(1-2):81-7) and lysophosphatidyl-glycerol compounds (U. S. Patent 5,725,871) are also well-known in the pharmaceutical arts. Likewise, illustrative transmucosal drug delivery in the form of a polytetrafluoroethylene support matrix is described in U. S. Patent 5,780,045.

10 In certain embodiments, liposomes, nanocapsules, microparticles, lipid particles, vesicles, and the like, are used for the introduction of the compositions of the present invention into suitable host cells/organisms. In particular, the compositions of the present invention may be formulated for delivery either encapsulated in a lipid particle, a liposome, a vesicle, a nanosphere, or a nanoparticle or the like. Alternatively, 15 compositions of the present invention can be bound, either covalently or non-covalently, to the surface of such carrier vehicles.

The formation and use of liposome and liposome-like preparations as potential drug carriers is generally known to those of skill in the art (see for example, Lasic, Trends Biotechnol 1998 Jul;16(7):307-21; Takakura, Nippon Rinsho 1998 20 Mar;56(3):691-5; Chandran *et al.*, Indian J Exp Biol. 1997 Aug;35(8):801-9; Margalit, Crit Rev Ther Drug Carrier Syst. 1995;12(2-3):233-61; U.S. Patent 5,567,434; U.S. Patent 5,552,157; U.S. Patent 5,565,213; U.S. Patent 5,738,868 and U.S. Patent 5,795,587, each specifically incorporated herein by reference in its entirety).

Liposomes have been used successfully with a number of cell types that 25 are normally difficult to transfect by other procedures, including T cell suspensions, primary hepatocyte cultures and PC 12 cells (Renneisen *et al.*, J Biol Chem. 1990 Sep 25;265(27):16337-42; Muller *et al.*, DNA Cell Biol. 1990 Apr;9(3):221-9). In addition, liposomes are free of the DNA length constraints that are typical of viral-based delivery systems. Liposomes have been used effectively to introduce genes, various drugs, 30 radiotherapeutic agents, enzymes, viruses, transcription factors, allosteric effectors and the like, into a variety of cultured cell lines and animals. Furthermore, the use of

liposomes does not appear to be associated with autoimmune responses or unacceptable toxicity after systemic delivery.

In certain embodiments, liposomes are formed from phospholipids that are dispersed in an aqueous medium and spontaneously form multilamellar concentric bilayer vesicles (also termed multilamellar vesicles (MLVs)).

Alternatively, in other embodiments, the invention provides for pharmaceutically-acceptable nanocapsule formulations of the compositions of the present invention. Nanocapsules can generally entrap compounds in a stable and reproducible way (see, for example, Quintanar-Guerrero *et al.*, Drug Dev Ind Pharm. 1998 Dec;24(12):1113-28). To avoid side effects due to intracellular polymeric overloading, such ultrafine particles (sized around 0.1  $\mu\text{m}$ ) may be designed using polymers able to be degraded *in vivo*. Such particles can be made as described, for example, by Couvreur *et al.*, Crit Rev Ther Drug Carrier Syst. 1988;5(1):1-20; zur Muhlen *et al.*, Eur J Pharm Biopharm. 1998 Mar;45(2):149-55; Zambaux *et al.* J Controlled Release. 1998 Jan 2;50(1-3):31-40; and U. S. Patent 5,145,684.

#### Cancer Therapeutic Methods

In further aspects of the present invention, the pharmaceutical compositions described herein may be used for the treatment of cancer, particularly for the immunotherapy of lung cancer. Within such methods, the pharmaceutical compositions described herein are administered to a patient, typically a warm-blooded animal, preferably a human. A patient may or may not be afflicted with cancer. Accordingly, the above pharmaceutical compositions may be used to prevent the development of a cancer or to treat a patient afflicted with a cancer. Pharmaceutical compositions and vaccines may be administered either prior to or following surgical removal of primary tumors and/or treatment such as administration of radiotherapy or conventional chemotherapeutic drugs. As discussed above, administration of the pharmaceutical compositions may be by any suitable method, including administration by intravenous, intraperitoneal, intramuscular, subcutaneous, intranasal, intradermal, anal, vaginal, topical and oral routes.

Within certain embodiments, immunotherapy may be active immunotherapy, in which treatment relies on the *in vivo* stimulation of the endogenous

host immune system to react against tumors with the administration of immune response-modifying agents (such as polypeptides and polynucleotides as provided herein).

Within other embodiments, immunotherapy may be passive immunotherapy, in which treatment involves the delivery of agents with established tumor-immune reactivity (such as effector cells or antibodies) that can directly or indirectly mediate antitumor effects and does not necessarily depend on an intact host immune system. Examples of effector cells include T cells as discussed above, T lymphocytes (such as CD8<sup>+</sup> cytotoxic T lymphocytes and CD4<sup>+</sup> T-helper tumor-infiltrating lymphocytes), killer cells (such as Natural Killer cells and lymphokine-activated killer cells), B cells and antigen-presenting cells (such as dendritic cells and macrophages) expressing a polypeptide provided herein. T cell receptors and antibody receptors specific for the polypeptides recited herein may be cloned, expressed and transferred into other vectors or effector cells for adoptive immunotherapy. The polypeptides provided herein may also be used to generate antibodies or anti-idiotypic antibodies (as described above and in U.S. Patent No. 4,918,164) for passive immunotherapy.

Effector cells may generally be obtained in sufficient quantities for adoptive immunotherapy by growth *in vitro*, as described herein. Culture conditions for expanding single antigen-specific effector cells to several billion in number with retention of antigen recognition *in vivo* are well known in the art. Such *in vitro* culture conditions typically use intermittent stimulation with antigen, often in the presence of cytokines (such as IL-2) and non-dividing feeder cells. As noted above, immunoreactive polypeptides as provided herein may be used to rapidly expand antigen-specific T cell cultures in order to generate a sufficient number of cells for immunotherapy. In particular, antigen-presenting cells, such as dendritic, macrophage, monocyte, fibroblast and/or B cells, may be pulsed with immunoreactive polypeptides or transfected with one or more polynucleotides using standard techniques well known in the art. For example, antigen-presenting cells can be transfected with a polynucleotide having a promoter appropriate for increasing expression in a recombinant virus or other expression system. Cultured effector cells for use in therapy must be able to grow and distribute widely, and to survive long term *in vivo*. Studies



have shown that cultured effector cells can be induced to grow *in vivo* and to survive long term in substantial numbers by repeated stimulation with antigen supplemented with IL-2 (*see, for example, Cheever et al., Immunological Reviews 157:177, 1997*).

Alternatively, a vector expressing a polypeptide recited herein may be introduced into antigen presenting cells taken from a patient and clonally propagated *ex vivo* for transplant back into the same patient. Transfected cells may be reintroduced into the patient using any means known in the art, preferably in sterile form by intravenous, intracavitary, intraperitoneal or intratumor administration.

Routes and frequency of administration of the therapeutic compositions described herein, as well as dosage, will vary from individual to individual, and may be readily established using standard techniques. In general, the pharmaceutical compositions and vaccines may be administered by injection (*e.g.*, intracutaneous, intramuscular, intravenous or subcutaneous), intranasally (*e.g.*, by aspiration) or orally. Preferably, between 1 and 10 doses may be administered over a 52 week period. Preferably, 6 doses are administered, at intervals of 1 month, and booster vaccinations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of a compound that, when administered as described above, is capable of promoting an anti-tumor immune response, and is at least 10-50% above the basal (*i.e.*, untreated) level. Such response can be monitored by measuring the anti-tumor antibodies in a patient or by vaccine-dependent generation of cytolytic effector cells capable of killing the patient's tumor cells *in vitro*. Such vaccines should also be capable of causing an immune response that leads to an improved clinical outcome (*e.g.*, more frequent remissions, complete or partial or longer disease-free survival) in vaccinated patients as compared to non-vaccinated patients. In general, for pharmaceutical compositions and vaccines comprising one or more polypeptides, the amount of each polypeptide present in a dose ranges from about 25  $\mu$ g to 5 mg per kg of host. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.1 mL to about 5 mL.

In general, an appropriate dosage and treatment regimen provides the active compound(s) in an amount sufficient to provide therapeutic and/or prophylactic benefit. Such a response can be monitored by establishing an improved clinical outcome (*e.g.*, more frequent remissions, complete or partial, or longer disease-free

survival) in treated patients as compared to non-treated patients. Increases in preexisting immune responses to a tumor protein generally correlate with an improved clinical outcome. Such immune responses may generally be evaluated using standard proliferation, cytotoxicity or cytokine assays, which may be performed using samples  
5 obtained from a patient before and after treatment.

#### Cancer Detection and Diagnostic Compositions, Methods and Kits

In general, a cancer may be detected in a patient based on the presence of one or more lung tumor proteins and/or polynucleotides encoding such proteins in a biological sample (for example, blood, sera, sputum urine and/or tumor biopsies)  
10 obtained from the patient. In other words, such proteins may be used as markers to indicate the presence or absence of a cancer such as lung cancer. In addition, such proteins may be useful for the detection of other cancers. The binding agents provided herein generally permit detection of the level of antigen that binds to the agent in the biological sample. Polynucleotide primers and probes may be used to detect the level of  
15 mRNA encoding a tumor protein, which is also indicative of the presence or absence of a cancer. In general, a lung tumor sequence should be present at a level that is at least three fold higher in tumor tissue than in normal tissue

There are a variety of assay formats known to those of ordinary skill in the art for using a binding agent to detect polypeptide markers in a sample. See, e.g.,  
20 Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In general, the presence or absence of a cancer in a patient may be determined by (a) contacting a biological sample obtained from a patient with a binding agent; (b) detecting in the sample a level of polypeptide that binds to the binding agent; and (c) comparing the level of polypeptide with a predetermined cut-off value.

25 In a preferred embodiment, the assay involves the use of binding agent immobilized on a solid support to bind to and remove the polypeptide from the remainder of the sample. The bound polypeptide may then be detected using a detection reagent that contains a reporter group and specifically binds to the binding agent/polypeptide complex. Such detection reagents may comprise, for example, a  
30 binding agent that specifically binds to the polypeptide or an antibody or other agent that specifically binds to the binding agent, such as an anti-immunoglobulin, protein G,

protein A or a lectin. Alternatively, a competitive assay may be utilized, in which a polypeptide is labeled with a reporter group and allowed to bind to the immobilized binding agent after incubation of the binding agent with the sample. The extent to which components of the sample inhibit the binding of the labeled polypeptide to the binding agent is indicative of the reactivity of the sample with the immobilized binding agent. Suitable polypeptides for use within such assays include full length lung tumor proteins and polypeptide portions thereof to which the binding agent binds, as described above.

The solid support may be any material known to those of ordinary skill in the art to which the tumor protein may be attached. For example, the solid support may be a test well in a microtiter plate or a nitrocellulose or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681. The binding agent may be immobilized on the solid support using a variety of techniques known to those of skill in the art, which are amply described in the patent and scientific literature. In the context of the present invention, the term "immobilization" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the agent and functional groups on the support or may be a linkage by way of a cross-linking agent). Immobilization by adsorption to a well in a microtiter plate or to a membrane is preferred. In such cases, adsorption may be achieved by contacting the binding agent, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and about 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of binding agent ranging from about 10 ng to about 10  $\mu$ g, and preferably about 100 ng to about 1  $\mu$ g, is sufficient to immobilize an adequate amount of binding agent.

Covalent attachment of binding agent to a solid support may generally be achieved by first reacting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the binding agent. For example, the binding agent may be covalently attached to supports

having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the binding partner (*see, e.g.,* Pierce Immunotechnology Catalog and Handbook, 1991, at A12-A13).

5           In certain embodiments, the assay is a two-antibody sandwich assay. This assay may be performed by first contacting an antibody that has been immobilized on a solid support, commonly the well of a microtiter plate, with the sample, such that polypeptides within the sample are allowed to bind to the immobilized antibody. Unbound sample is then removed from the immobilized polypeptide-antibody  
10 complexes and a detection reagent (preferably a second antibody capable of binding to a different site on the polypeptide) containing a reporter group is added. The amount of detection reagent that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.

          More specifically, once the antibody is immobilized on the support as  
15 described above, the remaining protein binding sites on the support are typically blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween 20™ (Sigma Chemical Co., St. Louis, MO). The immobilized antibody is then incubated with the sample, and polypeptide is allowed to bind to the antibody. The sample may be diluted with a suitable diluent, such as  
20 phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact time (*i.e.,* incubation time) is a period of time that is sufficient to detect the presence of polypeptide within a sample obtained from an individual with lung cancer. Preferably, the contact time is sufficient to achieve a level of binding that is at least about 95% of that achieved at equilibrium between bound and unbound polypeptide. Those of  
25 ordinary skill in the art will recognize that the time necessary to achieve equilibrium may be readily determined by assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

          Unbound sample may then be removed by washing the solid support  
30 with an appropriate buffer, such as PBS containing 0.1% Tween 20™. The second antibody, which contains a reporter group, may then be added to the solid support. Preferred reporter groups include those groups recited above.

The detection reagent is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound polypeptide. An appropriate amount of time may generally be determined by assaying the level of binding that occurs over a period of time. Unbound detection reagent is then removed and bound detection reagent is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

To determine the presence or absence of a cancer, such as lung cancer, the signal detected from the reporter group that remains bound to the solid support is generally compared to a signal that corresponds to a predetermined cut-off value. In one preferred embodiment, the cut-off value for the detection of a cancer is the average mean signal obtained when the immobilized antibody is incubated with samples from patients without the cancer. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value is considered positive for the cancer. In an alternate preferred embodiment, the cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett et al., *Clinical Epidemiology: A Basic Science for Clinical Medicine*, Little Brown and Co., 1985, p. 106-7. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (*i.e.*, sensitivity) and false positive rates (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest to the upper left-hand corner (*i.e.*, the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In

general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for a cancer.

In a related embodiment, the assay is performed in a flow-through or strip test format, wherein the binding agent is immobilized on a membrane, such as nitrocellulose. In the flow-through test, polypeptides within the sample bind to the immobilized binding agent as the sample passes through the membrane. A second, labeled binding agent then binds to the binding agent-polypeptide complex as a solution containing the second binding agent flows through the membrane. The detection of bound second binding agent may then be performed as described above. In the strip test format, one end of the membrane to which binding agent is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing second binding agent and to the area of immobilized binding agent. Concentration of second binding agent at the area of immobilized antibody indicates the presence of a cancer. Typically, the concentration of second binding agent at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of binding agent immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of polypeptide that would be sufficient to generate a positive signal in the two-antibody sandwich assay, in the format discussed above. Preferred binding agents for use in such assays are antibodies and antigen-binding fragments thereof. Preferably, the amount of antibody immobilized on the membrane ranges from about 25 ng to about 1  $\mu$ g, and more preferably from about 50 ng to about 500 ng. Such tests can typically be performed with a very small amount of biological sample.

Of course, numerous other assay protocols exist that are suitable for use with the tumor proteins or binding agents of the present invention. The above descriptions are intended to be exemplary only. For example, it will be apparent to those of ordinary skill in the art that the above protocols may be readily modified to use tumor polypeptides to detect antibodies that bind to such polypeptides in a biological sample. The detection of such tumor protein specific antibodies may correlate with the presence of a cancer.

A cancer may also, or alternatively, be detected based on the presence of T cells that specifically react with a tumor protein in a biological sample. Within certain methods, a biological sample comprising CD4<sup>+</sup> and/or CD8<sup>+</sup> T cells isolated from a patient is incubated with a tumor polypeptide, a polynucleotide encoding such a polypeptide and/or an APC that expresses at least an immunogenic portion of such a polypeptide, and the presence or absence of specific activation of the T cells is detected. Suitable biological samples include, but are not limited to, isolated T cells. For example, T cells may be isolated from a patient by routine techniques (such as by Ficoll/Hypaque density gradient centrifugation of peripheral blood lymphocytes). T cells may be incubated *in vitro* for 2-9 days (typically 4 days) at 37°C with polypeptide (e.g., 5 - 25 µg/ml). It may be desirable to incubate another aliquot of a T cell sample in the absence of tumor polypeptide to serve as a control. For CD4<sup>+</sup> T cells, activation is preferably detected by evaluating proliferation of the T cells. For CD8<sup>+</sup> T cells, activation is preferably detected by evaluating cytolytic activity. A level of proliferation that is at least two fold greater and/or a level of cytolytic activity that is at least 20% greater than in disease-free patients indicates the presence of a cancer in the patient.

As noted above, a cancer may also, or alternatively, be detected based on the level of mRNA encoding a tumor protein in a biological sample. For example, at least two oligonucleotide primers may be employed in a polymerase chain reaction (PCR) based assay to amplify a portion of a tumor cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is specific for (*i.e.*, hybridizes to) a polynucleotide encoding the tumor protein. The amplified cDNA is then separated and detected using techniques well known in the art, such as gel electrophoresis. Similarly, oligonucleotide probes that specifically hybridize to a polynucleotide encoding a tumor protein may be used in a hybridization assay to detect the presence of polynucleotide encoding the tumor protein in a biological sample.

To permit hybridization under assay conditions, oligonucleotide primers and probes should comprise an oligonucleotide sequence that has at least about 60%, preferably at least about 75% and more preferably at least about 90%, identity to a portion of a polynucleotide encoding a tumor protein of the invention that is at least 10 nucleotides, and preferably at least 20 nucleotides, in length. Preferably, oligonucleotide primers and/or probes hybridize to a polynucleotide encoding a

polypeptide described herein under moderately stringent conditions, as defined above. Oligonucleotide primers and/or probes which may be usefully employed in the diagnostic methods described herein preferably are at least 10-40 nucleotides in length. In a preferred embodiment, the oligonucleotide primers comprise at least 10 contiguous  
5 nucleotides, more preferably at least 15 contiguous nucleotides, of a DNA molecule having a sequence as disclosed herein. Techniques for both PCR based assays and hybridization assays are well known in the art (*see*, for example, Mullis et al., *Cold Spring Harbor Symp. Quant. Biol.*, 51:263, 1987; Erlich ed., *PCR Technology*, Stockton Press, NY, 1989).

10 One preferred assay employs RT-PCR, in which PCR is applied in conjunction with reverse transcription. Typically, RNA is extracted from a biological sample, such as biopsy tissue, and is reverse transcribed to produce cDNA molecules. PCR amplification using at least one specific primer generates a cDNA molecule, which may be separated and visualized using, for example, gel electrophoresis. Amplification  
15 may be performed on biological samples taken from a test patient and from an individual who is not afflicted with a cancer. The amplification reaction may be performed on several dilutions of cDNA spanning two orders of magnitude. A two-fold or greater increase in expression in several dilutions of the test patient sample as compared to the same dilutions of the non-cancerous sample is typically considered  
20 positive.

In another embodiment, the compositions described herein may be used as markers for the progression of cancer. In this embodiment, assays as described above for the diagnosis of a cancer may be performed over time, and the change in the level of reactive polypeptide(s) or polynucleotide(s) evaluated. For example, the assays may be  
25 performed every 24-72 hours for a period of 6 months to 1 year, and thereafter performed as needed. In general, a cancer is progressing in those patients in whom the level of polypeptide or polynucleotide detected increases over time. In contrast, the cancer is not progressing when the level of reactive polypeptide or polynucleotide either remains constant or decreases with time.

30 Certain *in vivo* diagnostic assays may be performed directly on a tumor. One such assay involves contacting tumor cells with a binding agent. The bound binding agent may then be detected directly or indirectly via a reporter group. Such



binding agents may also be used in histological applications. Alternatively, polynucleotide probes may be used within such applications.

As noted above, to improve sensitivity, multiple tumor protein markers may be assayed within a given sample. It will be apparent that binding agents specific  
5 for different proteins provided herein may be combined within a single assay. Further, multiple primers or probes may be used concurrently. The selection of tumor protein markers may be based on routine experiments to determine combinations that results in optimal sensitivity. In addition, or alternatively, assays for tumor proteins provided herein may be combined with assays for other known tumor antigens.

10 The present invention further provides kits for use within any of the above diagnostic methods. Such kits typically comprise two or more components necessary for performing a diagnostic assay. Components may be compounds, reagents, containers and/or equipment. For example, one container within a kit may contain a monoclonal antibody or fragment thereof that specifically binds to a tumor protein.  
15 Such antibodies or fragments may be provided attached to a support material, as described above. One or more additional containers may enclose elements, such as reagents or buffers, to be used in the assay. Such kits may also, or alternatively, contain a detection reagent as described above that contains a reporter group suitable for direct or indirect detection of antibody binding.

20 Alternatively, a kit may be designed to detect the level of mRNA encoding a tumor protein in a biological sample. Such kits generally comprise at least one oligonucleotide probe or primer, as described above, that hybridizes to a polynucleotide encoding a tumor protein. Such an oligonucleotide may be used, for example, within a PCR or hybridization assay. Additional components that may be  
25 present within such kits include a second oligonucleotide and/or a diagnostic reagent or container to facilitate the detection of a polynucleotide encoding a tumor protein.

The following Examples are offered by way of illustration and not by way of limitation.

### EXAMPLE 1

#### USE OF MOUSE ANTISERA TO IDENTIFY cDNA SEQUENCES ENCODING LUNG TUMOR ANTIGENS

5           This example illustrates the isolation of cDNA sequences encoding lung tumor antigens by screening of lung tumor cDNA libraries with mouse anti-tumor sera.

          A small cell cDNA lung tumor expression library was constructed using mRNA from the small cell carcinoma cell line NCIH69 employing the Lambda ZAP Express expression system (Stratagene, La Jolla, CA). Mouse anti-SCID mouse serum  
10 was developed by growing the lung small cell carcinoma cell lines NCIH69 and NCIH128 in SCID mice, removed SCID serum containing shed and secreted tumor antigens. These sera were pooled and injected into normal mice to produce anti-lung carcinoma serum. The antiserum was adsorbed with *E. coli* lysate and human GAPDH protein, and human PBMC lysate was added to the serum to block antibody to proteins  
15 found in normal tissue. The cDNA expression library was then screened with this anti-serum using a goat anti-mouse IgG-A-M (H+L) alkaline phosphatase second antibody developed with NBT/BCIP (Gibco BRL Labs., Gaithersburg, MD). Phage was purified and phagemid excised for clones with inserts in a pBK-CMV vector for expression in prokaryotic or eukaryotic cells.

20           The determined cDNA sequences for 76 isolated clones are provided in SEQ ID NO:1-76. Comparison of these sequences with those in the public database as described above, revealed no significant homologies to SEQ ID NO:7, 14, 21, 46 and 55. SEQ ID NO:11, 16, 20, 41, 49 and 74 were found to show some homology to previously identified expressed sequence tags (ESTs). The remaining clones were  
25 found to show some degree of homology to previously identified genes. The expression levels of certain of the isolated antigens in lung tumor tissues compared to expression levels in 36 normal tissues was determined by microarray technology. The results of these studies are shown below in Table 2, together with the database analyses for these sequences.

**Table 2**

Clone Name	SEQ ID NO:	Description	Lung Tumor Over-Expression ( $\geq 2$ )			
			LT+F/N	SCC+M/N	Squa/N	Aden/N
LSC-2	2	CDM, 6C6, BAP31/2	-	-	2.4	-
LSC-6	5	Motor protein p87/89	-	2.2	-	-
LSC-7	6	Ku autoantien 70 kDa	-	2.2	2.3	-
LSC-10	8	PIBF1 protein	-	2.4	-	-
LSC-11	9	Ku autoantien 70 kDa	-	2.4	-	-
LSC-15	11	Novel	-	-	2.9	-
LSC-29	19	Unknown DKFZp586N1020	-	2.5	-	-
LSC-33	22	10 methylene 4 hydrofolate DH	-	2.4	-	-
LSC-39	26	P1 protein	2.4	5.0	2.8	-
LSC-43	27	Minichrom maint deficient	2.3	7.1	2.8	-
LSC-46	28	Non-metastatic cell 1 NME1	2.6	2.5	2.7	2.1
LSC-49	29	GTPase act. Pro. ID- GAP	3.6	10.0	3.8	3.2
LSC-51	30	ZIC family member 2	-	3.4	-	-
LSC-55	32	Transmembrane(63 kDa) EK	2.7	2.2	4.2	2.3
LSC-64	35	Macrophage Migr Inhib Fac	2.6	3.2	3.9	-
LSC-72	38	hRif beta (p102 protein)	2.4	7.0	2.6	-
LSC-76	40	Pro Synth Init. Factor	-	-	-	2.1
LSC-78	42	Motor protein p87/89	-	2.7	2.2	-
LSC-81	43	Epidermal GFR subst 8 EPS8	-	-	2.7	2.1
LSC-101	45	Transmembrane(63 kDa) ER	2.7	-	4.3	-
LSC-103	47	Nuclear factor 4	-	4.3	2.8	-
LSC-134	51	Fumarase	-	3.6	-	-
LSC-142	52	Unknown BAC CTA363M4	-	-	2.5	-
LSC-144	53	Accessory Pro BAP31/BAP2	2.5	-	2.9	2.4
LSC-148	54	Unknown DKFZp586N1020	-	2.2	-	-
LSC-149	55	Novel / Novel	2.6	2.4	3.1	3.5
LSC-163	57	Unknown Ch8p11.2 sect2/19	-	-	-	2.4

LSC-170	58	Unknown PAC DJ0777023	2.2	3.0	2.2	-
LSC-210	74	Novel	-	2.6	2.1	-

LT+F/N = Lung Tumor plus Fetal tissue over Normal tissues

SC+M/N = Lung Small Cell carcinoma plus Metastatic over Normal tissues

Squa/N = Squamous lung tumor over Normal tissues

5 Aden/N = Adenocarcinoma over Normal tissues

## EXAMPLE 2

### ISOLATION OF LUNG TUMOR cDNA SEQUENCES

#### BY CONVENTIONAL SUBTRACTION

10 A human lung squamous cell carcinoma cDNA expression library was constructed from poly A<sup>+</sup> RNA from a pool of two patient tissues using a Superscript Plasmid System for cDNA Synthesis and Plasmid Cloning kit (BRL Life Technologies, Gaithersburg, MD) following the manufacturer's protocol. Specifically, lung carcinoma tissues were homogenized with polytron (Kinematica, Switzerland) and total RNA was  
15 extracted using Trizol reagent (BRL Life Technologies) as directed by the manufacturer. The poly A<sup>+</sup> RNA was then purified using an oligo dT cellulose column as described in Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989. First-strand cDNA was synthesized using the NotI/Oligo-dT18 primer. Double-stranded cDNA was synthesized, ligated with  
20 BstXI/EcoRI adaptors (Invitrogen, San Diego, CA) and digested with NotI. Following size fractionation with cDNA size fractionation columns (BRL Life Technologies), the cDNA was ligated into the BstXI/NotI site of pcDNA3.1 (Invitrogen) and transformed into ElectroMax *E. coli* DH10B cells (BRL Life Technologies) by electroporation.

Using the same procedure, a normal human lung cDNA expression  
25 library was prepared from a pool of normal lung, kidney, colon, pancreas, brain, resting PBMC, heart, skin and esophagus, with esophagus cDNAs making up one third of the material. For both libraries, sequence analysis showed that the majority of clones had a full length cDNA sequence and were synthesized from mRNA

cDNA library subtraction was performed using the above lung squamous  
30 cell carcinoma and normal cDNA library, as described by Hara *et al.* (*Blood*, 84:189-199, 1994) with some modifications. Specifically, a lung squamous cell carcinoma-specific subtracted cDNA library was generated as follows. To from the driver cDNA,

normal tissue cDNA library (80 µg) was digested with BamHI and XhoI, followed by a filling-in reaction with DNA polymerase Klenow fragment. After phenol-chloroform extraction and ethanol precipitation, the DNA was dissolved in 133 µl of H<sub>2</sub>O, heat-denatured and mixed with 133 µl (133 µg) of Photoprobe biotin (Vector Laboratories, Burlingame, CA). As recommended by the manufacturer, the resulting mixture was irradiated with a 270 W sunlamp on ice for 20 minutes. Additional Photoprobe biotin (67 µl) was added and the biotinylation reaction was repeated. After extraction with butanol five times, the DNA was ethanol-precipitated and dissolved in 23 µl H<sub>2</sub>O to form the driver DNA.

10 To form the tracer DNA, 10 µg lung squamous cell carcinoma cDNA library was digested with NotI and SpeI, phenol chloroform extracted and passed through Chroma spin-400 columns (Clontech, Palo Alto, CA). Typically, 5 µg of cDNA was recovered after the sizing column. Following ethanol precipitation, the tracer DNA was dissolved in 5 µl H<sub>2</sub>O. Tracer DNA was mixed with 15 µl driver DNA  
15 and 20 µl of 2 x hybridization buffer (1.5 M NaCl/10 mM EDTA/50 mM HEPES pH 7.5/0.2% sodium dodecyl sulfate), overlaid with mineral oil, and heat-denatured completely. The sample was immediately transferred into a 68 °C water bath and incubated for 20 hours (long hybridization [LH]). The reaction mixture was then subjected to a streptavidin treatment followed by phenol/chloroform extraction. This  
20 process was repeated three more times. Subtracted DNA was precipitated, dissolved in 12 µl H<sub>2</sub>O, mixed with 8 µl driver DNA and 20 µl of 2 x hybridization buffer, and subjected to a hybridization at 68 °C for 2 hours (short hybridization [SH]). After removal of biotinylated double-stranded DNA, subtracted cDNA was ligated into NotI/SpeI site of chloramphenicol resistant pBCSK<sup>+</sup> (Stratagene, La Jolla, CA) and  
25 transformed into ElectroMax *E. coli* DH10B cells by electroporation to generate a lung squamous cell carcinoma specific subtracted cDNA library (referred to as LST-69).

A cDNA library (referred to as mets3616A) was constructed from a metastatic lung adenocarcinoma. The mets3616A cDNA library was subtracted against a cDNA library prepared from a pool of normal lung, liver, pancreas, skin, kidney, brain  
30 and resting PBMC. To increase the specificity of the subtraction, the driver was spiked with genes that were determined to be most abundant in the mets3616A cDNA library, such as EF1-alpha, integrin-beta and anticoagulant protein PP4, as well as with cDNAs

that were previously found to be differentially expressed in subtracted lung adenocarcinoma cDNA libraries. The resulting subtracted library was referred to as mets3616A-S1.

The expression levels of 831 cDNAs from LST-S6 and 521 cDNAs from  
5 Mets3616A-S1 in lung tumor tissue and normal tissues was analyzed by microarray technology (Synteni, Palo Alto, CA). Briefly, the cDNAs were PCR amplified and the PCR amplification products were dotted onto slides in an array format, with each product occupying a unique location in the array. mRNA was extracted from the tissue sample to be tested, reverse transcribed, and fluorescent-labeled cDNA probes were  
10 generated. The microarrays were probed with the labeled cDNA probes, the slides scanned and fluorescence intensity was measured. This intensity correlates with the hybridization intensity. Thirty-four non-redundant cDNA clones showed 5-fold over-expression in lung tumors, compared with expression in normal tissues tested (lung, skin, lymph node, colon, liver, pancreas, breast, heart, bone marrow, large intestine,  
15 kidney, stomach, brain, small intestine, bladder and salivary gland). The determined cDNA sequences for the 34 isolated clones are provided in SEQ ID NO:77-110.

These sequences were compared to known sequences in the gene bank using the EMBL and GenBank databases. The sequences of SEQ ID NO:77, 86, 90 and  
108 were found to show some homology to previously identified expressed sequence  
20 tags (ESTs). The sequences of SEQ ID NO:78-85, 87-89, 91-107 and 109-110 were found to show some homology to previously identified genes.

The determined cDNA sequences of 54 clones isolated from lung tumor cDNA libraries that were shown to be differentially over-expressed in non-small cell lung carcinoma by are provided in SEQ ID NO:111-142 and 367-395.

25

### EXAMPLE 3

#### USE OF PATIENT SERA TO IDENTIFY DNA SEQUENCES ENCODING LUNG TUMOR ANTIGENS

30

This example illustrates the isolation of cDNA sequences encoding lung tumor antigens by expression screening of lung tumor samples with autologous patient sera.

A cDNA expression library was prepared using mRNA from the lung small cell carcinoma cell line NCIH69 in the lambda ZAP Express expression vector (Stratagene) as described above, and screened with a pool of lung small cell carcinoma patient sera. The sera pool was adsorbed with *E. coli* lysate and human PBMC lysate was added to the serum to block antibody to proteins found in normal tissue. Screening was performed as described in Sambrook et al., (*Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989), with the secondary antibody being goat anti-human IgG-A-M (H + L) conjugated with alkaline phosphatase, developed with NBT/BCIP (Gibco BRL). Positive plaques expressing immunoreactive antigens were purified. Phagemid from the plaques was rescued and the nucleotide sequences of the clones was determined.

The determined cDNA sequences of 86 isolated clones are provided in SEQ ID NO:143-228. The sequences of SEQ ID NO:153, 154, 163, 178, 186, 202, 203, 218 and 219 were found to show some homology to previously identified ESTs. The sequences of SEQ ID NO:143-152, 155-162, 164-177, 179-185, 187-201, 204-217 and 220-228 were found to show some homology to previously isolated genes. The sequences of an additional three isolated clones (referred to as SCC2-16, SCC2-28 and SCC2-62) are provided in SEQ ID NO:437-439.

The expression levels of certain of the isolated antigens in lung tumor tissues compared to expression levels in 36 normal tissues was determined using microarray technology and computer analysis. The results of these studies are shown below in Table 3, together with the database analyses for these sequences.

**Table 3**

Clone Name	SEQ ID NO:	Description	Lung Tumor Over-Expression ( $\geq 2$ )			
			LT+F/N	SC+M/N	Squa/N	Aden/N
SCC2-5	146	Unknown KIAA0878	-	3.2	-	2.2
SCC2-9	148	Tubulin K-alpha-1	-	2.2	-	-
SCC2-10	149	NY-REN-64 (pro kinase)	2.0	14.8	3.5	-
SCC2-11	150	TBP-assoc. fact. 2-170	-	5.4	-	-
SCC2-13	152	Centromere Pro F (CENPF)	2.3	5.4	2.8	-
SCC2-14	153	BRUNOL-4	2.7	9.4	3.1	2.3

SCC2-16	437	Non metastatic cells 2	2.3	2.1	2.7	-
SCC2-17	154	Novel (V87915)	2.0	-	2.8	-
SCC2-20	156	Cytoplas Linker Pro 170a2	2.1	3.0+	2.8	-
SCC2-23	157	Hypoxia-induc fact 1 a	2.2	3.0	2.7	-
SCC2-24	158	Actin gamma 1	-	3.8	2.0	-
SCC2-28	438	CHORD-containing pro 1	-	2.1	-	-
SCC2-29	160	Unk. DJ0669I17; ALR-like	2.2	4.0	3.0	2.2
SCC2-31	162	Unknown chrom 1	2.2	3.4	2.8	-
SCC2-36	165	Unknown (T20633)	3.3	2.6	5.5	3.4
SCC2-37	166	Sex-det reg Y Box 21 SOX 2	-	3.0	-	-
SCC2-43	170	CHORD-containing pro 1	-	2.1	-	-
SCC2-50	231	Hypoxia-induc fact 1 a	6.0	3.9	13.7	5.0
SCC2-51	175	Unknown KIAA1051	2.1	3.6	2.0	-
SCC2-54	178	Unknown FLJ20725	-	2.4	2.1	-
SCC2-60	181	Unknown Cosmid R32889	-	3.2	-	-
SCC2-62	439	CHORD-containing pro 1	-	2.1	-	-
SCC2-66	183	Novel, similar to transferase	-	2.2	-	-
SCC2-68	184	Ribosomal pro S7 (RPS7)	-	2.2	-	-

LT+F/N = Lung Tumor plus Fetal tissue over Normal tissues

SC+M/N = Lung Small Cell carcinoma plus Metastatic over Normal tissues

Squa/N = Squamous lung tumor over Normal tissues

5 Aden/N = Adenocarcinoma over Normal tissues

The expression levels of certain other of the isolated antigens in lung tumor tissues compared to expression levels in 36 normal tissues was determined using microarray technology and either computer or visual analysis. The results of these studies are shown below in Table 4, together with the databank analyses for these sequences. These results indicate that these antigens are over-expressed in lung tumor tissue compared to normal tissue.

10



**Table 4**

<b>Clone Name</b>	<b>SEQ ID NO:</b>	<b>Description</b>	<b>Ratio T/N Mean/Med</b>
SCC2-58	180	Sox-2	visual
SCC2-79	190	Mixed-lineage leukemia 4 / AF-6	2.0/2.0 sq
SCC2-91	194	Hepatocellular carcinoma-assoc Ag 58	visual
SCC2-100	200	F-Box protein FBW2	visual
SCC2-102	202	Novel	visual
SCC2-104	204	MAP-kinase act death domain MADD	visual
SCC2-143	214	Unknown HSPC232	2.8/2.1 sq
SCC2-266	226	HMG-2	visual

5 Ratio T/N = lung tumor tissues over normal tissues

#### **EXAMPLE 4**

#### **CLONING OF cDNAs ENCODING LUNG SMALL CELL CARCINOMA ANTIGENS**

10 Lung small cell carcinoma antigens were cloned by screening a small cell cDNA expression library with a mouse anti-SCID mouse serum. This antiserum was developed by growing lung small cell carcinoma cell lines NCIH69 and NCIH128 in SCID mice, removing SCID serum containing shed and secreted tumor antigens and immunizing normal mice with this serum. The library was constructed with mRNA  
15 from cell line NCIH128 in the lambda ZAP Express expression vector (Stratagene). The antiserum was adsorbed with *E. coli* lysate and human GAPDH protein and Ku autoantigens, and human PBMC lysate was added to the serum to block antibody to proteins found in normal tissue. Table 5 lists the data bank analyses for the nucleotide sequences. The determined cDNA sequences of the clones are provided in SEQ ID  
20 NO:258-317.

**Table 5**

SEQ ID NO.:	Clone ID #	Genbank Homologies
258	54533	Novel
259	54534	Homo sapiens mRNA for LAK-1
260	54536	Homo sapiens CGI-108 protein mRNA
261	54538	Human mRNA for HHR23A protein
262	54540	Homo sapiens chromosome 17, clone hRPC. 1030 0 14
263	55084	Homo sapiens homolog of rat elongation factor p18 (p18)
264	55086	Homo sapiens HSPC194 mRNA
265	54555	Homo sapiens accessory proteins BAP31/BAP29 (DXS1357E) mRNA
266	54557	Homo sapiens mesenchymal stem cell protein DSCD75 mRNA
267	54564	Homo sapiens prp28, U5 snRNP 100 kd protein (U5-100K) mRNA
268	55098	Novel
269	55473	Homo sapiens uroporphyrinogen III synthase (congenital erythropoietic porphyria) (UROS)
270	55104	Homo sapiens carbonyl reductase (LOC51181)
271	55105	Homo sapiens membrane component, chromosome 11, surface marker 1 (M11S1)
272	55107	H.sapiens mRNA encoding GPI-anchored protein p137
273	55108	Novel
274	55114	Homo sapiens mRNA; cDNA DKFZp56401716
275	55477	H.sapiens YB-1 gene promoter region
276	55482	Homo sapiens mRNA ; cDNA DKFZp434B0425
277	55483	Human Gu protein mRNA
278	55485	Homo sapiens 45kDa splicing factor mRNA
279	55487	Homo sapiens genomic DNA, chromosome 21q, section 72/105
280	55488	Homo sapiens chromosome 17, clone hCIT529110
281	55087	Novel (partial overlap of Unknown: Homo sapiens partial mRNA, clone c1-10e16)
282	55089	Homo sapiens scaffold attachment factor A (SAF-A) mRNA
283	55092	Homo sapiens density regulated protein drp1 mRNA
284	55093	H.sapiens mRNA encoding GPI-anchored protein p137
285	56926	Homo sapiens high-mobility group (nonhistone chromosomal) protein 17 (HMG17)
286	56930	Novel
287	56944	Homo sapiens KBNA-2 co-activator (100kD) (p100), mRNA
288	56945	Novel
289	55490	Homo sapiens death-associated protein 6 (DAXX) mRNA, and translated products.

SEQ ID NO.:	Clone ID #	Genbank Homologies
290	55495	Homo sapiens mRNA for MEGF6
291	55504	Mus musculus hairy / enhancer of split 6 mRNA
292	55506	Novel / (136bp: Mus musculus mRNA for Rab24 protein)
293	56480	Novel
294	56482	H.sapiens DNA from chromosome 19-cosmids R31158, R31874, & R28125, genomic seq.
295	56484	Novel
296	56487	Human L23 mRNA for putative ribosomal protein
297	56488	Homo sapiens cDNA FLJ10526 fis, clone NT2RP2000931, highly similar to MATRN 3
298	56490	Homo sapiens Sul1 isolog mRNA
299	56493	Novel
300	56494	Homo sapiens mRNA; cDNA DKFZp564B167 (from clone DKFZp564B167)
301	56495	Homo sapiens 12p13.3 BAC RPC111-543P15 (Roswell Park Cancer Inst. Human BAC lib.)
302	56499	Human DNA-binding protein B (dbpB) gene, 3' end
303	56517	Homo sapiens esterase D mRNA
304	56952	Homo sapiens 14q32 Jagged2 gene, complete cds; and unknown gene
305	56953	Homo sapiens DNA polymerase zeta catalytic subunit (REV3L) mRNA
306	56959	Novel
307	57139	Homo sapiens ribosomal protein, large, PO (RPLPO) mRNA
308	57078	Homo sapiens alpha-tubulin isoform 1 mRNA
309	57092	Novel
310	57099	Homo sapiens uncharacterized hypothalamus protein HBEX2 mRNA
311	57100	Novel (last 120 bp: Unknown: Canine 21 kDa Signal peptase subunit mRNA)
312	57105	Homo sapiens splicing factor, arginine/serine-rich 7 (35kD) (SFRS7)
313	57111	Human chromosome 14 DNA sequence
314	57117	Human DNA sequence from cosmid V857G56, between markers DXS366 and DXS87 on chromosome X contains ESTs
315	57121	Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 3/11
316	57124	H.sapiens MLN50 mRNA
317	57125	Homo sapiens calreticulin (CALR) , mRNA

EXAMPLE 5cDNAs ENCODING LUNG SMALL CELL CARCINOMA ANTIGENS

Lung small cell carcinoma antigens were cloned by screening a small cell  
 5 cDNA library (NCIH 128) with small cell carcinoma patient sera. The library was  
 constructed with mRNA from cell line NICH 128 in the lambda ZAP Express expression  
 vector (Stratagene). The antiserum was adsorbed with *E. coli* lysate and human  
 GAPDH protein, and human PBMC lysate was added to the serum to block antibody to  
 proteins found in normal tissue. Table 6 lists the homologies identified by database  
 10 analyses for nucleotide sequences shown in SEQ ID NO:318-364. An additional  
 isolated cDNA sequence (referred to as SCC3-90) is provided in SEQ ID NO:440.

Table 6

SEQ ID NO:	Clone ID #	Genbank Homologies
318	54800	Human Ig germline H-chain G-E-A region B
319	54802	Human mRNA for T-cell cyclophilin
320	54803	Unknown BAC clone GS1-11E15
321	54805	Unknown Homo sapiens cDNA FLJ20272 fis
322	54806	Unknown Homo sapiens mRNA for KIAA0713 protein
323	54809	Unknown Homo sapiens mRNA for RIE2 sid2705
324	54810	Homo sapiens glutamyl-prolyl-tRNA synthetase
325	54813	Unknown Human mRNA for KIAA0262 gene
326	54814	Hu.vacuolar proton pump delta polypeptide (VATD) mRNA
327	54816	Unknown Homo sapiens mRNA for KIAA0713 protein
328	54817	Unknown Hu.Chromosome 16 BAC clone CIT987SK-A-101F10
329	54819	Homo sapiens chromokinesin KIF4 (KIF4) mRNA
330	54821	Unknown Homo sapiens cDNA FLJ11101 fis
331	54823	Human mRNA for heat shock protein hsp86
332	54824	hinge=OXPHOS system complex III mitochondrial subunit
333	54825	H.sapiens mRNA for huntingtin interacting protein HIP-I
334	54826	Homo sapiens kinesin light chain mRNA
335	54827	Homo sapiens kinesin light chain mRNA
336	54829	Novel
337	54830	Unknown complete sequence
338	54832	Unknown Homo sapiens cDNA FLJ20272 fis
339	55800	Homo sapiens mRNA for E-MAP-115/105

SEQ ID NO:	Clone ID #	Genbank Homologies
340	55801	Hu. U-snRNP-associated cyclophilin (USA-CyP) mRNA
341	55803	Human chromosome 14 DNA sequence
342	55804	Human thymosin beta-4 mRNA
343	55805	Homo sapiens huntingtin interacting protein 1 (HIP1)
344	55806	Hu. protein kinase, interferon-inducible double stranded RNA
345	55808	Homo sapiens glutathione S-transferase A4 (GSTA4) mRNA
346	55810	Human chromosome 14 DNA sequence
347	55811	Unknown Homo sapiens mRNA for KIAA0713 protein
348	55812	Novel
349	55814	Human poly(ADP-ribose) synthetase mRNA
350	55816	Novel
351	55817	Homo sapiens centromere protein E (CENPE) mRNA
352	55819	Human poly(ADP-ribose) polymerase mRNA
353	55820	Novel
354	55823	Human mRNA for heat shock protein hsp86
355	55824	Novel
356	55826	Homo sapiens SOX18 mRNA, complete cds
357	55828	Novel
358	55829	Novel
359	55831	Unknown BAC sequence from the SPG4 candidate region
360	55832	Homo sapiens heat shock transcription factor 2 (HSF2)
361	55833	Homo sapiens vacuolar H-ATPase subunit D mRNA
362	55834	Homo sapiens clone 628 unknown mRNA
363	55835	Human mRNA for Cu/Zn superoxide dismutase (SOD).
364	55838	Homo sapiens cDNA FLJ20473 fis, clone KAT07092

The expression levels of certain of the isolated antigens in lung tumor tissues compared to expression levels in 36 normal tissues was determined using microarray technology and either computer or visual analysis. The results of these studies are shown below in Table 7, together with the databank analyses for these sequences. These results indicate that these antigens are over-expressed in lung tumor tissue compared to normal tissue.

**Table 7**

Clone Name	SEQ ID NO:	Description	Ratio T/N Mean/Med
SCC3-5	320	Novel	visual
SCC3-7	321	=SCC3-52; Unknown FLJ20272	visual
SCC3-17	325	Ring finger protein 10	2.1/3.0 ad
SCC3-30	330	Unknown FLJ11101	visual
SCC3-52	338	Unknown cDNA FLJ20272	2.7/1.2 sm
SCC3-64	340	U-snRNP-assoc. cyclophilin	visual
SCC3-71	341	TNG-2	visual
SCC3-79	345	GST A4	visual
SCC3-87	349	Poly(ADP-ribose) synthetase	visual
SCC3-90	440	Polyadenylate binding pro (TIA-1)	visual
SCC3-111	359	Unknown BAC	visual
SCC3-112	360	Heat-shock transcription factor 2	visual

5 Ratio T/N = lung tumor tissues over normal tissues

#### **EXAMPLE 6**

##### **ANALYSIS OF CDNA EXPRESSION USING MICROARRAY TECHNOLOGY**

In additional studies, sequences disclosed herein were found to be  
 10 overexpressed in specific tumor tissues as determined by microarray analysis. Using this approach, cDNA sequences are PCR amplified and their mRNA expression profiles in tumor and normal tissues are examined using cDNA microarray technology essentially as described (Shena *et al.*, 1995). In brief, the clones are arrayed onto glass slides as multiple replicas, with each location corresponding to a unique cDNA clone  
 15 (as many as 5500 clones can be arrayed on a single slide, or chip). Each chip is hybridized with a pair of cDNA probes that are fluorescence-labeled with Cy3 and Cy5, respectively. Typically, 1 $\mu$ g of polyA<sup>+</sup> RNA is used to generate each cDNA probe. After hybridization, the chips are scanned and the fluorescence intensity recorded for both Cy3 and Cy5 channels. There are multiple built-in quality control steps. First, the  
 20 probe quality is monitored using a panel of ubiquitously expressed genes. Secondly, the control plate also can include yeast DNA fragments of which complementary RNA may be spiked into the probe synthesis for measuring the quality of the probe and the sensitivity of the analysis. Currently, the technology offers a sensitivity of 1 in 100,000

copies of mRNA. Finally, the reproducibility of this technology can be ensured by including duplicated control cDNA elements at different locations.

Clones SCC2-5 (SEQ ID NO:229), SCC2-14 (SEQ ID NO:230), SCC2-50 (SEQ ID NO:231) and SCC2-51 (SEQ ID NO:232) were found to be overexpressed  
5 by microarray analysis in adenocarcinoma, lung pleural effusion, squamous cell carcinoma, small cell carcinoma, colon tumor, and ovarian tumor, with low levels of expression being detected in all normal tissues tested. The normal tissues included in the microarray were lymph node, salivary gland, lung, bladder, bone marrow, bronchus, esophagus, kidney, heart, liver, lung, skeletal muscle, spleen, stomach, PBMC, skin,  
10 thymus, tonsil, trachea, pituitary gland, adrenal gland, brain, pancreas, thyroid gland, adult lung, colon, small intestine, ovary, and peritoneal epithelium. These cDNAs were cloned from a lung small cell carcinoma expression library using small cell carcinoma patient sera as a probe. SCC2-14 has some similarity to an RNA-binding protein, and SCC2-50 is homologous to hypoxia-inducible factor 1 alpha. Amino acid sequences  
15 encoded by these cDNAs (SEQ ID Nos:229-232) are shown in SEQ ID NOs:233-236, respectively.

Also by microarray analysis, SCC2-54 (SEQ ID NO:178) was found to be over expressed in lung small cell and squamous carcinomas relative to normal tissues. An extended cDNA sequence for this clone is provided in SEQ ID NO:396,  
20 encoding the polypeptide sequence set forth in SEQ ID NO:397.

LSC-49 (SEQ ID NO:29) was found to be overexpressed in lung carcinomas, particularly small cell lung carcinomas. An extended sequence for this clone is provided in SEQ ID NO:412, encoding an amino acid sequence set forth in SEQ ID NO:413. Database searches of LSC-49 revealed sequence homology with a  
25 GTPase-activating protein for Rac (mgcRacGAP).

The results of an additional microarray analysis, performed using a criteria of greater than or equal to 2-fold over-expression in tumors and the average expression in normal tissues less than or equal to 0.2 (range from 0.01-10), are summarized in Table 8 below.

**Table 8**

Chip #	Clone ID #	Ratio	Mean Signal 1	Mean Signal 2	SEQ ID NO:
5	56908	3.78	0.837	0.221	398, 243
5	56911	2.29	0.453	0.198	399, 245
5	56912	2.57	0.265	0.103	400, 247
5	56913	2.21	0.306	0.138	401, 249
5	56916	2.44	0.449	0.184	402, 251
5	56917	2.29	0.479	0.209	403, 252
5	56921	2.54	0.418	0.165	404, 253
5	56922	5.05	0.613	0.121	405, 255
5	56923	2.74	0.426	0.155	406, 257

5           The ratio of signal 1 to signal 2 in Table 8 above provides a measure of the level of expression of the identified sequences in tumor versus normal tissues. For example, for SEQ ID NO:398, the tumor-specific signal was 3.78 times that of the signal for the normal tissues tested; for SEQ ID NO:399, the tumor-specific signal was 2.29 times that of the signal for normal tissues, etc.

10          Results from an additional microarray analysis, performed using visual analysis for identifying cDNAs over-expressed in selected tumor samples, are provided in Table 9 below. Some of these cDNAs were preferentially over-expressed in small cell lung carcinoma (SCLC) samples even though the original cDNAs were identified from subtracted NSCLC tumor samples.



**Table 9**

Chip #	Clone ID #	Ratio	Mean Signal 1	Mean Signal 2	SEQ ID NO:
5	60974	3.84	0.584	0.152	407
5	60976	3.73	0.58	0.155	408
5	60977	3.84	0.492	0.128	409
5	60978	4.63	0.476	0.103	410
5	60980	3.4	0.557	0.164	411

- 5 In further studies, the expression levels of certain of the isolated antigens in lung tumor tissues previously disclosed in Example 4 were compared to the expression levels in 36 normal tissues using microarray technology and computer analysis. The results of these studies are shown below in Table 10.

**Table 10**

Clone Name	Clone ID #	SEQ ID NO:	Squa/N	Aden/N	SC/N
LSCC2-1	54533	258	3	2	1
LSCC2-2	54534	259	5	3	5
LSCC2-4	54536	260	3	2	2
LSCC2-8	54540	262	0	3	2
LSCC2-18	55084	263	2	2	1
LSCC2-23	54555	265	2	3	3
LSCC2-25	54557	266	2	1	1
LSCC2-32	54564	267	2	3	2
LSCC2-48	55473	269	4	2	1
LSCC2-58	55104	270	3	5	2
LSCC2-61	55107	272	2	5	3
LSCC2-75	55483	277	2	4	2
LSCC2-79	55487	279	3	2	2
LSCC2-93	55089	282	5	4	4
LSCC2-121	55490	289	4	2	2
LSCC2-127	55495	290	2	4	1
LSCC2-137	55504	291	0	3	8
LSCC2-139	55506	292	3	4	1
LSCC2-161	56480	293	3	2	1
LSCC2-164	56482	294	2	4	2
LSCC2-171	56488	297	6	4	5
LSCC2-178	56494	300	3	5	3
LSCC2-191	56517	303	5	2	2

- 5 Squa/N = Squamous lung tumor over Normal tissues  
 Aden/N = Adenocarcinoma over Normal tissues  
 SC/N = Lung Small Cell carcinoma over Normal tissues

10

**EXAMPLE 7****FURTHER CHARACTERIZATION OF THE LUNG TUMOR ANTIGEN L43E**

- The predicted protein sequence shown in SEQ ID NO:436 represents a second open reading frame (ORF-2) encoded by the SCC2-51 cDNA nucleotide sequence (also referred to as L43E). The SCC2-51 nucleotide sequence is shown in
- 15 SEQ ID NO:175. This protein sequence has 33% identity and 49% similarity to the polypeptide of the fish Takifugu rubripes retrotransposon. Motif searches indicate potential protease signatures and protein translocation analysis indicates that the protein

could be cytoplasmic or membrane-associated due to a potential transmembrane region. Using realtime PCR, SCC2-51 was found to be over-expressed in primary small cell carcinoma and in atypical carcinoid metastatic tumors, but weakly expressed in other lung carcinomas and normal tissues except for pituitary gland and adrenal gland. The  
5 cDNA sequence and ORF-1 have homology to Takifugu rubripes gag polyprotein (28% identity and 45% similarity).

### EXAMPLE 8

#### ISOLATION OF cDNA SEQUENCES FOR ADDITIONAL LUNG TUMOR ANTIGENS

10 Additional cDNA clones were obtained from analysis II of LST-S6 and Mets3616-S1 libraries of Lung Chip V. These cDNAs were differentially expressed in lung squamous and/or adenocarcinoma tumors (greater than or equal to 2 fold), and the average expression values for these clones in normal tissues were below 0.1 (the range of value was between 0.001 and 10). A total of 29 non-redundant cDNA sequences were  
15 isolated and are disclosed in SEQ ID NO:367-395. A summary of these clones with respect to the Genbank searches is shown in Table 11.

**Table 11**

<u>SEQ ID NO:</u>	<u>Clone ID #</u>	<u>Chip #</u>	<u>GenBank</u>
367	49949	5	Novel
368	49952	5	Collagen type IV alpha-5
370	49960	5	h. mRNA for Pirin, isolate 17
371	49961	5	vector/Novel
372 and 373	49962	5	HBP, heme binding protein
374	49965	5	h. testitin
375	49966	5	KIAA 1077
376	49977	5	Cyclin B homologue
377	49975	5	Cat Eye 22q11.2
378	49982	5	Novel
379	49986	5	Novel
380	49988	5	KIAA0292, similar to AR1 protein
381	49993	5	transferrin receptor
382	49995	5	Cathepsin B
383	49996	5	RP3, similar to mouse tctex-1
384	49999	5	Novel, Cosmid g1572c198
385	50006	5	sheep and mouse <i>sox2</i> gene (HMG box, germ cell)
386	50007	5	Nrf3 for NF-E2 related factor 3
387	50009	5	vector/Novel, chrom. 10 seq
388	50014	5	clone RP5-1025A1 on 20p11.21
389	50016	5	Failed/h. MEGF9
390	50017	5	NH0160k17
391	50019	5	None
392	50022	5	h mitotic kinesin-like protein-1
393	50023	5	KIAA1077
394	50024	5	None
395	50033	5	None

### EXAMPLE 9

#### REAL-TIME PCR ANALYSIS OF L578S

5           As previously shown in Example 2, clone 48137 (SEQ ID NO:89), which is also referred to as L578S, and is predicted to have an extended cDNA sequence of SEQ ID NO:365, was shown to be 5-fold over-expressed in lung tumors as compared to the normal tissue by microarray analysis. Real-time PCR analysis confirmed that L578S is over-expressed in both lung squamous and adenocarcinoma  
10 tumors. Database analysis identified two human proteins showing some degree of homology to L578S, one corresponding to a putative type Ib membrane-bound protein. Protein alignment between this protein and SEQ ID NO:365 indicated that L578S full-length protein may also be a type Ib membrane-protein. This indicates that L578S is an attractive target for the development of antibody-based therapeutics.

15

### EXAMPLE 10

#### SYNTHESIS OF POLYPEPTIDES

20           Polypeptides are synthesized on a Perkin Elmer/Applied Biosystems Division 430A peptide synthesizer using Fmoc chemistry with HPTU (O-Benzotriazole-N,N,N',N'-tetramethyluronium hexafluorophosphate) activation. A Gly-Cys-Gly sequence is attached to the amino terminus of the peptide to provide a method of conjugation, binding to an immobilized surface, or labeling of the peptide. Cleavage  
25 of the peptides from the solid support is carried out using the following cleavage mixture: trifluoroacetic acid:ethanedithiol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for 2 hours, the peptides are precipitated in cold methyl-t-butyl-ether. The peptide pellets are then dissolved in water containing 0.1% trifluoroacetic acid (TFA) and lyophilized prior to purification by C18 reverse phase HPLC. A gradient of 0%-  
30 60% acetonitrile (containing 0.1% TFA) in water (containing 0.1% TFA) is used to elute the peptides. Following lyophilization of the pure fractions, the peptides are

characterized using electrospray or other types of mass spectrometry and by amino acid analysis.

From the foregoing it will be appreciated that, although specific  
5 embodiments of the invention have been described herein for purposes of illustration, various modifications may be made without deviating from the spirit and scope of the invention. Accordingly, the invention is not limited except as by the appended claims.

## CLAIMS

1. An isolated polynucleotide comprising a sequence selected from the group consisting of:

(a) sequences provided in SEQ ID NO:1-232, 243-396, 398-412, 414-424 and 437-440;

(b) complements of the sequences provided in SEQ ID NO:1-232, 243-396, 398-412, 414-424 and 437-440;

(c) sequences consisting of at least 20 contiguous residues of a sequence provided in SEQ ID NO:1-232, 243-396, 398-412, 414-424 and 437-440;

(d) sequences that hybridize to a sequence provided in SEQ ID NO:1-232, 243-396, 398-412, 414-424 and 437-440, under moderately stringent conditions;

(e) sequences having at least 75% identity to a sequence of SEQ ID NO:1-232, 243-396, 398-412, 414-424 and 437-440;

(f) sequences having at least 90% identity to a sequence of SEQ ID NO:1-232, 243-396, 398-412, 414-424 and 437-440; and

(g) degenerate variants of a sequence provided in SEQ ID NO:1-232, 243-396, 398-412, 414-424 and 437-440.

2. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of:

(a) SEQ ID NO:229-232, 237-242, 397, 413 and 425-436;

(b) sequences encoded by a polynucleotide of claim 1; and

(c) sequences having at least 70% identity to a sequence encoded by a polynucleotide of claim 1; and

(d) sequences having at least 90% identity to a sequence encoded by a polynucleotide of claim 1.

3. An expression vector comprising a polynucleotide of claim 1 operably linked to an expression control sequence.

4. A host cell transformed or transfected with an expression vector according to claim 3.

5. An isolated antibody, or antigen-binding fragment thereof, that specifically binds to a polypeptide of claim 2.

6. A method for detecting the presence of a cancer in a patient, comprising the steps of:

- (a) obtaining a biological sample from the patient;
- (b) contacting the biological sample with a binding agent that binds to a polypeptide of claim 2;
- (c) detecting in the sample an amount of polypeptide that binds to the binding agent; and
- (d) comparing the amount of polypeptide to a predetermined cut-off value and therefrom determining the presence of a cancer in the patient.

7. A fusion protein comprising at least one polypeptide according to claim 2.

8. An oligonucleotide that hybridizes to a sequence recited in SEQ ID NO:1-232, 243-396, 398-412, 414-424 and 437-440 under moderately stringent conditions.

9. A method for stimulating and/or expanding T cells specific for a tumor protein, comprising contacting T cells with at least one component selected from the group consisting of:

- (a) polypeptides according to claim 2;
- (b) polynucleotides according to claim 1; and
- (c) antigen-presenting cells that express a polypeptide according to claim 1,



under conditions and for a time sufficient to permit the stimulation and/or expansion of T cells.

10. An isolated T cell population, comprising T cells prepared according to the method of claim 9.

11.. A composition comprising a first component selected from the group consisting of physiologically acceptable carriers and immunostimulants, and a second component selected from the group consisting of:

- (a) polypeptides according to claim 2;
- (b) polynucleotides according to claim 1;
- (c) antibodies according to claim 5;
- (d) fusion proteins according to claim 7;
- (e) T cell populations according to claim 10; and
- (f) antigen presenting cells that express a polypeptide according to claim 2.

12. A method for stimulating an immune response in a patient, comprising administering to the patient a composition of claim 11.

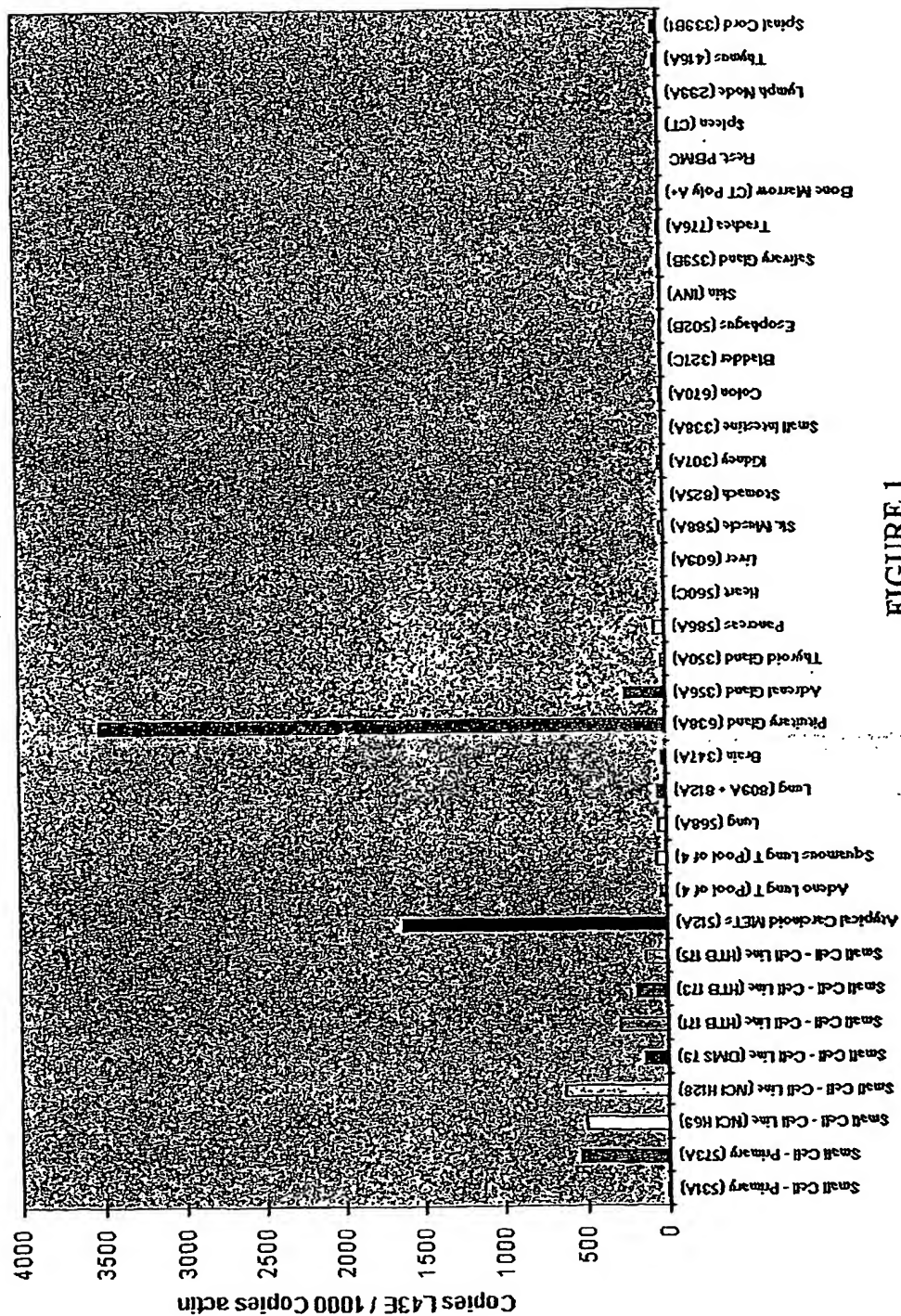
13. A method for determining the presence of a cancer in a patient, comprising the steps of:

- (a) obtaining a biological sample from the patient;
- (b) contacting the biological sample with an oligonucleotide according to claim 8;
- (c) detecting in the sample an amount of a polynucleotide that hybridizes to the oligonucleotide; and
- (d) compare the amount of polynucleotide that hybridizes to the oligonucleotide to a predetermined cut-off value, and therefrom determining the presence of the cancer in the patient.

14. A diagnostic kit comprising at least one oligonucleotide according to claim 8.

15. A diagnostic kit comprising at least one antibody according to claim 5 and a detection reagent, wherein the detection reagent comprises a reporter group.

**L43E: SC2-51**



## SEQUENCE LISTING

<110> Corixa Corporation  
Lodes, Michael J.  
Wang, Tongtong  
Mohamath, Raodoh  
Indirias, Carol Y.

<120> COMPOSITIONS AND METHODS FOR THE THERAPY  
AND DIAGNOSIS OF LUNG CANCER

<130> 210121.512PC

<140> PCT

<141> 2001-04-11

<160> 440

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 567

<212> DNA

<213> Homo sapien

<400> 1

gaattcgggc	acgaggcagc	gctctcggtt	gcagtaccca	ctggaaggac	ttaggcgctc	60
gcgtggacac	cgcaagcccc	tcagtagcct	cggcccaaga	ggcctgcttt	ccactcgcta	120
gccccgcggg	gggtccgtgt	cctgtctcgg	tggccggacc	cgggcccag	cccagcagc	180
agccggcgcc	atgtcgggtg	tgggcataga	cctgggcttc	cagagctgct	acgtcgctgt	240
ggcccgccgc	ggcgccatcg	agaatctcgc	taattgattt	agcgacccgt	gcacgcggcc	300
ttgcatttct	tttggctcta	agaatcgctc	aattggagca	gcagctaaaa	gccaggtaat	360
ttctaattgca	aagaacacag	tccaaggatt	taaaagattc	catggccgag	cattctctga	420
tccattttgtg	gaggcagaaa	aatctaacct	tgcataatgat	attgtgcagt	tgcctacagg	480
attaacagggt	ataaagggtga	catatatgga	ggaagagcga	aattttacca	ctgagcaagt	540
gactgccatg	cttttgtcca	aactgaa				567

<210> 2

<211> 413

<212> DNA

<213> Homo sapien

<400> 2

gaattcggta	cgagtgcacg	ttgactgtgg	gaaactcgga	aacaagctca	catcttcctg	60
tgggaaacct	tctagcaaca	ggatgagtct	gcagtggact	gcagttgcca	ccttcctcta	120
tgcggaggtc	tttgttgtgt	tgtttctctg	cattcccttc	atttctccta	aaagatggca	180
gaagattttc	aagtcccggc	tgggtggagt	gttagtgtcc	tatggcaaca	ccttctttgt	240
ggtttctcatt	gtcatccttg	tgtgtttggt	catcgatgcc	gtgcgcgaaa	ttcggaagta	300
tgatgatgtg	acggaaaaagg	tgaacctcca	gaacaatccc	ggggccatgg	agcacttcca	360
catgaagctt	ttccgtgccc	agaggaatct	ctacattgct	ggcttttcct	tgc	413

<210> 3

<211> 567

<212> DNA

<213> Homo sapien

<400> 3

2

&lt;400&gt; 3

gaattcggca	cgaggtcgcc	tgagaggtat	cacctcttct	gggctcaaga	tggaacaaca	60
gaagcgctg	gcctacgcca	tcattccagtt	cctgcatgac	cagctccggc	acgggggcct	120
ctcgtccgat	gctcaggaga	gcttggaggt	cgccatccag	tgcttgaga	ctgcgtttgg	180
gggtacggta	gaagacagt	accttgcgt	ccctcagact	ctgccggaga	tatttgaagc	240
ggctgccacg	ggcaaggaga	tgccgcagga	cctgaggagc	ccagcgcgaa	ccccgccttc	300
cgaggaggac	tcagcagagg	cagagcgct	caaaaccgaa	ggaaacgagc	agatgaaagt	360
ggaaaacttt	gaagctgccg	tgcatctcta	cggaaaagcc	atcgagctca	acccagccaa	420
cgccgtctat	ttctgcaaca	gagccgcagc	ctacagcaaa	ctcggcaact	acgcaggcgc	480
gggtgcaggac	tgtgagcggg	ccatctgcat	tgaccgggcc	tacagcaagg	cctacggcag	540
gatgggcctg	gcgtcttca	gcctcaa				567

&lt;210&gt; 4

&lt;211&gt; 454

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 4

gaattcggca	cgagctcccg	gccagctcgc	cttatttagt	gtctctgaca	aaaccggcct	60
tgtggaattt	gcaagaaacc	tgaccgctct	tggtttgaat	ctggtcgctt	ccggagggac	120
tgcaaaagct	ctcagggatg	ctggtctggc	agtcagagat	gtctctgagt	tgacgggatt	180
tctgaaatg	ttggggggac	gtgtgaaaac	tttgcacact	gcagtcctatg	ctggaatcct	240
agctcgtaat	attccagaag	ataatgctga	catggccaga	cttgatttca	atcttataag	300
agttgttgcc	tgcaatctct	atccctttgt	aaagacagt	gcttctccag	gtgtaactgt	360
tgaggaggct	gtggagcaaa	ttgacattgg	tggagtaacc	ttactgagag	ctgcagccaa	420
aaccacgctc	gagtgcagct	ggtgtgtgaa	ccag			454

&lt;210&gt; 5

&lt;211&gt; 424

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 5

gaattcggca	cgagggcagc	tcgagtcac	cagcagcgcc	gtccgcttga	ccgagatgct	60
gcgggcctgt	cagttatcgg	gtgtgaccgc	cgccgcccag	agttgtctct	gtgggaagtt	120
tgctctccgt	ccattgcgac	catgcgcag	atactctact	tcaggcagct	ctgggttgac	180
tactggcaaa	attgctggag	ctggcctttt	gtttgttgg	ggaggtattg	gtggcactat	240
cctatatgcc	aaatgggatt	cccatttccg	ggaaagtgt	gagaaaacca	taccttactc	300
agacaaaactc	ttcgagatgg	ttcttgggtc	tcagccttat	aatgttccat	tgccaaagaa	360
atcgattcag	tcgggtccac	taaaaatctc	tagtgtatca	gaagtaatga	aagaatctaa	420
acag						424

&lt;210&gt; 6

&lt;211&gt; 515

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 6

gaattcggca	cgagccaaag	tgtgtacatc	agtaagatca	taagcagtga	tcgagatctc	60
ttggctgtgg	tggtctatgg	taccgagaaa	gacaaaaatt	cagtgaattt	taaaaatatt	120
tacgtcttac	aggagctgga	taatccaggt	gcaaaacgaa	ttctagagct	tgaccagttt	180
aaggggcagc	agggacaaaa	acgtttccaa	gacatgatgg	gccacggatc	tgactactca	240
ctcagtgaag	tgctgtgggt	ctgtgccaac	ctcttttagt	atgtccaatt	caagatgagt	300
cataagagga	tcattgctgtt	caccaatgaa	gacaaccccc	atggcaatga	cagtgccaaa	360
gccagccggg	ccaggaccaa	agccggtgat	ctccgagata	caggcatctt	ccttgacttg	420
atgcacctga	agaaacctgg	gggctttgac	atatccttgt	tctacagaga	tatcatcagc	480
atagcagagg	atgaggacct	cagggttcac	tttga			515

3

<210> 7  
<211> 566  
<212> DNA  
<213> Homo sapien

<400> 7  
gaattcggca cgaggggacgc ggaggcgctg ggcgcacggc gcggagccag ccggagctcg 60  
aggccggcgg cggcgggaga gcgacccggg cggcctcgta gcggggcccc ggatccccga 120  
gtggcggccg gagcctcgaa aagagattct cagcgtgat tttagatga tgggcttggg 180  
aaacgggctg cgcagcatga agtcgccgcc cctcgtgctg gccgccctgg tggcctgcat 240  
catcgtcttg ggcttcaact actggattgc gagctcccg agcgtggacc tccagacacg 300  
gatcatggag ctggaaggca gggtcgcgag ggcggctgca gagagaggcg ccgtggagct 360  
gaagaagaac gagttccagg gagagctgga gaagcagcgg gagcagcttg acaaaatcca 420  
gtccagccac aacttccagc tggagagcgt caacaagctg taccaggacg aaaaggcggt 480  
tttggtgaat aacatcacca cagggtgagag gctcatccga gtgctgcaag accagttaaa 540  
gacctgcag aggaattacg gcaggc 566

<210> 8  
<211> 515  
<212> DNA  
<213> Homo sapien

<400> 8  
gaattcggca cgagctgtcc tccttgccgg tgccggagatg gttgtcttgg ttacgggtcc 60  
taacgggtccc ctgccttgaa atcccttgtt gagggcctgc aaccttgtgc ttccgactgg 120  
agacgccttt ggtccctcgg tgtctgcaact ggctgctggt caaggcttca gtgtggagta 180  
attgacactt tcgagaatat taaaatcaaa ttagagaaga aaactgatcc ataataataa 240  
aaatgtctcg aaaaatttca aaggagtcaa aaaaagtga catctctagt tctctggaat 300  
ctgaagatat tagtttagaa acaacagttc ctacggatga tatttcctca tcagaagagc 360  
gagagggcaa agtcagaatc accaggcagc taattgaacg aaaagactac ttcataatat 420  
tcagttacta aaaattgagc tatcccagaa aactatgatg atcgacaatt tgaaagtgga 480  
ttatcttaca aagattgaag aattggaggga gaaac 515

<210> 9  
<211> 415  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)... (415)  
<223> n = A,T,C or G

<400> 9  
gaattcggca cgaggctcgtc ttctgtccaa gttggtcgct tccttgcgcc aaagtgagca 60  
gtagccaaca tgtcagggtg ggagtcatat tacaaaaccg agggcgatga agaagcagag 120  
gaagaacaag aagagaacct tgaagcaagt ggagactata aatattcagg aagagatagt 180  
ttgatttttt tggttgatgc ctccaaggct atgtttgaat ctgagagtga agatgagttg 240  
acaccttttg acatgagcat ccagtgtatc caaagtgtgt acatcagtaa gatcataagc 300  
agtgatcgag atctcttggc tgtggtgttc tatggtaccg agaaagacaa aaattcantg 360  
aattttaaaa atatttacct cttacaggag ctggataatt cagggtgcaa acnaa 415

<210> 10  
<211> 565  
<212> DNA  
<213> Homo sapien

<400> 10  
gaattcggca cgagctcggg cagccttgtg cccgaaggag gaaacagtga cagacctgga 60

4

gactgcagtt	ctctatcctt	cacacagctc	tttcaccatg	cctggatcac	ttcctttgaa	120
tgcagaagct	tgctggccaa	aagatgtggg	aattgttgcc	cttgagatct	attttccttc	180
tcaatatgtt	gatcaagcag	agttggaaaa	atatgatggt	gtagatgctg	gaaagtatac	240
cattggcttg	ggccaggcca	agatgggctt	ctgcacagat	agagaagata	ttaactctct	300
ttgcatgact	gtggttcaga	atcttatgga	gagaaataac	ctttcctatg	attgcattgg	360
gcggtcgaa	gttggaaacag	agacaatcat	cgacaaatca	aagtctgtga	agactaattt	420
gatgcagctg	tttgaagagt	ctgggaatac	agatatagaa	ggaatcgaca	caactaatgc	480
atgctatgga	ggcacagctg	ctgtcttcaa	tgctgttaac	tggattgagt	ccagctcttg	540
ggatggacgg	tatgccctgg	tagtt				565

<210> 11  
 <211> 505  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(505)  
 <223> n = A,T,C or G

<400> 11						
gaattcggca	cgaggcagcg	acagactcgg	ggtgctggca	gcggcagccc	acgcctccca	60
gggattgcag	gcctgggcgc	cgggggttga	ccagtctccc	gggcatggca	cgccctgggt	120
attctgtacc	cgtgatttgt	ggcggggcaa	gacgttaagt	tgggtgacac	cgaggtgagc	180
cacggctctc	ggcaccagat	gaggaaccac	tgtctcaata	agtgcacca	gtgatgctgt	240
taaacaaggga	caatccggtt	catggattgt	gacaacgcac	gctgacatca	agcagaccct	300
gccgtcaggt	acagagggca	ccacagtgc	caggaactgc	tgtcctttca	taccangttt	360
tangaggctt	taccanaagg	aatggaaaat	gctggtgggc	aagtaagatt	gaaacagcat	420
ctgaggactg	gttctgcaca	aaaccttaaa	ttcttcaagg	actttgacat	ttgtttattc	480
ttgtaacaaa	ttaaaacctt	ttctt				505

<210> 12  
 <211> 513  
 <212> DNA  
 <213> Homo sapien

<400> 12						
gaattcggca	cgaggcgcca	cgatgtccgg	ggagtcagcc	aggagcttgg	ggaagggaa	60
cgcgcccccg	gggcccgtcc	cggagggtcc	gatccgcac	tacagcatga	ggttctgccc	120
gtttgtgag	aggacgcgtc	tagtcctgaa	ggccaaggga	atcaggcatg	aagtcaccaa	180
tatcaacctg	aaaaataagc	ctgagtgggt	ctttaagaaa	aatccctttg	gtctggtgcc	240
agttctggaa	aacagtcagg	gtcagctgat	ctacagctct	gccatcacct	gtgagtacct	300
ggatgaagca	taccaggga	agaagctggt	gccggatgac	ccctatgaga	aagcttgcca	360
gaagatgatc	ttagagttgt	tttctaaggt	gccatccttg	gtaggaagct	ttattagaag	420
ccaaaataaa	gaagactatg	atggcctaaa	agaagaattt	cgtaaagaat	ttaccaagct	480
agaggaggtt	ctgactaata	agaagacgac	ctt			513

<210> 13  
 <211> 375  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(375)  
 <223> n = A,T,C or G

<400> 13						
gaattcggca	cgaggcagcc	ccagtgcgga	gggaggagac	tgccgcgaca	tggagctggt	60

## 5

cctcgcgggc	cgccgggtgc	tggtcaccgg	ggcaggcaaa	ggtatagggc	gcggcacggg	120
ccaggcgctg	cacgcgacgg	gcgcgcgggt	ggtggctgtg	agccggactc	aggcggatct	180
tgacagcctt	gtccgcgagt	gcccggggat	agaacccgtg	tcgctggacc	tgggtgactg	240
ggaggccacc	gancgggcgc	tgggcaacgt	gggccccgtg	gacctgctgg	tgaacaacgc	300
ccctgtcccc	tgcttcaacc	ctttctggaa	gtcaccaaa	aagcctttga	cagatccttt	360
taagtgaacc	tgctg					375

<210> 14  
 <211> 298  
 <212> DNA  
 <213> Homo sapien

<400> 14						
gaattcggca	cgagacagaa	attaaagtga	aaagaccttt	acgtggagaa	tttgcattgcg	60
taatatagga	aggtgttctt	taggtatgtt	acaggattac	tttaaaccat	ttgactttcg	120
ctccaaagt	atgttggtag	tatagcaaat	tatgatgaat	agctttaatt	gtatgtttaa	180
aaagtctcata	tggtcacatg	cttaaatctg	ggtatcagaa	tttaagcaat	tcttgaaatg	240
tattgtctcc	ttaatatata	aattacaaag	caaaaaaaaa	aaaaaaaaaa	aactcgag	298

<210> 15  
 <211> 506  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(506)  
 <223> n = A,T,C or G

<400> 15						
gaattcggca	cgagccggcg	aggaatagga	atcatggcgg	ctgcgctgtt	cgtgctgctg	60
ggattcgcgc	tgctgggcac	ccacggagcc	tccggggctg	ccggcacagt	cttcactacc	120
gtagagagac	ttggctccaa	gataacctc	acgtgctcct	tgatgacag	cgccacagag	180
gtcacagggc	accgttggtt	gaaggggggc	gtggtgctga	aggaggacgc	gctgcccggc	240
cagaaaacgg	agttcaaggt	ggactccgac	gaccagtggg	gagagtactc	ctgcgtcttc	300
ctccccgagc	ccatgggcac	ggccaacatc	cagctccacg	ggcctccan	agtgaagggt	360
tgtagagtcg	tcaagaacac	atcaacgagg	gggagacggc	catgctggtc	tgcaagtcag	420
agtcogtgcc	accttgctac	ttgactgggc	ctggtacaaa	gatcacttga	cttttgaagg	480
acaaggccct	tattgaaccg	gcttcc				506

<210> 16  
 <211> 286  
 <212> DNA  
 <213> Homo sapien

<400> 16						
gaattcggca	cgagctttta	aggagaaaat	gtgacacttg	tgaaaaagct	tgtaagaaag	60
ccccctccctt	ttttctttta	accttttaaat	gacaaatcta	ggtaattaag	gttgtgaatt	120
tttatTTTTg	ctttgttttt	aatgaacatt	tgtctttcag	aataggattg	tgtgataatg	180
tttaaatggc	aaaaacaaaa	catgattttg	tgcaattaac	aaagctactg	caagaaaaat	240
aaaacacttc	ttggtaacac	aaaaaaaaaa	aaaaaaaaaa	ctcgag		286

<210> 17  
 <211> 387  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature



6

&lt;222&gt; (1)...(387)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 17

gaattcggca	cnaggcaagg	tgtgcgggcg	ggaaggggca	cgggcacccc	cgcggtcccc	60
gggaggctag	agatcatgga	aggggaagtgg	ttgctgtgta	tggtactggg	gcttggaact	120
gctattgttg	aggctcatga	tggacatgat	gatgatgtga	ttgataattga	ggatgacctt	180
gacgatgtca	ttgaagaggt	agaagactca	aaaccagata	ccactgctcc	tccttcatct	240
cccaagggtta	cttacaaagc	tccagttcca	acaggggaag	tatatatttc	tgattctttt	300
gacagaggaa	ctctgtcagg	gtggatttta	tccaaagcca	agaaagacna	tcccgatgat	360
gaaattgccca	aatatgatgg	aaagtgg				387

&lt;210&gt; 18

&lt;211&gt; 415

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 18

gaattcggca	cgagccaaag	tgagcagtag	ccaacatgtc	agggtgggag	tcatattaca	60
aaaccgaggg	cgatgaagaa	gcagagggaag	aacaagaaga	gaaccttgaa	gcaagtggag	120
actataaata	ttcaggaaga	gatagtttga	tttttttggg	tgatgcctcc	aaggctatgt	180
ttgaatctca	gagtgaagat	gagttgacac	cttttgacat	gagcatccag	tgtatccaaa	240
gtgtgtacat	cagtaagatc	ataagcagtg	atcgagatct	cttggtctgtg	gtgttctatg	300
gtacccgaga	aagacaaaaa	ttcagtgaat	tttaaaaata	tttacgtctt	acaggagctg	360
gataatccag	gtgcaaaaacg	aattctagac	tttgccagtt	taaggggcag	caggg	415

&lt;210&gt; 19

&lt;211&gt; 466

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(466)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 19

gaattcggca	cnagcgggga	tcggtcgcct	gagaggtatc	acctcttctg	ggctcaagat	60
ggacaacaag	aagcgcttg	cctacgccat	catccagttc	ctgcatgacc	agctccggca	120
ggggggcctc	tcgtccgatg	ctcaggagag	cttggaagtc	gccatccagt	gcctggagac	180
tcggtttggg	gtgacggtag	aagacagtga	ccttgcgctc	cctcagactc	tgccggagat	240
atttgaagcg	gctgccacgg	gcaaggagat	gccgcaggac	ctgaggagcc	ccgcgcgaac	300
cccgcctttc	cgaagaagga	ctcancaaga	agggcaagaa	gccgccttca	aaacccgaaa	360
gggaaaaccg	aagccagaat	gaaaaagtgg	gaaaaacttt	tgaaagcttg	cccgtgccat	420
ttttcttacc	gggaaaaaag	cccattcggg	agcttcaaac	cccca		466

&lt;210&gt; 20

&lt;211&gt; 296

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(296)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 20

gaattcggca	cnagggtggtg	tgtggctgcg	gcctgggcaa	gagccgccgc	ggaccatgag	60
ctgagtaagt	tctggaggga	tctgcctct	tggagccttc	gcagccaggc	agctgtgaac	120

7

tgtgagctag	agtgaagcag	aaatctagga	agatgagctc	caagatgggtc	ataagtgaac	180
caggactgaa	ttgggatatt	tccccaaaa	atggccttaa	gacatttttc	tctcagaaaa	240
ttataaagat	cattccatgg	cttccaagtt	taaaaagaac	ttacgtggtt	tttatc	296

<210> 21  
 <211> 328  
 <212> DNA  
 <213> Homo sapien

<400> 21						
gaattcggca	cgagcccgcg	ctgcacttgc	tgcgcgcgtg	actggaggac	cgagccccc	60
cattttcttt	atgtggttgt	ggtgggggca	cagtaatgcc	ctgtgcgccg	tagcgttcct	120
gtggggatgt	ggccgggggg	cgtcgggaag	cgctcactgt	tgatgtccga	gctcagcgat	180
gaagccagcg	agccggaact	cctgaaccgc	agcttgtcca	tgtggcacgg	gctcgggaca	240
caggtcagcg	gggaggagct	ggatgtcccc	ctggatcttc	acacagctgc	ttcattggcc	300
agtatgaagt	ggtgaaggaa	tgtgtgca				328

<210> 22  
 <211> 466  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(466)  
 <223> n = A,T,C or G

<400> 22						
gaattcggca	cgaggcggac	taataaaggc	catggcgcca	gcagaaatcc	tgaacgggaa	60
ggagatctcc	gcgcaaataa	ggcgagact	gaaaaatcaa	gtcactcagt	tgaaggagca	120
agtacttgtt	ttcacaccac	gcctggcaat	attacagggt	ggcaacagag	atgattccaa	180
tctttatata	aatgtgaagc	tgaaggctgc	tgaagagatt	gggatcaaa	ccactcacat	240
taagtctact	gtacatgggt	tcttagtgca	gtacacttta	gattcagaga	attccattaa	300
cactgaagaa	gtgatcaatg	ctattgcacc	cganaaggat	gtggatggat	tgactagcat	360
caatgctggg	aaacttgcta	gaggtgacct	caatgactgt	ttcatt		420
						466

<210> 23  
 <211> 517  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(517)  
 <223> n = A,T,C or G

<400> 23						
gaattcggca	cgagcagagg	tctccagagc	cttctctctc	ctgtgcaaaa	tggcaactct	60
taaggaaaaa	ctcattgcac	cagttgcgga	agaagaggca	acagttccaa	acaataagat	120
cactgtagtg	ggtgttggac	aagttgggtat	ggcgtgtgct	atcagcattc	tgggaaagtc	180
tctggctgat	gaacttgctc	ttgtggatgt	tttggaagat	aagcttaaa	gagaaatgat	240
ggatctgcag	catgggagct	tatttcttca	gacacctaaa	attgtggcag	ataaagatta	300
ttctgtgacc	gccaattcta	agattgtagt	ggtaactgca	ggagtccgtc	agcaagaagg	360
ggagagtcgg	ctcaatctgg	tgagagaaaa	tgtaaatgtc	ttcaaattca	ttattcctca	420
gatcgtaag	tacagtctctg	attgcatcat	aattgtgnt	tccaaccag	tggacattct	480
tacgtatgtt	acctggaaac	taagtggatt	acccaaa			517

<210> 24

<211> 196  
 <212> DNA  
 <213> Homo sapien

<400> 24  
 gaattcggca cgaggggtggc actatgtggc gcgtctgtgc gcgacgggct cagaatgtag 60  
 ccccatgggc gggactcgag gctcgggtgga cggccttgca ggaggtaccc ggaactccac 120  
 gagtgcaccc gcgatctggc ccggtcccg ctcgtcgcaa cagcgtgact acagggtatg 180  
 gcgggggtccg ggcact 196

<210> 25  
 <211> 365  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)... (365)  
 <223> n = A,T,C or G

<400> 25  
 gaattcggca cgaggttggg cgggtctggt ttttcgctcg tcgactgcgg ctcttcctcg 60  
 ggcagcggaa gcggcgcggc ggtcggagaa gtggcctaaa acttcggcgt tgggtgaaag 120  
 aaaatggccc gaaccaagca gactgctcgt aagtcaccgc gtgggaaagc cccccgcaaa 180  
 cagctggcca cgaaagccgc caggaaaagc gtcacctcta ccggcggggt gaagaagcct 240  
 catcgctaca ggcccgggac cgtggcgctt cganagattc gtcgttatca gaagtcgacc 300  
 gagctgctca tccggaagct gcccttcag angttggtga gggagatcgc gcaggatttc 360  
 aaac 365

<210> 26  
 <211> 321  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)... (321)  
 <223> n = A,T,C or G

<400> 26  
 ctcgagtttt tttttttttt tttttttgta cgaaatggct aagttttattc aacatctcgg 60  
 atattcatct ggatattggg ttgtttttgt gatacaatac atattcacct taactggtgc 120  
 tactgcaaag aaagctttct tgacctgcat gacgtgcctc anagcttctc tccaccaatt 180  
 ggaaccaccc aaagcctagt ctanaccaa gtgctctgga gaaaaaaaac aaaacaaaaa 240  
 aacagcaaac agaaaacagt tgtgccccca aaagtactca gaagtcatat gttatttaca 300  
 attgggtttg tgtgggatgg g 321

<210> 27  
 <211> 454  
 <212> DNA  
 <213> Homo sapien

<400> 27  
 gaattcggca cgagcaagga tgaggagaac aatcccccttg agacagaata tggcctttct 60  
 gtctacaagg atcaccagac catcaccatc caggagatgc cggagaaggc ccagccggc 120  
 cagctccccc gctctgtgga cgtcattctg gatgatgact tgggtggataa agcgaagcct 180  
 ggtgaccggg ttcaggtggt gggaacctac cgttgccctc ctggaaagaa gggaggctac 240  
 acctctggga ccttcaggac tgtcctgatt gcctgtaatg ttaagcagat gagcaaaagga 300  
 tgctcagccc tctttctctg ctgaggatat agccaagatc aagaagttca gtaaaaccgc 360

9

atccaaggat atctttgacc atctggccaa gtcattggcc ccaagtatcc atgggcatga 420  
 ctatgtcaag aaagcaatcc tctgcttgc tttg 454

<210> 28  
 <211> 285  
 <212> DNA  
 <213> Homo sapien

<400> 28  
 gaattcggca cgagggttgg ctgaaattca tgcaagcttc cgaagatctt ctcaaggaac 60  
 actacgttga cctgaaggac cgtccattct ttgccggcct ggtgaaatac atgcactcag 120  
 ggccggtagt tgccatggtc tgggaggggc tgaatgtggt gaaaacgggc cgagtcatgc 180  
 tcggggagac caaccctgca gactccaagc ctgggaccat cgtggagac ttctgcatac 240  
 aagttggcag gaacattata catggcagtg attctgtgga gagtg 285

<210> 29  
 <211> 512  
 <212> DNA  
 <213> Homo sapien

<400> 29  
 gaattcggca cgagcaacct tgtaaatgtg aaagtacaac tcgtatttat ctctgatgtg 60  
 ccgctggctg aactttgggt tcatttgggg tcaaagccag tttttctttt aaaattgaat 120  
 tcattctgat gcttggccccc cataccccca accttgtcca gtggagccca acttctaaag 180  
 gtcaatatat catcctttgg catcccaact aacaataaag agtaggctat aagggaagat 240  
 tgtcaatatt ttgtggtaag aaaagctaca gtcatttttt ctttgcactt tggatgctga 300  
 aatttttccc atggaacata gccacatcta gatagatgtg agctttttct tctgttaaaa 360  
 ttattcttaa tgtctgtaaa aacgattttc ttctgtagaa tgtttgactt cgtattgacc 420  
 cttatctgta aaacacctat ttgggataat atttggaaaa aaagtaaata gctttttcaa 480  
 aatgaaaaaa aaaaaaaaaa aaaaaactcg ag 512

<210> 30  
 <211> 464  
 <212> DNA  
 <213> Homo sapien

<400> 30  
 gaattcggca cgaggccagg tgggcagccc ggggaccgac ccctactcgg cggcgcaact 60  
 ccacaaccag tacggcccca tgaatatgaa catgggtatg aacatggcag cagccgcggc 120  
 ccaccaccac caccaccacc accaccacc cgggtgcctt ttcccgtat atgcggcagc 180  
 agtgcacaa gcaggagcta atctgcaagt ggatcgaccc cgagcaactg agcaatccca 240  
 agaagagctg caacaaaact ttcagcacca tgcacgagct ggtgacacac gtctcgtggtg 300  
 agcacgtcgg cggcccggag cagagcaacc acgtctgctt ctgggaggag tgtccgcgcg 360  
 agggcaagcc cttcaaggcc aaatacaaac tggtaacca catccgcgtg cacacaggcg 420  
 agaaaccctt cccctgcccc ttcccggtct gtggcaaatg ctcc 464

<210> 31  
 <211> 317  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)... (317)  
 <223> n = A, T, C or G

<400> 31  
 gaattcggca cgagcagagg tgagcaagct ggaacagcaa tgccagaagc agcaggagca 60  
 ggctgacagc ctggaacgca gcctcgaggc tgagcgggcc tcccgggctg agcgggacag 120

## 10

tgctctggag	actctgcagg	gccagttaga	ggagaaggcc	cangagctag	ggcacagtca	180
gagtgcctta	gcctcggccc	aacgggagtt	ggctgccttc	cgcaccaagg	tacaagacca	240
cagcaaggct	gaagatgagt	ggaaggccca	gttggcccgg	ggccggcaag	aggctganag	300
gaaaaatagc	ctcatca					317

<210> 32  
 <211> 275  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)... (275)  
 <223> n = A,T,C or G

<400> 32						
gaattcggca	cgagcgaagg	aggacggagg	cttcagacac	tcggaagcct	ttgaggcact	60
ccagcaaaag	agtcagggac	tggaactccag	gtccagcac	gtggaggatg	gggtgctctc	120
catgcagggtg	gcttctgcgc	gccagaccga	gagcctggag	tccctcctgt	ncaagagcca	180
ggagcacgag	cagcgccctgg	ccgccctgca	ggggcgccctg	gaaggccctcg	ggtcctcata	240
ggcanaccan	gatggcctgc	cagcacgggtg	aggag			275

<210> 33  
 <211> 516  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)... (516)  
 <223> n = A,T,C or G

<400> 33						
gaattcggca	cgagggggcc	tgggcgttga	ctgtgggaaa	ctcggaaaca	agctcacatc	60
ttcctgtggg	aaaccttcta	gcaacaggat	gagtctgcag	tggaactgcag	ttgccacctt	120
cctctatgcy	gaggtctttg	ttgtgttgct	tctctgcatt	tccttcattt	ctcctaaaag	180
atggcagaag	attttcaagt	cccggctggt	ggagttgtta	gtgtccatag	gcaacacctt	240
ctttgtgggt	ctcattgtca	tccttgtgct	gttggatcatc	gatgccgtgc	gcgaaattcg	300
gaagtatgat	gatgtgacgg	aaaagggtgaa	cctccagaac	aatccccggg	ccatggagca	360
cttcacatg	aagnttttcc	gtgccagag	gaatctctac	attgctggct	tttccttgct	420
gctgtccttc	ctgcttagac	gcctgggtgac	tctcatttcc	aacaggccac	gctgctggcc	480
ttcaatgaac	ctttaaaaac	aggcggagag	tntcat			516

<210> 34  
 <211> 446  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)... (446)  
 <223> n = A,T,C or G

<400> 34						
gaattcggca	cgagacagaa	atgntctaaag	aagagaagga	ccctggaatg	ggtgcaatgg	60
gtggaatggg	aggtggtatg	ggaggtggca	tgttctaact	cctagactag	tgctttacct	120
ttattaatga	actgtgacag	gaagcccaag	gcagtgttcc	tcccaataac	ttcagagaag	180
tcanttgagg	aaaatgaaga	aaaaggctgg	ctgaaaatca	ctataaccat	cagttactgg	240
tttcagttga	caaatatat	aatggtttac	tgctgtcatt	gtccatgcct	acagataatt	300

11

tat	tttt	gtat	tttt	gaataa	aaaacatttg	tacattcctg	atactgggta	caagagccat	360
gtaccagtg	actgctttca	acttaaatca	ctgaggcatt	tttactacta	ttctgttaaa				420
atcaggattt	tagtgcttgc	ccccca							446

<210> 35  
 <211> 440  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(440)  
 <223> n = A,T,C or G

<400> 35									
gaattcggca	cgaggtttat	ttgtcccccac	cagaagggtg	gggtggg	cgcg	gcctagaaca		60	
cagcgtgcg	cggttccc	ggtggagcca	gcgcagacag	cgtgggtccc	tgcggtctt			120	
angcgaaggt	ggagttgttc	canccacat	tgccccgct	ttcattgtcg	taatagttga			180	
tgtagaccct	gtccgggctg	atgcgcaggc	gctctgccag	caggccgcac	agcagcttgc			240	
tgtaggagcg	gttctgcgcg	ccgcgatct	tgccgatgct	gtgcangctg	canagcgcg			300	
acggctcgt	ggagccgccc	aaggccatga	gctgggtccg	gaccacgtgc	accgctatgt			360	
actggggggg	cttgccggtg	gcctgcgcca	nctgctgggt	gagctcggag	aggaaccgtc			420	
cggcacggag	gcgcggggca							440	

<210> 36  
 <211> 373  
 <212> DNA  
 <213> Homo sapien

<400> 36									
gaattcggca	cgaggccaaa	cgtaccaaga	aagtcgggat	cgtcggtaaa	tacgggaccc			60	
gctatggggc	ctccctccg	aaaatggtga	agaaaattga	aatcagccag	cacgccaagt			120	
acacttgctc	tttctgtgga	anacccaga	tgagagacg	agctgtggg	atctgggact			180	
gtgttctctg	catgaagaca	gtggctggcg	gtgcctggac	gtacaatacc	acttccgctg			240	
tcacggtaaa	gtccgccatc	agaagactga	aggagttgaa	agaccagtag	acgtcctct			300	
actctttgag	acatcactgg	cctataataa	atgggttaat	ttatgtaaca	aaaaaaaaaa			360	
aaaaaaactc	gag							373	

<210> 37  
 <211> 565  
 <212> DNA  
 <213> Homo sapien

<400> 37									
gaattcggca	cgaggggggca	cgggcacccc	cgcggtcccc	gggaggctag	agatcatgga			60	
aggggaagtgg	ttgctgtgta	tgttactggt	gcttggaaact	gctattgttg	aggctcatga			120	
tggaacatgat	gatgatgtga	ttgatattga	ggatgacctt	gacgatgtca	ttgaagaggt			180	
agaagactca	aaaccagata	ccactgctcc	tccttcatct	cccaaggtta	cttacaagc			240	
tccagtcca	acaggggaag	tatatatttc	tgattctttt	gacagaggaa	ctctgtcagg			300	
gtggatttta	tccaaagcca	agaagacga	taccgatgat	gaaattgcc	aatatgatgg			360	
aaagtgggag	gtagaggaaa	tgaaggagtc	aaagcttcca	ggtgataaag	gacttgtgtt			420	
gatgtctcgg	gccaagcatc	atgccatctc	tgctaaactg	aacaagccct	tcctgtttga			480	
caccaagcct	ctctgtttca	gtatgagggtt	aatttccaaa	atggaataga	atgtggtggt			540	
gcctatgtga	aactgctttc	taaaa						565	

<210> 38  
 <211> 566  
 <212> DNA  
 <213> Homo sapien

12

<220>  
 <221> misc\_feature  
 <222> (1)...(566)  
 <223> n = A,T,C or G

<400> 38  
 gaattcggca cgagcccaac tttagccagg aagatcagca ggacaccag atttatgaga 60  
 agcatgacaa ccttctacat gggaccaaga agaaaaagga gaagatggtg agtcagcat 120  
 tcatgaagaa gtacatccat gtggccaaaa tcatcaagcc tgtctgaca caggagtcgg 180  
 ccacctacat tgcagaagag tattcacgcc tgcgcagcca ggatagcatg agctcagaca 240  
 ccgccaggac atctccagtt acagcccgaa cactggaaac tctgattcga ctggccacag 300  
 ccctatgcgaa ggcccgcag agcaagactg tggacctgca ggatgcagag gaagctgtgg 360  
 agttggtcca gtatgcttac ttttaagaagg ttctggagaa ggagaagaaa cgtaagaagc 420  
 gaagtgagga tgaatcagag acagaagatg aagaggagaa aagccaagag gaccaggagc 480  
 agaagaggaa gagaaggaag actcgccagc cagatgccaa agatggggat tcatacgacc 540  
 cctatgactt cagtgcacaca gaggan 566

<210> 39  
 <211> 364  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(364)  
 <223> n = A,T,C or G

<400> 39  
 gaattcggca cgaggtctca cagaaagttc tccgctccca gacatgggtc cctcggttc 60  
 ctgcctcgga agcgcagcag caggcatcgt gggaaggtga agagcttccc taaggatgac 120  
 ccgtccaagc cgggccacct cacagccttc ctgggataca aggctggcat gactcacatc 180  
 gtgagggaag tgcacggcc gggatccctg gtgacacaga cggaggtggt ggaggctgtg 240  
 accattgtag agacaccacc catggtggtt gtgggcattg tgggtacgt ggaaaccct 300  
 ngaggcctcc ggacctttaa gactgtcttt gcttgagcac atcantgatg aatgcaagag 360  
 gcgt 364

<210> 40  
 <211> 336  
 <212> DNA  
 <213> Homo sapien

<400> 40  
 gaattcggca cgagcccaga tctctaccac agcctcccag ggggcctact acatccctgg 60  
 acaggggagc tccacatacg ttgtcccagc acagcagtac cctgtgcagc caggagcccc 120  
 aggttcttat ccaggtgcaa gccctacaga atttgggacc tacgctggcg cctactatcc 180  
 agcccaaggg gtgcagcagt ttcccactgg cgtggccccc gccccagttt tgatgaacca 240  
 gccaccccag attgctccca agagggagcg taagacgatc cgaattcgag atccaaacca 300  
 aggaggaaag gatatcacag aggagatcat gtctgg 336

<210> 41  
 <211> 566  
 <212> DNA  
 <213> Homo sapien

<400> 41  
 gaattcggca cgagacttgg gaaaatgaat tcagaggagg aagatgaagt gtggcaggtg 60  
 atcataggag ccagagctga gatgacttca aaacaccaag agtacttgaa gctggaaacc 120  
 acttggatga ctgcagttgg tctttcagag atggcagcag aagctgcata tcaaactggc 180

## 13

gcagatcagg	cctctataac	cgccaggaat	cacattcagc	tggtgaaact	gcaggtggaa	240
gaggtgcacc	agctctcccc	gaaagcagaa	accaagctgg	cagaagcaca	gatagaagag	300
ctccgtcaga	aaacacagga	ggaaggggag	gagcgggctg	agtcggagca	ggaggcctac	360
ctgcgtgagg	attgagggcc	tgagcacact	gccctgtctc	cccactcagt	ggggaagca	420
ggggcagatg	ccaccctgcc	cagggttggc	atgactgtct	gtgcaccgag	aagaggcggc	480
aggtcctgcc	ctgccaatca	ggcgagacgc	ctttgtgagc	tgtgagtgcc	tcctgtggtc	540
tcaggcttgc	gcttggacct	ggttct				566

&lt;210&gt; 42

&lt;211&gt; 386

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 42

gaattcggca	cgagggcagc	tcgagtccac	cagcagcgcc	gtccgcttga	ccgagatgct	60
gcgggcctgt	cagttatcgg	gtgtgaccgc	cgccgcccag	agttgtctct	gtgggaagtt	120
tgtcctccgt	ccatttgcgac	catgccgcag	atactctact	tcaggcagct	ctgggttgac	180
tactggcaaa	attgctggag	ctggcctttt	gtttgttggg	ggaggtattg	gtggcactat	240
cctatatgcc	aaatgggatt	cccatttccg	ggaaagtgtg	gagaaaacca	taccttactc	300
agacaaactc	ttcgagatgg	ttcttgggtc	tgcagcttat	aatgttccat	tgccaaagaa	360
atcgattcaa	gtcgggtcca	ctaaaa				386

&lt;210&gt; 43

&lt;211&gt; 514

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 43

gaattcggca	cgagggcaaa	acctccacct	cctgatgaat	ttcttgactg	tttccaaaag	60
tttaaacacg	gatttaacct	tctggccaaa	ctgaagtctc	atattcagaa	tcctagtgtc	120
gcagatttgg	ttcacttttt	gtttactcca	ttaaataatg	tggtgcaggc	aacaggaggt	180
cctgaactag	ccagttcagt	acttagtccc	ctattgaata	aggacacaat	tgattttcta	240
aaagccagag	cagagtggcc	aaaagaacag	tttattccac	catatgttcc	acgattccgc	300
aatggctggg	agcccccaat	gctgaacttt	atggggagcca	caatggaaca	agatctttat	360
caactggcag	aatctgtggc	aaatgtagca	gaacatcagc	gcaaacagga	aataaaaaaga	420
ttatcccaga	gcatttcagt	gtatcagaat	atta			480
						514

&lt;210&gt; 44

&lt;211&gt; 467

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 44

gaattcggca	cgagactaga	gccgcatcac	atggggactt	ctgcaaatac	agagactcgg	60
attaaagggtg	gagaagatgg	agctaaagga	actgcttatt	taatacatit	gaacaacttt	120
tggggctactt	agaaggtgct	ttgaaacctg	catttgatta	agcaagaatt	cgcttgcaag	180
tttaaggggca	ctccacagaa	ggaatgttatt	atcaagtcag	atgcaccgga	cactttgtta	240
ttggagaaac	atgcagatta	tatcgcatcc	tatggctcaa	agaaagatga	ttatgaatac	300
tgtatgtctg	agtatttgag	aatgagtggc	atctattggg	gtctgacagt	aatggatctc	360
atgggacaac	ttcatcgcat	gaatagagaa	gagattctgg	catttattaa	gtcttgccaa	420
catgaatgtg	gtggaataag	tgctagtatc	ggacatgatc	ctcatct		467

&lt;210&gt; 45

&lt;211&gt; 344

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;



14

<221> misc\_feature  
 <222> (1)...(344)  
 <223> n = A,T,C or G

<400> 45  
 gaattcggca cgaggagagac tggaggaaga gctccgccag ctgaagtccg attcccacgg 60  
 gccgaaggag gacggaggct tcagacactc ggaagccttt gaggcactcc agcaaaagag 120  
 tcagggactg gactccaggc tccagcacgt ggaggatggg gtgctctcca tgcaagtggc 180  
 ttctgcgcgc cagaccgaga gcctggagtc cctcctgtcc aagaaccagg aacacgagca 240  
 gcgcctggcc gcctgcaggg gcgcctggaa agcctcgggt cctcagaagc agaccangat 300  
 ggcctgccag cacngtgagg agcctgggag agaccagct ggtg 344

<210> 46  
 <211> 303  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(303)  
 <223> n = A,T,C or G

<400> 46  
 gaattcggca cgagngggaa cacaagtatg tgccaccaca ccttggtaac ttttaaattg 60  
 tttttagata tgaggctctga ccatgttgcc catgccatta ttattccttt tgataaaggt 120  
 gaatttaggc taaactgtga aagaatgtac agcaaatggc tctgttaatt cttctcatag 180  
 gaggacaggt tactgttaat agagaacata tgtatgtaat ggctaaaaat agggcagtag 240  
 aaaaggaatg taacttctca cctcctttga gaatgnaaag aaagaaagaa aaaaggatgg 300  
 tac 303

<210> 47  
 <211> 364  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(364)  
 <223> n = A,T,C or G

<400> 47  
 gaattcggca cgaganatag ttccctttctc taaagtggat gaggaacaaa tgaaatataa 60  
 atcggagggg aagtgccttct ctgttttggg attttgtaaa tcttctcagg ttcagagaag 120  
 attcttcatt ggaaatcaag ttctaaaggt ctttgcagca agagatgatg aggcagctgc 180  
 agttgcactt tctcctctga ttcatgcttt ggatgactta gacatggttg ccatagtctg 240  
 atatgcttat gacaaaagag ctaatcctca agtcggcgtg gcttttcctc atatcaagca 300  
 taactatgag tgtttagtgt atgtgcagct gcctttcatg gaagacttgc ggcaatacat 360  
 gttt 364

<210> 48  
 <211> 284  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(284)  
 <223> n = A,T,C or G

## 15

```

<400> 48
gaattcggca cgagagcagc tggaggcact ggagaaggag aaggctgcc aagctggagat      60
tctgcagcag caacttcagg tggctaata agcccgggac agtgcccaga cctcagtgac      120
acaggcccag cgggagaagg cagagctgag ccggaagggt gaggaactcc aggcctgtgt      180
tgagacagcc cgccaggaac agcatgaggc ccaggcccag gttgcagagc tagagttgca      240
gctgcggtct gaggcagcaa aagcaactga ganagaaagg gtgg                          284

<210> 49
<211> 313
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(313)
<223> n = A,T,C or G

<400> 49
gaattcggca cgagggtttat tatagctcat acctgggacc gattaagggt tcaacatttt      60
aaaattactc aagatatttaa ccagaaaaga tgattatggc ctttaaaaact attggacaaa      120
ctgatgctat ttaacattgt tcacagccat ttaatttgaa taacaaattt tagattctaa      180
gtaggccata acttcttttc aaaacaattg atttataaag gtacagtttc agaagгнаac      240
agcatgagac tagtcttcct ataggcacat tttagtagac tgctcttctc atccctgggc      300
aaggagcttc tct                          313

<210> 50
<211> 522
<212> DNA
<213> Homo sapien

<400> 50
gaattcggca cgaggggacag ccaacaaaag cagcttcttg aagttcaact tcagcaaaat      60
aaggagcttg aagatattta tgctaaatta gaggagaga tgaaggatc tgaggagaa      120
aatgaggatc tgcggaggtc ctttaatgcc ctacaagaag agaaacaaga tttatctaaa      180
gagattgaga gtttgaaagt atctatatcc cagctaacaa gacaagtaac agccttgcaa      240
gaagaaggta ctttaggact ctatcatgcc cagttaaaag taaaagaaga agaggtacac      300
aggttaagtg ctttgttttc ctctctctca aagagaattg cagaactgga agaagaattg      360
gtttgtgttc aaaaggaagc tgccaagaag gtaggtgaaa ttgaagataa actgaagaaa      420
gaattaaagc atcttcacat tgatgcaggg ataattgagaa atgaaactga aacagcagaa      480
gagagagtgg cagagctagc aagagatttg gtggagatgg aa                          522

<210> 51
<211> 463
<212> DNA
<213> Homo sapien

<220>
<221> misc_feature
<222> (1)...(463)
<223> n = A,T,C or G

<400> 51
gaattcggca cgaggagcac ttcggctcct cgcgcgctcg cgtcccctcg tgcgggctcc      60
agccgcagcc ttagcttcgg ctcccggtt ggggtggcgg gccgtgccct cgttttggcc      120
tccgaacgcg gctcgaatgg caagccaaaa ttccttcagg atagaatatg atacctttgg      180
tgaactaaag gtgccaaatg ataagtatta tggcgcccag accgtgagat ctacgatgaa      240
ctttaagatt ggaggtgtga cagaacgcac gccaacccca gttattaaag cttttggcat      300
cttgaaagcg cgggcccgtg aagtaaacca ggattatggt cttgatccaa agattgctan      360
tgcaataatg aaggcagcag angaggtagc tgaaggtaaa ttaaatgac attttctct      420

```

16

cggtggtatgg cagactggat caggaactca gacaaatatg aat 463

<210> 52

<211> 423

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)... (423)

<223> n = A,T,C or G

<400> 52

gaattcggca	cgagaaagcg	cagccgagcc	cagcgccccg	cacttttctg	agcagacgtc	60
cagagcagag	tcagccagca	tgaccgagcg	ccgcgtcccc	ttctcgctcc	tgcgggggccc	120
cagctgggac	cccttcgcg	actggtacc	gcatagccgc	ctcttcgacc	aggccttcgg	180
gctgcccccg	ctgccggagg	agtggtcgca	gtggttaggc	ggcagcagct	ggccaggcta	240
cggtgcgccc	ctgcccccg	ccgccatcga	gagccccgca	gtggccgcgc	ccgcctacag	300
ccgcgcgctc	agccggcaac	tcagcagcgg	ggtctcggag	atccggcaca	ctgcggaccg	360
ctggcgcggtg	tccttggtatg	tcaaccactt	cgccccggac	gagctgacgg	tcaagaccaa	420
nga						423

<210> 53

<211> 474

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)... (474)

<223> n = A,T,C or G

<400> 53

gaattcggca	cgaggggaatc	tctacattgc	tggcttttcc	ttgctgctgt	ccttcctgct	60
tagacgcctg	gtgactctca	tttcgcagca	ggccacgctg	ctggcctcca	atgaagcctt	120
taaaaagcag	gcggagagtg	ctagtgaggc	ggccaagang	tacatggagg	agaatgacca	180
gctcaagaan	ggagctgctg	ttgacggagg	caagttggat	gtcgggaatg	ctgaggtgaa	240
gttgaggagg	gagaacagga	gcctgaaggc	tgacctgcag	aagctaaagg	acgagctggc	300
cagcactaag	caaaaactag	agaaaagctga	aaaccagggt	ctggccatgc	ggaagcagtc	360
tgagggcctc	accaaggagt	acgaccgctt	gctggaggag	cacgcaaagc	tgaggctgc	420
agtagatggt	cccatggaca	agaaggaaga	gtaaggcct	tccttcctcc	cctg	474

<210> 54

<211> 473

<212> DNA

<213> Homo sapien

<400> 54

gaattcggca	cgagctcgtg	ccgaatcggc	acgagggatc	ggtcgcctga	gaggtatcac	60
ctcttctggg	ctcaagatgg	acaacaagaa	gcgcctggcc	tacgccatca	tccagttcct	120
gcatgaccag	ctccggcacg	ggggcctctc	gtccgatgct	caggagagct	tggagtcgc	180
catccagtgc	ctggagactg	cgtttgggg	gacggtagaa	gacagtgacc	ttgcgctccc	240
tcagactctg	ccggagatat	ttgaagcggc	tgccacgggc	aaggagatgc	cgcaggacct	300
gaggagccca	gcgcgaaccc	cgccttcgga	ggaggactca	gcagaggcag	agcgctcaa	360
aaccgaagga	aacgagcaga	tgaagtgga	aaactttgaa	gctgccgtgc	atttctacgg	420
aaaagccatc	gagctcaacc	cagccaacgc	cgtctatttc	tgcaacagaa	gcc	473

<210> 55

<211> 365

17

<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)...(365)  
<223> n = A,T,C or G

<400> 55  
gaattcggca cgagtgattg aggatcagtt ggggtgccaga cactctctta ggtgtcagag 60  
ctccagttta cattacacag ataagggtccc tgcccccag cgaagctggc attaaagtca 120  
gcaataaat gttcaggatt ttgataagt ctgtaaagga aaaaagacct gtaacagggt 180  
ggaatgactg gggagggggc gaggtctctat ctaggcaggg atggaccaga cntgagagtg 240  
accaggaggt tcgagccagt tgcagaggga caagaaaggc cttctgggca ggggcactta 300  
caggtacaga gccctgcag cagaataagc ttctcctacc ggagaggcaa aaagaaggcc 360  
ttttg 365

<210> 56  
<211> 517  
<212> DNA  
<213> Homo sapien

<400> 56  
gaattcggca cgagggacgc cgctttgttg cctgagatga agttggagcc cttgtttttg 60  
acattggatc ctatactgtg agagctgggt atgctgggtga ggactgcccc aagggtgatt 120  
ttcctacagc tattggtatg gtggtagaaa gagatgacgg aagcacatta atggaaatag 180  
atggcgataa aggcaaacaa ggcggtccca cctactacat agatactaata gctctgcgtg 240  
ttccgaggga gaatatggag gccatttcac ctctaaaaaa tgggatgggt gaagactggg 300  
atagtttccá agctattttg gatcatacct acaaaatgca tgtcaaatca gaagccagtc 360  
tccatcctgt tctcatgtca gaggcaccgt ggaatactag agcaaagaga gagaaactga 420  
cagagttaat gtttgaacac tacaacatcc ctgccttctt cctttgcaaa actgcagttt 480  
tgacagcatt tgctaattggt ccgttctact gggcttg 517

<210> 57  
<211> 237  
<212> DNA  
<213> Homo sapien

<400> 57  
gaattcggca cgagctatga gatagtatta agcaattaaa agaatatatg acttttctac. 60  
atcaaaattt gaaacttctg tgcatacaag gacacaatca acagagtga gaggaactt 120  
acagaatggg agaaaatatt tgtaaatcat gtatctcata aggattaata tccaggctat 180  
gtaaagaact acatctcaac acaaaaacac aaacagcttg attaaaaaat gggcaaa 237

<210> 58  
<211> 485  
<212> DNA  
<213> Homo sapien

<400> 58  
gaattcggca cgagcgcggc ggtcactgcg ccggggtagt gggccccagt gttgcgctct 60  
ctggccggtc cttacacttt gcttcaggct ccagtgcagg ggcgtagtgg gatatggcca 120  
actcggtctg caaggacgtc acgggtccag atgaggagag ttttctgtac ttgcctacg 180  
gcagcaacct gctgacagag aggatccacc tccgaaaccc ctgcggcgcg ttcttctgtg 240  
tgccccgcct gcaggatttt aagcttgact ttggcaattc ccaaggcaaa acaagtcaaa 300  
cttggcatgg agggatagcc accatttttc agagtccctg cgatgaagtg tggggagtag 360  
tatggaaaat gaacaaaagc aatttaaatt ctctggatga gcaagaaggg gttaaaagtg 420  
gaaatgtatg ttgtaataga agttaaaagt tgccaacttc aagaaaggaa aaaaaaata 480  
acctg 485

18

<210> 59  
 <211> 514  
 <212> DNA  
 <213> Homo sapien

<400> 59  
 gaattcggca cgagtggcgt tggaggtcgg cgatatggaa gatgggcagc tttccgactc 60  
 ggattccgac atgacggtcg caccacgca caggccgctg caattgcca aagtgcagg 120  
 tggcgacagt gctatgaggg ccttcagaa caggcgaact gcattgacac cagtatcaca 180  
 ttatcgagct gttgaaagtg tggattcaag tgaagaaagt tttctgatt cagatgatga 240  
 tagctgtctt tggaaacgca aacgacagaa atgttttaac cctcctccca aaccagagcc 300  
 ttttcagttt ggccagagca gtcagaaacc acctgttgct ggaggaaaga agattaacaa 360  
 catatggggt gctgtgctgc aggaacagaa tcaagatgca gtggccactg aacttggtat 420  
 cttgggaatg gagggcacta ttgacagaag cagacaatcc gagacctaca attatttgc 480  
 tgccaagaaa cttaggaagg aatctcaaga gcat 514

<210> 60  
 <211> 336  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)... (336)  
 <223> n = A,T,C or G

<400> 60  
 gaattcggca cgaggccgcc ggtgtgctgt caccggggca ggcaaaggta tagggcgagg 60  
 caggtgccag gcgtgcacg cgacgggcgc gcgggtggtg gctgtgagcc ggactcaggc 120  
 ggaatctgac agccttgctc gcgagtgccc ggggatagaa cccgtgtgag tggacctggg 180  
 tgactgggag gccaccgagc gggcgctggg cagcgtgggc cccgtggacc tgctggtgaa 240  
 caagcgagct gtcgagctgc tgcagccctt cagggaggtc aacggggagg ctttgaagg 300  
 atcctttgag gtgaacctgc gtgcggtcat ccagggt 336

<210> 61  
 <211> 515  
 <212> DNA  
 <213> Homo sapien

<400> 61  
 gaattcggca cgaggtcgcc tgagaggat cactcttctt gggctcaaga tggacaacaa 60  
 gaagcgccctg gcctacgcca tcatccagtt cctgcatgac cagctccggc acgggggcct 120  
 ctgctccgat gctcaggaga gcttggaagt cgccatccag tgcctggaga ctgcttttgg 180  
 ggtgacggta gaagacagt accttgctgt cctcagact ctgcccggaga tatttgaagc 240  
 ggctgccacg ggcaaggaga tgccgcagga cctgaggagc ccagcgcgaa cccgccttc 300  
 cgaggaggac tcagcagagg cagagcgctt caaaaccgaa ggaaacgagc agatgaaagt 360  
 ggaaaacttt gaagctgccg tgcatctcta cggaaaagcc atcgagctca acccagccaa 420  
 cgccgtctat ttctgcaaca gagccgcagc ctacagcaaa ctcggcaact acgcaggcgc 480  
 ggtgcaggac tgtgagcggg ccattctcat tgacc 515

<210> 62  
 <211> 417  
 <212> DNA  
 <213> Homo sapien

<400> 62  
 gaattcggca cgagagccaa cctcctggaa gggcacgcgc gtgctgaggt gtacccttca 60  
 gccaaagcaa tgatcaaat ccaatcacc tatgaggaa agttggaaca gcagagactg 120

## 19

gcagtgcagc	aggtggagga	ggcccagcag	ctgcgggaac	accaggaagc	tttgaccag	180
cagaggctgc	aggggcactt	actacggcag	caggaacagc	agcagcagca	ggtggcaaga	240
gagatggccc	tgcagaggca	ggctgagctt	gaggagggcc	ggccgcagca	ccaggagcag	300
ctccggcagc	aagctcatta	tgatgctatg	gataatgata	tcgttcaggg	agcagaggac	360
cagggaatcc	aaggagagga	aggagcctat	gaaagagaca	accagcacca	agatgaa	417

<210> 63  
 <211> 455  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(455)  
 <223> n = A,T,C or G

<400> 63	
gaattcggca	cgagggccgg gcttgggctg cgtggagaat actttttgcg atgcctactg 60
gagactttga	ttcgaagccc agttgggccc accaggtgga ggaggagggg gaggacgaca 120
aatgtgtcac	cagcgagctc ctcaagggga tccctctggc cacaggtgac accagcccag 180
agccaganc	actgccggga gctccactgc cgcctcccaa ggaggtcatc aacggaaaca 240
taaagacagt	gacagagtac aagatagatg aggatggcaa gaagttcaag attgtccgca 300
ccttcaggat	tgagaccggg aaggcttcaa aggctgtcgc aaggaggag aactggaaga 360
agttcgggaa	ctcagagttt gacccccccg gacccaatgt ggccaccacc actgtcagt 420
acgatgtctc	tatgacgttc atcaccagca aagag 455

<210> 64  
 <211> 517  
 <212> DNA  
 <213> Homo sapien

<400> 64	
gaattcggca	cgagggccgg gcttgggctg cgtggagaat actttttgcg atgcctactg 60
gagactttga	ttcgaagccc agttgggccc accaggtgga ggaggagggg gaggacgaca 120
aatgtgtcac	cagcgagctc ctcaagggga tccctctggc cacaggtgac accagcccag 180
agccaganc	actgccggga gctccactgc cgcctcccaa ggaggtcatc aacggaaaca 240
taaagacagt	gacagagtac aagatagatg aggatggcaa gaagttcaag attgtccgca 300
ccttcaggat	tgagaccggg aaggcttcaa aggctgtcgc aaggaggag aactggaaga 360
agttcgggaa	ctcagagttt gacccccccg gacccaatgt ggccaccacc actgtcagt 420
acgatgtctc	tatgacgttc atcaccagca aagag 455

<210> 65  
 <211> 519  
 <212> DNA  
 <213> Homo sapien

<400> 65	
gaattcggca	cgagtggagg tcggcgatat ggaagatggg cagctttccg actcggattc 60
cgacatgacg	gtcgcaccca gcgacaggcc gctgcaattg ccaaaagtgc taggtggcga 120
cagtgtatg	agggccttcc agaacacggc aactgcatgt gcaccagtat cacattatcg 180
agctgttgaa	agtgtggatt caagtgaaga aagtttttct gattcagatg atgatagctg 240
tctttgaaaa	cgaaaacgac agaaatgttt taacctcctt cccaaaccag agccttttca 300
gtttggccag	agcagtcaga aaccacctgt tgctggagga aagaagatta acaacatag 360
gggtgctgtg	ctgcaggaac agaatacaga tgcagtggcc actgaacttg gtatcttggg 420
aatggagggc	actattgaca gaagcagaca atccgagacc tacaattatt tgcttgccaa 480
gaaacttagg	aaggaatctc aagagcattc caaaagatc 519

<210> 66

20

<211> 517  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(517)  
 <223> n = A,T,C or G

<400> 66  
 gaattcggca cgagggcggc tgaggaaagc aggaggaggt ggcgggcgcg ggaagatggc 60  
 tccttcacct accaaacgca aagaccgctc agatgagaag tccaaggatc gctcaaaaga 120  
 taaaggggccc accaaggagt cgagtggaga ggatcgcggc cgggacaaaa cccgaaagag 180  
 gcgcagcgct tccagtggta gcagcagtac caggtctcgg tccagctcga cttccagctc 240  
 aggtccagc accagcactg gctcaagcag tggctccagc tcttcctcag catccagccg 300  
 ctcaggaagc tccagcacct cccgcagctc cagctctagc agctcttctg gctctccaag 360  
 tccttctcgg cgcanacag acaacaggag gcgctccgcg tccaaatcca aaccacctaa 420  
 aagagatgaa aaggagagga aaaggcgag cccatctcct aagcccacca aagtgcacat 480  
 tgggagactc acccggaatg tgacaaagga tcacatc 517

<210> 67  
 <211> 517  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(517)  
 <223> n = A,T,C or G

<400> 67  
 gaattcggca cgagggcgcg tgcagcggtc gagggtgngc ggcgggcgag gcaaaccggg 60  
 agctgagggc cggcgcgagg gaggagggac cgggtgaggc ccaggaaacg gaggcggggc 120  
 cggaggctcc atgttgaggaa gcggcgccgt tcgtgcttgt tagcgggaat ccgggagccg 180  
 cggggtgagc tggcgggggc cgggccctaa gtgaagatgg aggcccgct gcggcctgcc 240  
 gcggacatcc tgaggcgga aacgcagcag gactacgaac tcgtccagag ggtcggcagc 300  
 ggcacctacg gggacgtcta taaggccaga aatgtacaca caggagagct ggctgcagta 360  
 aaaatcatta aattggagcc tggagatgat ttttctttga ttcaacaaga aatatttatg 420  
 gttaaagaat gtaaacattg taacatcggt gcctaacttg ggagttatct tagtcgggaa 480  
 aaactatgga tttgtatgga atactgtggt ggcggat 517

<210> 68  
 <211> 516  
 <212> DNA  
 <213> Homo sapien

<400> 68  
 gaattcggca cgaggtcggt tcctgctatt ccggtttctc cactccgtcc cccgcgggtc 60  
 tgctctgtgt gccatggacg gcattgtccc agatatagcc gttggtaca agcggggatc 120  
 tgacgagctt ttctctactt gtgtcactaa cggaccgttt atcatgagca gcaactcggc 180  
 ttctgcagca aacggaaatg acagcaagaa gttcaaaggc gacagccgaa gtgcaggcgt 240  
 cccctctaga gtgatccaca tccggaagct ccccatcgac gtcacggagg gggaagtcac 300  
 ctccctgggg ctgccctttg ggaagggtcac caacctcctg atgctgaagg ggaaaaacca 360  
 ggcccttcac gagatgaaca cggaggaggc tgccaacacc atggtgaact actacacctc 420  
 ggtgaccctc gtgctgcgag gccagcccat ctacatccag ttctccaacc acaaggagct 480  
 gaagaccgac agctctccca accaggcgcg ggccca 516

<210> 69  
 <211> 455

## 21

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 69

gaattcggca	cgaggagcca	tagagcctct	gcctcgatgc	cgttttgccc	ccgctctttg	60
gacacgccga	cccggcgctc	cccaagggaat	gctgtcccaa	caagattccc	gtgaaagagc	120
accggtgtcg	ccccctcccg	tggacttctg	tgccgccccg	tccacacctg	ttcttggtg	180
catgtgggtt	ttcggttcct	ggcgggtccag	gacggggcgg	gggctccccct	cccatctcgt	240
gctgggaggt	ctcagcgcg	tctcctgtcc	ctgggacgtg	cgtctctcct	totcatgccg	300
ttctggaaaa	tgctcttgct	gtagagagca	gctgcttctg	ccagggtgtt	ggaggtgggtg	360
gagcgcttc	cgattccatt	catggcattt	tgtgatgtga	tgtaattgga	atagagctgt	420
tgatttaagg	caaaaaaaaa	aaaaaaaaac	tcgag			455

&lt;210&gt; 70

&lt;211&gt; 569

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)... (569)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 70

gaattcggca	cgagcagaac	gcagctctgc	tctgctngag	gaggtgcaga	gcctccggga	60
ggaggtgag	aaacagcggg	tggcttcaga	gaacctgcgg	caggagctga	cctcacaggc	120
tgagcgtcg	gaggagctgg	gccaaagatt	gaaggcgtgg	caggagaagt	tcttcagaa	180
agagcaggcc	ctctccaccc	tgagctcga	gcacaccagc	acacaggccc	tggtgagtga	240
gctgctgcc	gctaagcacc	tctgccagca	gctgcaggcc	gagcaggccg	ctgccagaa	300
acgccaccgt	gaggagctgg	agcagagcaa	gcaggccgct	gggggactgc	gggcagagct	360
gctgcgggcc	cagcgggagc	ttggggagct	gattcctctg	cggcagaagg	tggcagagca	420
ggagcgaaca	gctcagcagc	tgcgggcaga	gaaggccagc	tatgcagagc	agctgagcat	480
ccttgcccg	cagtttctgg	aagtggagt				569

&lt;210&gt; 71

&lt;211&gt; 555

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 71

gaattcggca	cgagtggcga	cgccccctaa	gcggcgggcg	gtggaggcca	cgggggagaa	60
agtgtgcgc	tacgagacct	tcattcagtga	cgtgtctgcag	cgggacttgc	gaaaggtgct	120
ggaccatcga	gacaaggtat	atgagcagct	ggccaaatac	cttcaactga	gaaatgtcat	180
tgagcgactc	caggaagcta	agcactcgga	gttatatatg	caggtggatt	tggtgtgtaa	240
cttcttcgtt	gacacagtgg	tcccagatac	ttcacgcata	tatgtggccc	tggtgatagg	300
ttttttcctg	gagttgacac	tgccagaagc	tctcaagttc	attgatcgta	agagctctct	360
cctcacagag	ctcagcaaca	gcctcaccaa	ggactccatg	aatatcaaag	cccatatcca	420
catgttgcta	gaggggctta	gagaactaca	aggcctgcag	aatttcccag	agaagcctca	480
ccattgactt	cttcccccca	tcctcagaca	ttaaagagcc	tgaatgccaa	aaaaaaaaaa	540
aaaaaaaaac	tcgag					555

&lt;210&gt; 72

&lt;211&gt; 567

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature



&lt;222&gt; (1)...(567)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 72

gaattcggca	cgagggtctg	tggagttgtt	agtgttctat	ggcaacacct	tctttgtggt	60
tctcattgtc	atccttgtgc	tgttggatcat	cgatgccgtg	cgcgaaattc	ggaagtatga	120
tgatgtgacg	gaaaagggtga	acctccagaa	caatcccggg	gccatggagc	acttccacat	180
gaagcttttc	cgtgccccaga	ggaatctcta	cattgctggc	ttttccttgc	tgctgtcctt	240
cctgcttaga	cgctctggtga	ctctcatttc	gcagcaggcc	acgctgctgg	cctccaatga	300
agcctttaa	aagcaggcgg	agagtgtctag	tgaggcggcc	aagaagtaca	tggaggagaa	360
tgaccagctc	aagaaggag	ctgctgttga	cggaggcaag	ttggatgtcg	ggaatgctga	420
ggtgaagttg	gaggaagaga	acaggagcct	gaaggctgac	ctgcagaagc	taaaggacga	480
gctggccagc	actaagcaaa	aactagagaa	agctgaaaac	caggttctgg	ccatgcggaa	540
gcagtctgag	ggcctcacca	aggagta				567

&lt;210&gt; 73

&lt;211&gt; 254

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(254)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 73

gaattcggca	cgagcctgga	caaggagaga	gtgcggntgc	tgagagccga	gcccagcaat	60
cccgatccctc	tgagtcgtga	agaaggagg	cagcgagggg	gttggggttg	gggcctgagg	120
caagccccc	ggctccgctc	ttgccagagg	gacaggagcc	atggctcaga	aaatggactg	180
tggtgcgggc	ctcctcggct	tccaggctga	ggcctccgta	gaagacagcg	ccttgcttat	240
gcagaccttg	atgg					254

&lt;210&gt; 73

&lt;211&gt; 516

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 74

gaattcggca	cgagcagccc	tgggtgagc	cgcgccgcac	catgcccgcc	gtggacaagc	60
tctgtctaga	ggaggcggtg	caggacagcc	cccagactcg	ctctttactg	agcgtgtttg	120
aagaagatgc	tggcaccctc	acagactata	ccaaccagct	gctccaggca	atgcagcgcg	180
tctatggagc	ccagaatgag	atgtgcctgg	ccacacaaca	gctttctaag	caactgctgg	240
catatgaaaa	acagaacttt	gctcttggca	aaggtgatga	agaagtaatt	tcaacactcc	300
actatttttc	caaaagtggg	gatgagctta	atcttctcca	tacagagctg	gctaaccagt	360
tggcagacac	aatggttcta	cctatcatac	aattccgaga	aaaggatctc	acagaagtaa	420
gcacttttaa	ggatctatct	ggactcgcta	gcaatgagca	tgacctctca	atggcaaaat	480
acagcaggct	gcctaagaaa	aaggagaatg	agaagg			516

&lt;210&gt; 75

&lt;211&gt; 468

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 75

gaattcggca	cgagcagggg	cgacgcccgag	aatgggagct	gactgatatg	gtggtgtggg	60
tgactggagc	ctcgagtggg	attggtgagg	agctggctta	ccagttgtct	aaactaggag	120
tttctcttgt	gctgtcagcc	agaagagtgc	atgagctgga	aagggtgaaa	agaagatgcc	180
tagagaatgg	caatttaaaa	gaaaaagata	tacttgtttt	gcccttgac	ctgaccgaca	240
ctggttccca	tgaagcggct	accaaagctg	ttctccagg	gtttggtaga	atcgacattc	300

## 23

tggtcaacaa	tggtggaatg	tcccagcgtt	ctctgtgcat	ggataccagc	ttggatgtct	360
acagaaagct	aatagagctt	aactacttag	ggacggtgtc	cttgacaaaa	tgtgttctgc	420
ctcacatgat	cgagaggaag	caaggaaaga	ttgttacttg	tgaatagc		468

<210> 76  
 <211> 349  
 <212> DNA  
 <213> Homo sapien

<400> 76						
gaattcggca	cgagctcgac	tcttagcttg	tcggggacgg	taaccgggac	ccggtgtctg	60
ctctgtgcgc	cttcgcctcc	taatccctag	ccactatgcg	tgagtgcac	tccatccacg	120
ttggccaggc	tggtgtccag	attggcaatg	cctgctggga	gctctactgc	ctggaacacg	180
gcattccagcc	cgatggccag	atgccaaagt	acaagaccat	tgggggagga	gatgactcct	240
tcaaacacctt	cttcagttag	acggggcgctg	gcaagcacgt	gccccgggct	gtgtttgtag	300
acttgaacc	cacagtcatt	gatgaagttc	gcactggcac	ctaccgcca		349

<210> 77  
 <211> 469  
 <212> DNA  
 <213> Homo sapien

<400> 77						
ataggcacat	acacatacac	agtctcagca	aggttataaa	gaaccctgtc	aggtccactt	60
gcaacatggc	cttgctactt	ggattagctc	ctttaagcct	gaaaataact	ttcctgggtca	120
tggaagaact	ggacgcatct	tttaacttat	gaaatagaag	ttgaacttga	aaactctttt	180
taaaaaatcc	tggttttgca	ggacagctac	ataatgaatg	tatatattaa	gactgtagct	240
gaattgcaca	tgaaatcaga	ttgccaaactt	cttgactttc	aatgttagac	atttatcctt	300
aagtgtgag	cgatatatgt	agcatgctgt	gaaatgtctg	ttatagctct	ttaattcatc	360
agtattaata	cagaattatc	atttgcgttt	cttggtaactt	tttattcaat	gtaatcagaa	420
gctgtgatgt	tttgcctttg	tagtcctgtg	ctttgggtact	gtaattttt		469

<210> 78  
 <211> 399  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(399)  
 <223> n = A,T,C or G

<400> 78						
gcgctcgggt	tgagggctcg	gcgcgggggtt	tctgtttcct	tcttctgcgc	ggctgcagct	60
cgggacttcg	gcctgaccca	gcccccatgg	cttcagaaga	gctacagaaa	gatctagaag	120
aggtaaaggt	gttgctggaa	aaggctacta	ggaaaagagt	acgtgatgcc	cttacagctg	180
aaaaatccaa	gattgagaca	gaaatcaaga	acaagatgca	acagaaatca	cagaagaaag	240
canaacttct	tgataatgaa	aaaccagctg	ctgtgggtgc	tcccattaca	acgggctata	300
cggtgaaaat	cagtaattat	ggatgggac	aagtcagata	agtttgtgaa	aatctacatt	360
accttaactg	gagttcatca	agttcccact	gagaatgtg			399

<210> 79  
 <211> 439  
 <212> DNA  
 <213> Homo sapien

<400> 79						
ccgagaagct	gggctttgct	ggtcttgtac	aggagatctc	atttgggaca	actaaggata	60
aaatgctggt	catcgagcag	tgtaagaact	ccagagctgt	aaccattttt	attagaggag	120

24

gaaataagat gatcattgag gaggcgaaac gatcccttca cgatgctttg tgtgtcatcc	180
ggaacctcat ccgcgataat cgtgtggtgt atggaggagg ggctgctgag atatcctgtg	240
ccctggcagt tagccaagag gcggataagt gccccacctt agaacagtat gccatgagag	300
cgtttgccga cgactggag gtcattcccca tggccctctc tgaaaacagt ggcatgaatc	360
ccatccagac tatgaccgaa gtccgagcca gacaggtgaa ggagatgaac cctgctcttg	420
gcatcgactg ttgcacaa	439

&lt;210&gt; 80

&lt;211&gt; 437

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(437)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 80

aattaacatc ttttttgttt aggcattgtc aattaatgct gtagctatca tagctntgct	60
cttacctgaa gccttgtccc caccacacag gacagccttc ctactgaaga gaatgtcttt	120
gtgtgtccga agttgagatg gcctgcccta ctgccaaaga ggtgacagga aggctgggag	180
cagctttgtt aaattgtgtt cagttctgtt acacagtgc tggccctttg ttgggggtat	240
gcatgtatga acacacatgc ttgtcggaaac gctttctcgg cgtttgtccc ttgggtctca	300
tctcccccac tcctgtgcct actttgcctg agttcttcta ccccgagcag tggcagccac	360
attgggagtc tgtttgttcc agtggggttg agctgtcttt gtcgtggaga tcttggaact	420
ttgcacatgt cactact	437

&lt;210&gt; 81

&lt;211&gt; 472

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(472)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 81

atattttant aatgcagagc tatagtctca attgttactt tataaggtgg ttttattaac	60
aaacccaaat cctggatttt cctgtctttg ctgtattttg aaaaacacgt gttgactcca	120
ttgttttaca ttagcaaaag tctgccatct gtgtctgctg tattataaac agataagcag	180
cctacaagat aactgtattt ataaaccact cttcaacagc tggctccagt gctgggttta	240
gaacaagaat gaagtcattt tggagtcttt catgtctaaa agatttaagt taaaaacaaa	300
gtgttacttg gaaggttagc ttctatcatt ctggatagat tacagatata ataaccatgt	360
tgactatggg ggagagacgc tgcattccag aaacgtctta acacttgagt gaatcttcaa	420
aggaccctga cattaaatgc tgaggcttta atacacacat attttatccc aa	472

&lt;210&gt; 82

&lt;211&gt; 448

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(448)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 82

gttcagtgnr gccctcagag ctcttgctgt tagctggcag ctgacgctgc taggatagtt	60
---	----

25

```
<210> 83
<211> 270
<212> DNA
<213> Homo sapien
```

```
<210> 84
<211> 359
<212> DNA
<213> Homo sapien
```

```
<220>
<221> misc_feature
<222> (1)...(359)
<223> n = A,T,C or G
```

```
<210> 85
<211> 371
<212> DNA
<213> Homo sapien
```

```
<220>
<221> misc_feature
<222> (1)...(371)
<223> n = A,T,C or G
```

$\langle 210 \rangle$	86
$\langle 211 \rangle$	500

26

<212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(500)  
 <223> n = A,T,C or G

<400> 86  
 ctgcagcccg ggggatccac tagtttincta tgatcattaa actcattctc agggttaaga 60  
 aaggaatgta aattttctgcc tcaatttgta cttcatcaat aagtttttga agagtgcaga 120  
 ttttttagtca ggtcttaaaa ataaactcac aaatctggat gcattttctaa attctgcaaa 180  
 tgtttctctgg ggtgacttaa caaggaataa tcccacaata tacctagcta cctaatacat 240  
 ggagctgggg ctcaaccacac tgtttttaag gatttgcgct aacttggggc tgaggaaaaa 300  
 taagtagtnc gaggaagtag tttttaaatg tgagcttata gatanaaaca gaatatcaac 360  
 ttaattatga aattgttaga acctgttctc ttgtatctga atctgattgc aattactatt 420  
 gtactgatag actccagcca ttgcaagtct cagatatctt agctgtgtag tgattcttga 480  
 aattcttttt aagaaaaatt 500

<210> 87  
 <211> 550  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(550)  
 <223> n = A,T,C or G

<400> 87  
 ctgcagcccg ggggatccac tagtccantg tgggtggaatt ccaggaactg gaccagggnnc 60  
 tggagcggat ctccaccatg cgccttccgg atgagcgggg ccctctggag cacctctact 120  
 gctggaactb ccccaactgt gacagcatg gctgtacaa cctcaaacag tgcagatgt 180  
 ctctgaacgg gcagcgtggg gagtgtgtgt gtgtgaaccc caacaccggg aagctgatcc 240  
 agggagcccc caccatccgg ggggaccccg agtgcacat cttctacaat gagcagcagg 300  
 aggtctcggg ggtgcacacc cagcgggatgc agtagaccgc agccagccgg tgcttggcgc 360  
 ccctgcccc cgcctctctc caaacaccgg cagaaaacgg agagtgttg ggtggtgggt 420  
 gctggaggat tttccagttc tgacacacgt atttatattt ggaaagagac cagcaccgag 480  
 ctcggcacct cccgggcctc tctcttccca ngctgcagat gccacacctg ctcttcttg 540  
 ctttccccgg 550

<210> 88  
 <211> 429  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(429)  
 <223> n = A,T,C or G

<400> 88  
 gggaccagac tcgtctcagg ccanttgcag ctttctcagc caaacgcoga ccaaggaaaa 60  
 ctactacca tgagaattgc agtgatttgc ttttgcctcc taggcatcac ctgtgccata 120  
 ccagttaaac aggtgatctc tggagttctt gaggaaaagc agcttttaca caaataccca 180  
 gatgtctgtg ccacatggct aaaccctgac ccatctcaga agcagaatct cctagcccca 240  
 cagaatgctg tgtcctctga agaaccaat gacttttaac aagagacctt tccaagtaag 300  
 tccaacnaaa gccatgacca catggatgat atggatgatg aagatgatga tgaccatgtg 360  
 gacagccagg actccattga ctcgaaacac tctgatgatg tanatgacac tgatgattct 420

27

caccagtct

429

&lt;210&gt; 89

&lt;211&gt; 477

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(477)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 89

ttttaattta	caccaagaac	ttctcaataa	aagaaaatca	tgaatgctcc	acaatttcaa	60
cataccacaa	gagaagttaa	tttcttaaca	ttgtgttcta	tgattatttg	taagaccttc	120
accaagtctt	gatattcttt	aaagacatag	ttcaaaattg	cttttgaaaa	tctgtattct	180
tgaaaaatct	cttgttgtgt	attaggtttt	taaataccag	ctaaaaggatt	acctcactga	240
gtcatcaggt	accctcctat	tcagctcccc	aagatgatgt	gtttttgctt	accctaagag	300
aggntttctt	cttattttta	gataattcaa	gncttagat	aaattatggt	ttctttaagt	360
gtttatggta	aactctttta	aagaaaattt	aatatgttat	agctgaatct	ttttggtaac	420
tttaaatctt	tatcatagac	tctgtacata	tgttcaaatt	agctgcttgc	ctgatgt	477

&lt;210&gt; 90

&lt;211&gt; 310

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(310)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 90

ctgcagcccg	ggggatccac	tagtcanttt	attgacacta	tttgaaactt	ttgaaatata	60
aacggagagg	ctttctgttg	agacattgtc	accaaaca	tttttgaaa	tgttcctgaa	120
actaatttgg	gtttaaagat	taaaagggtt	gttaccatto	ttatctgagt	agttgggagg	180
aggggaatac	cacttttagt	catttgga	atatagacat	atttcttttg	ctttcttaaa	240
acagcttaaa	atgatgaact	tttataattt	taatttgaag	attgaataaa	tattttttat	300
aaagataaaa						310

&lt;210&gt; 91

&lt;211&gt; 532

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(532)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 91

ctgcagcccg	ggggatccac	tagtcatgat	gtgtgttgta	ttttaaaaat	tatctgcaac	60
cttaattcag	ctgaagtact	ttatatttca	aaagaatgaa	taacattgat	aataaaatcg	120
ctactttaag	gggtttgtcc	aaaataaata	ttgtggcctt	atatatcaca	ctattgtaga	180
aagtattatt	taattttaat	ggatgcaggt	tgtctactaa	agaaagatta	tatataacta	240
tgctaattgt	tcataatcaa	cagaaaccaa	gatagagcta	caaactcagc	tgtacagttc	300
gtacactaaa	ctcttcttgc	ttttgcatta	taaggaaatta	agtctccgat	tattagggtga	360
tcaccctgga	tgatcagttt	tctgctgaag	gcacctactc	agtatctttt	cctctttatc	420
actctgcatt	ggtgaattta	atcctctcct	ttgtgttcaa	cttttgtgtg	cttttaaaat	480

28

cagctttatt ctaaagcaaa tctgtgtcta ctttaaaaaa ctgnaaatgg aa 532

<210> 92  
 <211> 608  
 <212> DNA  
 <213> Homo sapien

<400> 92  
 .cactactgtc ttctccttgt agctaatacaa tcaatattct tcccttgccct gtgggcagtg 60  
 gagagtgtcg ctgggtgtac gctgcacctg cccactgagt tggggaaaga ggataatcag 120  
 tgagcactgt tctgctcaga gctcctgac taccacccc cctaggatcc aggactgggt 180  
 caaagctgca tgaaccagg ccctggcagc aacctgggaa tggctggagg tgggagagaa 240  
 cctgacttct ctttccctct ccctcctcca acattactgg aactctatcc tgttaggac 300  
 ttctgagctt gtttccctgc tgggtgggac agaggacaaa ggagaaggga gggctagaa 360  
 gaggcagccc ttctttgtcc tctggggtaa atgagcttga cctagagtaa atggagagac 420  
 caaaagcctc tgatttttaa tttccataaa atgttagaag tatatatata catatatata 480  
 tttctttaaa tttttgagtc tttgatatgt ctaaaaatcc attccctctg ccctgaagcc 540  
 tgagtgaagc acatgaagaa aactgtgttt catttaaaga tgttaattaa atgattgaaa 600  
 cttgaaaa 608

<210> 93  
 <211> 519  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)... (519)  
 <223> n = A,T,C or G

<400> 93  
 ctgcagcccc ggggatccac tagtccagtg tgggtgaatt ctaaagaagt aggtgctgca 60  
 ttttaataat tgctttttct gtgtattttg tattgggctg ggggatagca tcaaaggttg 120  
 aactttttga gctttctatg aaaaacccca ggaccttctt tctttggcca tttctatgga 180  
 aatgcgatgt cagatggatg gtaatgggtc cctccagtggt ctgtgagacc tcattgcgca 240  
 ttgtctactg gagctttagt cttctgagac ggaggaaaac tgctgaatac tctggattca 300  
 tctatgtcta caatgttgca tttatgaaaa actacactgn gctaggcgca ttctaggaca 360  
 tgaatatgac cacacctctt ttcaccgggt gtttctgtag caagttttca tattcttttc 480  
 aaacaatggt ttctctgcgt taattattga ggaaaaaaa 519

<210> 94  
 <211> 569  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)... (569)  
 <223> n = A,T,C or G

<400> 94  
 ctgcagcccc ggggatccac tagtccantg tgggtgaatt cgtctgcgag ccaggattcc 60  
 cgatccagag acaatggccc cgatgggatg gagccgaag gcgtcatcga gagtaactgg 120  
 aatgagattg ttgacagctt tgatgacatg aacctctcgg agtcccttct ccgtggcatc 180  
 tacgctatg gttttgagaa gccctctgcc atccagcagc gagccattct acctgtatc 240  
 aagggttatg atgtgattgc tcaagcccaa tctgggactg ggaaaacggc cacatttgcc 300  
 atatcgattc tgcagcagat tgaattagat ctnaagcca cccaggcctt ggtcctagca 360  
 cccactcgag aattggctca gcagatacag aagtggtcn tggcactagg agactacatg 420

29

ggcgctcct	gtcacgcctg	tatcgggggc	accaacgtgc	gtgctgaggt	gcagaaactg	480
cagatggaag	ctccccacat	catcgtgggt	acccttgcc	gtgtgttga	tatgcttaac	540
cggagatacc	tgtcccccaa	atacatcaa				569

<210> 95  
<211> 260  
<212> DNA  
<213> Homo sapien

gacaagctcc	tggtcttgag	atgtcttctc	gttaaggaga	tgggcctttt	ggaggtaaag	60
gataaaatga	atgagttctg	tcatgattca	ctattctaga	acttgcatga	cctttactgt	120
gttagctctt	tgaatgttct	tgaatattta	gactttcttt	gtaaacaaat	gatatgtcct	180
tatcattgta	taaaagctgt	tatgtgcaac	agtgtggaga	ttccttgctc	gatttaataa	240
aatacttaaa	cactgaaaaa					260

<210> 96  
<211> 438  
<212> DNA  
<213> Homo sapien

atttctcttt	agttctttgc	aagaaggtag	agataaagac	actttttcaa	aatggcaat	60
ggtatcagaa	ttcctcaagc	aggcctggtt	tattgaaaat	gaagagcagg	aatatgttca	120
aactgtgaag	tcatccaaag	gtggtcccg	atcagcgggt	agcccctatc	ctaccttcaa	180
tccatcctcg	gatgtcgtcg	ccttgcataa	ggccataatg	gttaaagggt	tggatgaagc	240
aaccatcatt	gacattctaa	ctaagcgaaa	caatgcacag	cgtcaacaga	tcaaagcagc	300
atatctccag	gaaacaggaa	agcccctgga	tgaacactg	aagaaagccc	ttacagggtca	360
ccttgaggag	gttgttttag	ctctgctaaa	aactccggcg	caatttgatg	ctgatgaact	420
tcgttgctgc	catgaagg					438

<210> 97  
<211> 471  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)... (471)  
<223> n = A, T, C or G

tcgttatccg	cgatngttt	cctggcagct	acattcctgc	tcctggcgct	cagcacccgt	60
gccaggccg	aaccgggtgca	gttcaaggac	tgcatatttc	agtctaaaag	cagcaaggcc	120
gtggtgcatg	gcatcctgat	ggcggtccca	gttccctttc	ccattcctga	gcctgatggt	180
tgtaagagt	gaattaaactg	ccctatccaa	aaagacaaga	cctatagcta	cctgaataaa	240
ctaccagtga	aaagcgaata	tcctctata	aaactgggtg	tggagtggca	acttcaggat	300
gacaaaaacc	aaagtctctt	ctgctgggaa	atcccagtac	agatcgtttc	tcatctctaa	360
gtgcctcatt	gagttcggtg	catctggcca	atgagtctgc	tgagactctt	gacagcacct	420
ccagctctgc	tgcttcaaca	acagtgaact	gctctccaat	ggtatccagt	g	471

<210> 98  
<211> 578  
<212> DNA  
<213> Homo sapien

ccagtgtggt	ggaattcgca	gccaccgcca	cccattggaa	tggccaacag	gggacctgca	60
tatggcctga	gccgggaggt	gcagcagaag	attgagaaac	aatatgatgc	agatctggag	120



## 30

cagatcctga	tccagtggat	caccacccag	tgccgaaagg	atgtgggccc	gccccagcct	180
ggacgcgaga	acttccagaa	ctggctcaag	gatggcacgg	tgctatgtga	gctcattaat	240
gcactgtacc	ccgaggggca	ggccccagta	aagaagatcc	aggcctccac	catggccttc	300
aagcagatgg	agcagatctc	tcagttcctg	caagcagctg	agcgctatgg	cattaacacc	360
actgacatct	tccaaactgt	ggacctctgg	gaaggaaaga	acatggcctg	tgtgcagcgg	420
acgctgatga	atctgggtgg	gctggcagta	gcccagatg	atgggctctt	ctctggggat	480
cccaactggt	tccttaagaa	atccaaggag	aatcctcgga	acttctcgga	taaccagctg	540
caagagggca	agaacgtgat	cgggttacag	atgggcac			578

&lt;210&gt; 99

&lt;211&gt; 416

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(416)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 99

caagaatgtg	cctaactggc	atanagatct	ggtacgagtg	tgtgaaaaca	tccccattgt	60
gntgngtggc	aacaaagtgg	atattaagga	caggaaagtg	aaggcgaaat	ccattgtctt	120
ccaccgaaag	aagaatcttc	agtactacga	catttctgcc	aaaagtaact	acaactttga	180
aaagcccttc	ctctggcttg	ctaggaagct	cattggagac	cctaacttgg	aatttgttgc	240
catgcctgct	ctcgcccac	cagaagtgtg	catggacca	gcttggcag	cacagtatga	300
gcacgactta	gaggttctc	anacaactgc	tctcccggat	gaggatgatg	acctgtgaga	360
atgaagctgg	agccancn	cagaagtcta	gttttatang	cagctgtcct	gtgatg	416

&lt;210&gt; 100

&lt;211&gt; 441

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(441)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 100

agacaatgac	cccacgntc	ctccttatga	ctccattcaa	atctacgggt	atgaaggcag	60
gggctcagtg	gccgggtccc	tgagctccct	agagtcggcc	accacagatt	cagacttgga	120
ctatgattat	ctacagaact	ggggacctcg	ttttaagaaa	ctagcagatt	tgtatggttc	180
caaagacact	tttgatgacg	attcttaaca	ataacgatac	aaatttggcc	ttaagaactg	240
tgtctggcgt	tctcaagaat	ctanaagatg	tgtaaacagg	tattttttta	aatcaaggaa	300
aggctcattt	aaaacaggca	aagttttaca	gagaggatac	atttaataaa	actgcgagga	360
catcaaagtg	gtaaatactg	tgaaatacct	tttctcacia	aaaggcaaatt	attgaagttg	420
tttatcaact	tcgctagaaa	a				441

&lt;210&gt; 101

&lt;211&gt; 521

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 101

ccagcgccca	gagagacacc	agagaaccca	ccatggcccc	cttgagccc	ctggcttctg	60
gcacctgtgt	gttgctgtgg	ctgatagccc	ccagcagggc	ctgcacctgt	gtcccacccc	120
accacagac	ggccttctgc	aattccgacc	tcgtcatcag	ggccaagttc	gtggggacac	180
cagaagtcaa	ccagaccacc	ttataccagc	gttatgagat	caagatgacc	aagatgtata	240
aagggttcca	agccttaggg	gatgccgctg	acatccggtt	cgtctacacc	cccgcctagg	300

31

```

agagtgtctg cggatacttc cacaggctcc acaaccgcag cgaggagttt ctctattgctg 360
gaaaactgca ggatggactc ttgcacatca ctacctgcag ttctgtggct ccctggaaca 420
gcctgagctt agctcagcgc cggggcttca ccaagaccta cactgttggc tgtgaggaat 480
gcacagtgtt tccctgttta tccatcccct gcaaaactgca g 521

```

```

<210> 102
<211> 520
<212> DNA
<213> Homo sapien

```

```

<400> 102
gaagaaaaag aaattctgat acgggacaaa aatgctcttc aaaacatcat tctttatcac 60
ctgacaccag gagttttcat tggaaaagga tttgaacctg gtgttactaa cattttaaag 120
accacacaag gaagcaaaat ctttctgaaa gaagtaaag atacacttct ggtgaatgaa 180
ttgaaatcaa aagaatctga catcatgaca acaaatgggt taattcatgt ttagataaaa 240
ctcctctatc cagcagacac acctgttgga aatgatcaac tgctggaaat acttaataaa 300
ttaatcaaat acatccaaat taagtttgtt cgtggtagca ccttcaaaga aatccccgtg 360
actgtctata gaccacact aacaaaagtc aaaattgaag gtgaacctga attcagactg 420
attaagaag gtgaaacaat aactgaagt atccatggag agccaattat taaaaaatc 480
accaaataca ttgatggagt gcctgtggaa ataactgaaa 520

```

```

<210> 103
<211> 479
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(479)
<223> n = A,T,C or G

```

```

<400> 103
ctgattctca ggcctagaagt gtcacttttc ttctctgtac ttccaaagca ctctctgata 60
tttttattat ggcatttata tatagttcat ttatatttaa attttaattc catgaacaat 120
caagtaccaa gtataatgga gaaggtgctc atcctctgcc ttcttgagc ttctgggtga 180
tgccaggccc aagtctttgt ggcacccagc tccatgcttt gaatactatg tggctgaatg 240
aatttttaaa atctcaaagc agttaaacag caggaaagcc cattaacttc gtactgaaaa 300
agcaacatac tgtgatgata cgggatgaca tcatttcagg ttgggcatac aaaaaagtaa 360
ggaagctaaa ctaagactat actcaccagg ccatttagaa gttttaaata atgcctccac 420
tatttttttt cttanacata gcttttaatg gggaaatgga attagtaaat gactatttt 479

```

```

<210> 104
<211> 324
<212> DNA
<213> Homo sapien

```

```

<400> 104
tgaccatcca tatccaatgt tctcatttaa acattaccca gcatcattgt ttataatcag 60
aaactctggt ccttctgtct ggtggcactt agagtctttt gtgcataat gcagcagtat 120
ggagggagga ttttatggag aaatggggat agtcttcatt accacaaata aataaaggaa 180
aactaagctg cattgtgggt ttgaaaagg ttattatact tcttaacaat tctttttttc 240
agggactttt ctactgttat gactgttact tgaccttctt tgaaaagcat tcccaaatg 300
ctctatttta gatagattaa catt 324

```

```

<210> 105
<211> 541
<212> DNA
<213> Homo sapien

```

32

&lt;400&gt; 105

cttggttcca	gaacctgacg	acccggcgac	ggcgacgtct	cttttgacta	aaagacagtg	60
tccagtgtc	cagcctagga	gtctacggg	accgcctccc	gcgccgccac	catgccaac	120
ttctctggca	actggaaaat	catccgatcg	gaaaacttcg	aggaattgct	caaagtgtcg	180
ggggtgaatg	tgatgctgag	gaagattgct	gtggctgcag	cgtccaagcc	agcagtggag	240
atcaaacagg	agggagacac	tttctacatc	aaaacctcca	ccaccgtgcg	caccacagag	300
attaacttca	aggttgggga	ggagtgtgag	gagcagactg	tggatgggag	gcctgtgaag	360
agcctggtga	aatgggagag	tgagaataaa	atggtctgtg	agcagaagct	cctgaaggga	420
gaggggccca	agacctcgtg	gaccagagaa	ctgaccaacg	atggggaact	gatcctgacc	480
atgacggcgg	atgacgttgt	gtgcaccagg	gtctacgtcc	gagagtga	ggccacaggt	540
a						541

&lt;210&gt; 106

&lt;211&gt; 391

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 106

cagaagtctt	ggactgcaac	tacatacatg	gaatatgaga	ctcttaccct	gggagatatg	60
attaggagaa	gtggtggcca	cagtcgaaaa	atcccaaggc	ccaaacctgc	accactgact	120
gctgaaatac	agcaaaagat	tttgcatctt	ccaacatctt	gggactggag	aaatgttcat	180
ggtatcaatt	ttgtcagtc	tgctcgaac	caagcatcct	gtggcagctg	ctactcattt	240
gcttctatgg	gtatgctaga	agcgagaatc	cgtataactaa	ccaacaattc	tcagacccca	300
atcctaagcc	ctcaggaggt	tgtgtcttgt	agccagtatg	ctcaaggctg	tgaaggcggc	360
ttcccatacc	ttattgcagg	aaagtacgcc	c			391

&lt;210&gt; 107

&lt;211&gt; 462

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; miss feature

&lt;222&gt; (1)...(462)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 107

cgtgacctca	agatgngcca	ctctgactgg	aagagtggag	agtactggat	tgaccccaac	60
caaggctgca	acctggatgc	catcaaagtc	ttctgcaaca	tggagactgg	tgagacctgc	120
gtgtacccca	ctcagcccag	tgtggcccag	aagaactggt	acatcagcaa	gaaccccaag	180
gacaagaggc	atgtctgggt	cggcgagagc	atgaccgatg	gattccagtt	cgagtatggc	240
ggccagggct	ccgaccctgc	cgatgtggcc	atccagctga	ccttcctgcg	cctgatgtcc	300
accgaggcct	cccagaacat	cacctaccac	tgcaagaaca	gcgtggccta	catggaccag	360
cagactgggn	acctcaataa	ggccctgctc	ctccagggct	ccaacganat	ngagatccgc	420
gccgagggca	acagccgctt	cacctacagc	gtcactgtcg	at		462

&lt;210&gt; 108

&lt;211&gt; 580

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 108

atataccatt	taatacatctt	acactttctt	atttaagaag	atattgaatg	caaaataatt	60
gacatataga	actttacaaa	catatgtcca	aggactctaa	attgagactc	ttcccatgtt	120
acaatctcat	catcctgaag	cctataatga	agaaaaagat	ctagaaactg	agttgtggag	180
ctgactctaa	tcaaatgtga	tgattggaat	tagaccattt	ggcctttgaa	ctttcatagg	240
aaaaatgacc	caacatttct	tagcatgagc	tacctcatct	ctagaagctg	ggatggactt	300
actatttctg	tttatatttt	agatactgaa	aggtgctatg	cttctgttat	tattccaaga	360
ctggagatag	gcagggctaa	aaaggtatta	ttatttttcc	tttaatgatg	gtgctaaaat	420

## 33

tcttcctata	aaattcctta	aaaataaaga	tggtttaatc	actaccattg	tgaaaacata	480
actgttagac	ttccccgttc	tgaaagaaag	agcatcggtc	caatgcttgt	tcactgttcc	540
tctgtcatat	tgtatctgga	atgctttgta	atacttgcat			580

&lt;210&gt; 109

&lt;211&gt; 482

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(482)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 109

caggcgtgca	gtttcccggc	tctccgcgcg	gccggggaag	gtcagcgcgc	taatggcggt	60
cttggcgctc	ggaccctacc	tgacccatca	gcaaaagggt	ttgcggcttt	ataagcgggc	120
gctacgccac	ctcgagtcgt	ggtgcgtcca	gagagacaaa	taccgatact	ttgcttggtt	180
gatgagagcc	cggtttgaag	aacataagaa	tgaaaaggat	atggcgaagg	ccacccagct	240
gctgaaggag	gccgaggaag	aattctggta	ccgtcagcat	ccacagccat	acatcttccc	300
tgactctcct	gggggcacct	cctatgagag	atacnattgc	tacaagggtc	cagaatgggtg	360
cttagatgac	tggcatcctt	ctgagaaggc	aatgtatcct	gattactttg	ccaagagaga	420
acagtggaag	aaactgcgga	gggaaagctg	ggaacgagag	gttaagcagc	tcaggaggga	480
aa						482

&lt;210&gt; 110

&lt;211&gt; 286

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 110

aatcattctg	cactcactgg	gtgcatagea	tggtagagg	ggctagagat	ggacagtcac	60
gcaataacag	acagagcttt	tgtagagctg	taactgagct	atggaatagc	ttotttgatg	180
tactctttg	ccttaaatg	ctttttagtt	ctaagattgt	agaatgatcc	tttcaaattg	240
taattctttt	taacagagat	attttaatat	acttgctttc	ttaaaa		286

&lt;210&gt; 111

&lt;211&gt; 465

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(465)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 111

agctactggt	aagatttgac	agattgtctt	gtctttttcc	agtatatata	ggtatctata	60
tatgtatata	ctgtatatata	ttatatatat	ttattgtatt	aaatatatac	atatgtatat	120
gtatatataa	gtatgtgtat	atatgtatat	atttaataca	attattaaat	tgtattattg	180
tattaaatgt	atacatatat	acacacatat	atacatatat	gcataatatt	aacacagtta	240
aaataacact	aaatgtacca	ttttgtttct	ggccttttca	gntaatgtta	tgaagaattt	300
ttctattttg	ttaaactttc	ccaaaaacat	taaactgcat	tatgtttctga	gagtagatgt	360
accacaatta	attctacccat	ttctgtattg	ttggccatgt	aggttgttct	taattttctc	420
attattatga	atgcatgtga	caatcattgg	ttttgcctaa	agttg		465

&lt;210&gt; 112

&lt;211&gt; 773

34

<212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(773)  
 <223> n = A,T,C or G

<400> 112  
 ttttttttca gttttttgcag ttggtgtggt tagcagatac tttcttagaa taaaattgat 60  
 aactcaattt gattttttaaa aagttgtttt agtgatttaa aatgttgata tggaaaaata 120  
 ttaaacatta tatagatagt aggcaaattc atataccta atgcataatta gcttgtagca 180  
 ttttaaatata aaatctaaat ttcttgatat attgccacat tagttgtaat gtttaataaaa 240  
 tgggtggttaa agattttattt gtaatttaaat ctgtgtactt agttgccatg gacctctctt 300  
 ttagcttttc ataaataaat atcctttaat accttacctc ctcccttcaa ttgactgatg 360  
 ctgggatagg gtgttctttg gagcttatct tggtaaagaa ggtcagaagt gacatataac 420  
 cctattccct aggggccgag ggtgctttcc ttacagagtt gtattttaag tgagtcaact 480  
 cctgagccag catctactaa gagaaccttc aaacataatc ataggcattt aaataatttg 540  
 aaaaatcaaa ttcttgcat taaaaacatt tatccttang ttcatttctt tataanggtt 600  
 ctctttttaa aaaaaaggat tggattttat gaaaggaat ggtggctggg tttttcttaa 660  
 gcattatgna aagggggagt acccctattt ttctttctcc ccanggaaa tgggtgaagg 720  
 gaacctgggc aatgcccatg attgnaaaaa ttccacttcc nttgaacaat ggg 773

<210> 113  
 <211> 543  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(543)  
 <223> n = A,T,C or G

<400> 113  
 gtttttctga tttgaaaaat tgtttataat attactataa gatgagatta acaatctttg 60  
 taaaaatcag attatgtttt gggcttaaaa aaaaccctag tgttttctac tattagtgtgta 120  
 ctcaaagtat ttgtgagtga tagtactcaa atgagaattg catttaattt gtacatagtt 180  
 aaatcgtctt gttttgaagc acaaagtcag gatgtttctc atcagaattt tctgtttgaa 240  
 tagggaaaag tggcatttgt catgaggcat cattaaaaac ggaaagcaga ggaataattg 300  
 gaaagctaca gaaaaaagat tcacatgaaa aaccaagctg aagaaaaaag ctgcagaaca 360  
 gtttcgaatg cgacttaaaa aattaagcca agatgnaaat gaagctagaa agggagatct 420  
 cagaaagaag ccagccgagc ctgtcaaaca actggatgtc cagaaaaata ttcaggttcc 480  
 ccaggggaaa gcatgggtac tgggtttgan gcttgaaga nggagactgg aaggaaagaa 540  
 tga 543

<210> 114  
 <211> 550  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(550)  
 <223> n = A,T,C or G

<400> 114  
 ggaaagaggt aagcggtaaa ttacatagac tgctggagga agagtgttcc agtggagaga 60  
 aacagagcta gtgcaaagc cctgaggtga gagcatgcct ggtgtgatcc ggggatggca 120  
 aggaggccag ggtggtgat gaggagttag caaggaggan agtacgagga taagaagcca 180

35

```

ncaaggaaaa atggcagtgg ggcggatcac ctangggctc agtacgccat tgtgaagact      240
ttgcccttttg ctcccaantg gaatgggtac tcnttgaagg cttttaancc caggaanaaa      300
cattgattga tttanaagtt taaanggatc acntttgggt attgtggcca acaagacact      360
gcgggaagaa gcaagaaggg tagaaagcca gnaaaccaac tnaggaggct ttgacagtaa      420
tcctggntga nanacantgg tggctcnggt taaaaagttt tggaaaaaat taaaactggt      480
tgatggtttg tttcctgttc ttgggggcnt aggcattcca actccttacc gaaagggtta      540
ccccttttga

```

&lt;210&gt; 115

&lt;211&gt; 550

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(550)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 115

```

caatgtggca ottaacttan tgggtacaac tgtatcacat catgtgtgaa tcgtgagacc      60
actcaaactc ctctctggga aaacncggct gctccccga tggctggcag gtgttggaac      120
ctcgggtctc cgtccgtctc tggggcaagg tgggtttcct catgtatngc aagagtctat      180
cgtgccgtgc ttctctcttg gcatacagct cacagctctt tggcctatac agtgtggaaa      240
tttatnctcc ggtgctggag gtgttaatgg gaaagagctc ggtaaatgc acttctcact      300
tggcccggtg gtgatgctct acatgactga attcctctct nacggggact gacattgtat      360
ctatacacta natccttcca ccanagtggc gttaaggacg gtgtctggga tggaaactga      420
cggtaacang cccanctctc tgaaatgagt ccananatga actacctgca tacctctcta      480
aatcactctg gtctggcatg ntctccgtgc cgaacatat atagtatgt ctctccncaat      540
acgaaaaana

```

&lt;210&gt; 116

&lt;211&gt; 463

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(463)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 116

```

cacaatgtgg tactttactt agttggtaca actgtatcat atcatgtggt gaatcacgtg      60
tgacgtgact ccgcaactcc gcaccagact aactgcacg taatnacagc cngcacncca      120
ggtggacaaa nattgacgca atgttgtgtc antgccaccg tgccacacca cctgtggagg      180
acgtcagttc tctcttcccc caaaaccag gacctctmtg atctcccgac cngaggtcct      240
nggttgtggt gactgagcnc aaaaccgagg tcgttcaact gtacttgacg ctggagtcac      300
atccaganaa agcccgaag acatcacngc cttcgtgtgt cncctctcag tctgcacaga      360
cggctaacgc aggatcattc angtccacaa gctccacccc tcanaaactc tcnaacaagg      420
cagccgaaac acgtttccct gccctccgga gaatacanaa cag

```

&lt;210&gt; 117

&lt;211&gt; 503

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(503)

&lt;223&gt; n = A,T,C or G

```

<400> 117
nncactnatg tgctacgta acttagttgt acaactcgat cctatccatg tggatgaattc 60
tctccagcag tacactgang atacanctta ttgttattga cgtgcgctgc gctcactacc 120
gncagccagg gaatgcgcct caggaaccct ggtgccacc ctggctggca tngccattgt 180
caagggaagag aaacgagntg ccattggagc cctcctactg ccatgagggc ctgaaacaaa 240
ctgtgntatg ctctgcgaag gtctgggtgct aaggtcccgc tggctcacta tggcacacca 300
ctcngggctg aagtttgtgt cctgaaggta ctcancccag tgtggccggg acctggatac 360
gtgcacattg cctgtgcgca aaaccagcat tgtatgtgca catgtagttt gttccactga 420
atgtcncctg gcgctcagat ttcagggaga ttgactctca tctccttgtc ctactaagag 480
agagcacctc acctgaatgt caa 503

```

<210> 118

<211> 560

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(560)

<223> n = A,T,C or G

```

<400> 118
tgggggnnca ctaagtgcta cgttacttag ttgtacgact cgatcctatc atgtggtgaa 60
ttctgnagcn tgggtctcatg agcctctctg gtgcgctgtg tgtatnggta cggcgctctc 120
tatcgcttta tctcttctga ctgcaccgg ggcggcgggc atcacgggcc aagaccctgc 180
acaatgaaga ctgcaggagc aggcgggtgg cccacctggc cctggacctg aagaccnaaa 240
ctggagcagg ctcgngccgg aggactgggc accgcctaca ggccacgtca cccacgggtg 300
ctggnanaac aatgaaaaca agaagaactt ctctacccaa gagagaagtt caaaaccnnc 360
aactcactgt cgggaaattg actaaaactg cngaactgaa gaaaacaacn caaagccnnc 420
tnaagcanag aagngaactg agacgaacat catccnccna actaatgaaa agagagacgt 480
tccctgnaga gacnaagaga gagaaagagc cccagacngc cccggactaa gattctaata 540
agagcttgtt gtaagagaag 560

```

<210> 119

<211> 638

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(638)

<223> n = A,T,C or G

```

<400> 119
acaaaagtgc tacgttactt agctgtacga ctgcgtcatat ccatgtggtg aatcatacgc 60
tattttatat acngtngatc aacatgaagg gttngtgtct gatcccgcgc atcaaaacac 120
gtgttacttt gactccccaa acctactcta gtaataccta ctattgacca gaaccttaca 180
ttacataaac agttncata ttctgtatat atatgtatac tgtattctta ataagtaagc 240
taagaaatgt tattgaaatc ataaggaaa gaaatgtatt atacactgta tgtattgtct 300
gtantgtact gtctgttaca agatgatcgt ctgatgaatg atgcgctgca ccccaactat 360
gtattacaaa caatcncctt tcatttgttc tgacttgctt ctgaaatact ccacacncta 420
tngctttata tggctctggg gtattcaggt tatntatgcc taactgaaaa tcccagaacc 480
tgaagatatg tttctgtgat cncattactg ganaaagaac gcccatcaat actcnccgng 540
tttaacggat cccacactga cncgcatac acagagtgtg naatttgtnt acacttntca 600
cgtanctagc tttgaataac gctcttcttt ttcttccc 638

```

<210> 120

<211> 434

37

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)... (434)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 120

ngnnggggca	caaaagctgc	tatgtttaac	ttagcttggg	tacgactcgt	tcatatccat	60
gtgnttgant	caccgctcta	ctgccaagca	tcatttttgg	tctacgnctc	aanctgtgna	120
aangatgtgg	gttaggggan	tgaagatgca	aacncctagg	gtangggcat	ttanaactga	180
aaagganagg	aaganaagac	ctgcgaacgt	gggggataag	actanaagaa	agacgggaga	240
naatantgtc	tttgancctc	aaatggaaca	tntcccatcc	tatctgttan	aaancaccan	300
gtaaaatggg	atgtntgcac	naaagaataa	gttaaaactaa	acnccggacn	gtgactanaa	360
aatgaangac	cacanatgaa	aaggcgatga	ctngcctgtt	tacctancct	gtanacctat	420
attttcnggg	ttat					434

&lt;210&gt; 121

&lt;211&gt; 631

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)... (631)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 121

caaagcgcta	tggttaatgag	cttgtacgac	tcgtcatatc	ttgtggtgta	tcatattctc	60
tctctctttc	aacaaactcc	ccagctccac	ccgggctcta	cctccgagac	cagganccaa	120
aacgancgaa	gatggctgct	ctgcgcgcc	cgccgcgcc	ctcccgctgc	ccccggcccc	180
gctcgcggtt	ccggctccgg	gtcggatgct	gcaaatgctg	ggatgccgag	ntgtgcgcgg	240
gcccagntgc	gcacggttac	acacaccact	ctggactgga	gaagaatcat	ttatanttct	300
gtgcgcgacc	cgcgctcaaat	gcgcttgctg	aactcacgaa	agnagtcaat	ntgttctaac	360
gngctgaaca	cacgcagacc	ncacnaaagc	gccgatggga	ctgctgcgcg	aacctggaga	420
ctctcaactc	caagaaccgc	gcaaccgggc	ggcctccgct	ccggcgntgg	gaactgtntc	480
cccccgaaat	tggtccggnt	taacgcgacc	cggttanctt	cgtnaaaggg	ngggcctnaa	540
ttcggtgccct	tncnggcggg	gggtgaccgc	c			600
						631

&lt;210&gt; 122

&lt;211&gt; 678

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)... (678)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 122

caaagcggtt	angttaatta	gctggtacga	ctcgtcatat	catgtggtgn	atccacacat	60
ggaatgaggg	tcccgtccac	tctggggctc	tgctgctctg	gtccatgtgc	cagatntaaa	120
tccagatgac	cagttctcctc	ctccctgtct	gcctcggttg	ganacgaatc	accatcactt	180
gncgggcaat	caganattan	aatgattaa	cctggtatca	gcagaaacca	gggaaaccct	240
aagctctgat	ctttgtgca	tcagttacaa	gtggggctct	tcncgcttca	cggcagtgn	300
ctggcacaga	ttcatctcac	atcncagctg	cagcctgaaa	aatttacact	tatactgtct	360
acggataaca	ataccctgna	cttcggcaag	gactanggtg	gaatnaaacn	aatgtggctg	420



38

cacatctgtc	ttctcttccc	gctctgataa	cagtnaaatc	tgaactgctc	tgttggtgtgc	480
tgctgatact	tctatccana	aaagccaagt	acatggaagt	gaatacgcct	ccaatcggtt	540
atccagaaat	gtccaaanag	gaacaggacg	nctacgctcg	cacnccctgac	ctaaccanen	600
aatcnaaaac	caatctnccc	gcaatccctc	gggctgaccc	ctccaaaact	ccngggaatt	660
taaggaaatc	cccccccc					678

&lt;210&gt; 123

&lt;211&gt; 445

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(445)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 123

gaggggggng	caaaagcgct	acttaattag	ctgtacgact	cgtcatatca	tgtggtggat	60
cagcatccag	atggcataat	cggctaattg	cctgggggttc	agatgtatgc	gatgtccggc	120
taatgtgaca	tcttgccanc	tagcttaagg	anggctggct	agaagacatt	gcagaaacag	180
gagctcggcc	cacangtttc	ccaaggctct	caccccatto	catctccagg	gaagctcgcc	240
cagtggcact	gaatggcctc	ctcagcggag	ggtttggaat	caggetgggc	aagaactgct	300
aatctttgcg	ggactgggaa	cagctctccg	gccttctctg	gctccttggt	tctggtgggg	360
aagggagag	ggaaaagaaa	ggaaatctcc	nggcanaaga	ngggacaccc	canacaccga	420
agacacnccc	ccctcctgta	actgt				445

&lt;210&gt; 124

&lt;211&gt; 641

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(641)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 124

gagggggggg	ncaaagcgct	acgttaatta	gctgtacgac	tcgtcatatc	atgtggtgga	60
tcccactaca	angttgtcac	tatatattan	atctatagtn	gagtcngtnt	tcccatcccc	120
tgtaaacgaa	tttactattg	ttggggtagt	gtccctactt	tcctgattaa	ggatctgtgc	180
tggggaacaa	gcnttgcata	ccttatatgt	agttaanatt	tattaacata	tctcatgan	240
ctcattcaca	ctgnanctct	cctnaaaatn	gtgtgctcct	gttacattan	aactaatctg	300
aaataaagac	tctcnaatgc	tgtgcaacat	anttactgtt	tgaaggagca	gtgtnaattg	360
agtaccaatt	tagcatcgat	ttgaaacgca	ccttatttga	actgtgaata	aacactttct	420
gcgtatacta	ctgcttacat	ccaattcngt	gatttaagat	actcgtggta	tagatacact	480
gattgaagtc	cgatatatgc	aaaactcctt	cataggattg	acatgctgat	ntnagtnggc	540
nttcaatgtg	gagtatactt	acntaattgc	taacgtataa	agtattgaan	gttnaatagt	600
cagcttcngt	gnaaaatnng	aaattagtat	ggtncngttc	c		641

&lt;210&gt; 125

&lt;211&gt; 285

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(285)

&lt;223&gt; n = A,T,C or G

39

<400> 125  
 aggggngcac aaagcgctac gttaatnag tgtacgaccg tccatatcag gtgggtggatc 60  
 catatgtccg gtattctctg atgtcangct tattataata gtaccaaccc ttcattctctg 120  
 aaatgtctgg ttctgggtcc ctattatata ccagcactga aaatattcgt atcttagnan 180  
 caaaagcatt taaaaagagt taaaaattta ntcactacta tgcacttcaa ggggagaagc 240  
 tncactgcnt ncttgagnct angcaagatg cnagcncctt ggaag 285

<210> 126  
 <211> 282  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(282)  
 <223> n = A,T,C or G

<400> 126  
 aggggnntgac aaagcggcta cgtaatnag ctggtacgac cgtcatatcn tgtgggtggat 60  
 ccngaacang tagcctcata atcacaacat ccattagcca cagtaaacctg attctgtaac 120  
 tccactggca atgctgattg gtaatggctg cataaaccga gtgtatcaat ttantttcgg 180  
 ttttgagaca aaatctcata ttatacnctg acatctcnaa cttcgatata tgaccaaata 240  
 cgggnagaca ttattcaaan atatttacct tacanaaaaa aa 282

<210> 127  
 <211> 634  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(634)  
 <223> n = A,T,C or G

<400> 127  
 acaaagcggc tacgttantic agctggtagc accgtccata tcatgtgggtg gatcntgaaa 60  
 anctttgatc ggctgcggtg gaaacgttgt cngggccggc aagaagagcc gctgtgnacaa 120  
 tgggtgcatg agttcagccg aacgcangac ggttctcaca cccgtgctgc ggtgttgcca 180  
 tgtccgcacg ggacaatato ctggggaccg gtactggttag taactatgat gcattntgct 240  
 gantgtgaat gatctcaact catgccagct gtcacattca tagaattctc gtaatatatc 300  
 ntcgaaaaat ggtaanatgc tgtgtctttt gccgtcctgt tctatgttta tatcagtcag 360  
 ctgttatgac attctatcag tggttggctg atccatctct gttacnactt tgactcgtct 420  
 cattgccgtt gctatagtc tcaactattgc cagatcaaaa tactgatcac tactaattcc 480  
 nacaananac tctggctgga ccaactgccn gtcattgtctg tgtcttgcta tcacatttaa 540  
 gctactatta ctgtgttgga atgcataatc tcacaacnaa gtgcgaaatg ngtttccgcc 600  
 ttgaatacnc cctactttgc ccctataaag gcgg 634

<210> 128  
 <211> 180  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(180)  
 <223> n = A,T,C or G

<400> 128  
 caaagcgcta cgtaatnag ctgtacgacc gtccatngtc aggtgggtgga tccctgttat 60

40

gtcaagaaaa gtaaatcgtc tcttcaataa ggccttttatt tgggacaggt ttatttcctg 120  
 atatnatntc ttttatactc ttttctctca gaaanaaaaa agtngtntnc tcttattgtc 180

&lt;210&gt; 129

&lt;211&gt; 567

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(567)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 129

acaaagcgct atgttaactt agctgtacga ccgtccatng tcaggtggtg gatcctcccg 60  
 tgtgctggat tcataatgga tctatttaga cagttgagaa taaattattc tattacaata 120  
 atagatgcta atatatatat tatgctgttt ggatatctaa atatttgctc acatccttaa 180  
 tataattttta aaattctaac aatagtactg ttganataaa gttgagccat attganacnc 240  
 tcccanattg gtctagaaaa gttacactgg ttgtctctcc ttatgtcctg ttatccaccc 300  
 tgacgtgccc gctttatatt cttaatgant tggacggaca gtggtatccg atcgttttga 360  
 cgacgtttaca ntactnacca tctatacgtc tacttaattg acagcagatt tcgtagcnct 420  
 cattaggatc tgttccaacn gttggcaaat naccncggan gaagttccng tagttgtcnn 480  
 ctccccctat tgaaacttat gaccnatctt cctttacnca catatcgacc ttcctgacaa 540  
 cncctttttn aaagaactct tcnccca 567

&lt;210&gt; 130

&lt;211&gt; 557

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(557)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 130

agggnntcac aaaagcgcta cgtaaataatnag ctgtacgact cgtcatatca tgtggtggat 60  
 ccgcggcgct ggcgactgga tgtcaaaactc tgccctgcggc gatgcgcgca tcggcgcccg 120  
 ggatacgtgg caagcgcggg cccggcgcca gccgcactct cccancctgg cgtggccacc 180  
 cggccaagca gaattgggtcc tgcagctgcn gtctagcngt ctgcaccaac acgggtggtg 240  
 gtgcagcnaa gtctccggaa tcncaagggt ctattnaatt ctgtgggaaa ttanatctca 300  
 actcaatagc cctttccaaa gaactattgc atgatattca acaagtaatt tcttatttca 360  
 atacactccg tatcagaatc atgttctttc tcgatctctt ccatcctccg aacagcctgc 420  
 antgactggt tcacctagac aannaatata tccttggtat tgggactcag cataactgtc 480  
 aaatatgcta tcnactccna tcnagaagaat ctttccgaag ctgtatttga ttcattaatt 540  
 tatccacatt actggat 557

&lt;210&gt; 131

&lt;211&gt; 655

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(655)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 131

aggngggcac aaagcgctat gttactgagc tgtacgnctc gtccattgtc ntgtggtgga 60

41

tcntcggatn	aggtctgata	tacttcctgt	gngatcnaga	tgnatctncg	tagntcccc	120
cggttgatgc	tgctcatnac	tgctgcattt	ccacgatcca	ccctgtnatg	gctatcctgc	180
tatacacaac	ngcatgatnn	gatatggaat	cctccacaat	ggaagtgttc	tggtatgacc	240
caccacctta	tatncngccg	ctgtctgaaa	ctcaaacctt	ttgcctgtnt	cagancacga	300
tcngttatgt	tactgatgaa	gaaatggaat	actcccaaaa	acagtgtcn	gccgcaaatc	360
ctacttcnng	caaatcnact	gcgtctctta	atcctaactc	ctctccatan	aanctacagt	420
tactccgtga	agcctgaag	gaaatggan	agttatagga	aactntcatc	gttataagcc	480
anaatgcntg	attaaataaa	tcgtctttng	tgataacctc	atcttctactc	ngttatacct	540
atcgttactn	canaancctt	attgaanttg	aattgtnttg	aaactgccga	aaaaaacgtt	600
cttatgtttc	ccggaccttg	ggggatcaat	aatccaatag	cntactcttc	ncgcc	655

&lt;210&gt; 132

&lt;211&gt; 566

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(566)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 132

agggtmncac	aaagcgctat	gttacttagc	tgtacgtgtc	gtcattntca	tgtggtggat	60
tcgagcatca	cagctctacg	tgtgtcagct	ctcacgtctg	caccagacgc	tgaagcaaga	120
gtacagtga	agtctccaca	agcctcccag	ccccatcgag	aaacatctcc	aaagccaaag	180
ggcgccnnaa	aaccacngtg	tacacctgcc	ccatcccggg	agaaatgacc	agaacaagtc	240
gctgacctgc	tggtcaagct	ctatccagca	ctccctggaa	tgggaaacat	ggcanccgaa	300
acactacana	cacnctcccg	tgctggatcg	acgtctctcc	tctatgcanc	tcacgtggac	360
aaacagttgc	acagggaaact	ctctctgtcg	tgatgtgtgan	ggtctgcaa	cactacccaa	420
aaanctctcc	tgttcccggt	tataatgcga	aggcggcanc	ccnctcccg	gntctcgcg	480
tcacacaagat	gntgcacntn	cccgtctatt	cttccagcac	ccanctggaa	ataagcnccn	540
ccatgnccctg	ggccctgaaa	aaaaaa				566

&lt;210&gt; 133

&lt;211&gt; 816

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(816)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 133

agctnngggt	nagcgtataa	aacttaagct	tgggtnaccg	agctcgggat	ccactcagtc	60
cagtngtggg	tgggnaattc	ctngnagcca	ccctnacagc	cagtaagnag	atatngtagg	120
gtaaaattgtt	aagggnaagt	cagcacttac	attaaagtaa	aattgggctc	acaaaccccg	180
nacacagtna	gcattttgtg	gccaatttct	gggttgggaa	tgggtgaaca	aacattgctg	240
ggaagccaag	tngctnaaca	ttgccttggt	ttcaaggggg	natgggnaaa	gtcaccctgt	300
aaggggatgg	gcaattgcca	gtgggaaacc	caccgcttgc	ttgaaggctc	tgggacttgc	360
atccttacca	cccaaaactcc	gtccaaacttg	gacaaagccc	ttggccgctt	tgctctcca	420
ggaatgtctt	acaaaaattg	ggtgggttat	tgggttactg	gttccttgtt	gggcccgaa	480
ttgggaaaaa	cttgggttgt	tctcaaaacc	cgggttattg	ggttgggtca	ccttttggct	540
cccagnttca	aacgtttaca	aacggggaaa	gtnaaaaaatc	ttgttcgaaa	aattgccacc	600
cattgnaaaa	gcttttggaa	nttggaaaac	tcttctcttg	gggggacaaa	ttgtttgggg	660
gctttccaat	tgntcaaaaa	aattgttgtt	cttgttcaaa	agggatgttt	nccgttccgt	720
ggggccaaac	cgttttgctt	gggttgaaca	gccaaaaaaa	tttgnancc	ccaccaant	780
tggggaaagc	caagcnttgg	ggtttactg	gcttcc			816

42

<210> 134  
 <211> 451  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(451)  
 <223> n = A,T,C or G

<400> 134  
 ttgtnangag aggggtcacct gggcagccct gacttttgtc ccctggcaaa gggacettca 60  
 gtgaccttgg ccctaggaga gcctctgagc acgtcagcca tgtcgaaccg ctcagggaagg 120  
 gcagcaagaa ttgggtctct gacctctgcc tctcctactc gccatctgca ctgggtgtgg 180  
 ttgtgcccat ttacagatg aggaggctgg ggcacgcacc agctgaatgc ctgtcccag 240  
 gtactgcgta agcagagctg gcagttgaac cccgtgtcct ggttgcgct gggggtgggc 300  
 tgcaccctga cttgtgaggc cagnagcaag gnttgacgt gacttcgtga ccgtcaccca 360  
 gctctgcagc acatcccgtg acccanctca tccaggccgn atgcaaacct gttgccaggc 420  
 ganaaaacca agtcaccgca canctgtggg t 451

<210> 135  
 <211> 658  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(658)  
 <223> n = A,T,C or G

<400> 135  
 gtggtatctg ccttcccagg aggcaggagt ggggccccca actgatgagc tcatggtgca 60  
 ctctttagctt ttaagacttg tctacagggg tgaataaata caaatgtgc caatcaaat 120  
 gtactttttt ggtatatttt gatcttgcgt ttaagagggg ctacaattca gagaggctgc 180  
 agacacagaa atagccctga aaagctttct tctctggcag agatttgcaa gtgctgagga 240  
 aatacacggt agtgaagtga acagaggaga aaagcatttc tctgaggcac accccacccc 300  
 caccttatct gcctaattgg atcaaggaaa gattaactcc caggaaaaac agactgagat 360  
 cctaattgct taaaggtctg actgagaaac ttctccatag gccactgtct atcttctga 420  
 gggcancctg ggggagcccc tgagagactc acatcttgtg tggggacagc cttggctcac 480  
 caagcatacc tctctctctt cccattacc tgaaaccac ctccnaaaa cccagcccc 540  
 tattctctct gtgcctcag gatgtgaaga aatcttcac attgggctc ttggagctca 600  
 tatttgcgtc tcntgtnttg tatatnaatt attgcattta tggtaatatt cctttgcc 658

<210> 136  
 <211> 478  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(478)  
 <223> n = A,T,C or G

<400> 136  
 gaagtctcgc gagtataaga acagtaacca gctccgggag taccagctgg aagggatgaa 60  
 ctggcttctt tttactgggt ataacagaaa aaactgtatt ttggctgatg agatgggcct 120  
 agggaaaacc atccagtcca tcacattcct ttcagaaata tttctgagag gaatccacgg 180  
 cccttttctc attatcgccc ctctctccac catcactaac tgggagcggg agttccggac 240  
 atggacagag atgaatgcca ttgtgtacca cggcagccag atcagcaggc agatgatcca 300

43

gcagtatgaa	atggtgtaca	gagacgccca	gggaacccct	ttcaggagtc	ttcaagttcc	360
acgtcgatc	cacaacnttt	gaatgatcct	agcagactgc	ccagagttga	agaagaattc	420
actggaactg	tgtggataat	tggatgaaac	ccccagact	ggaagaatan	ggaactgc	478

<210> 137  
 <211> 612  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)... (612)  
 <223> n = A,T,C or G

<400> 137	
gcaggggctc	ttgcaaatta acacaaaata ataattaaaa atgaaacgaa attgaggata 60
ttcttagaaa	gggtgaagga catgaaatac attactatct gggatttcaa cctttccaaa 120
ggtcaataaa	tccccaaata aaatgtaaat ccaaggctac ctgagaattc catttctgtt 180
gcatctttgt	tcatgatgag catatgtctt ttcattttga ggacttttta aaagagaaga 240
gtgacacaca	atgcaacatg gacaaggaat gaaaattgct ttagacactg cactttgaac 300
atacaaacct	gggagggtgcc agggctctgac actgtatatt tcttcctttg atctgattct 360
tccaaacagg	atccatgtac tggcaaattt ccctagtgtt ccctggtaag catcaaagta 420
aaccactggt	tggcctcggt atttctacat tggctttctc cattgntttt atacataaaa 480
aaaanaaaaa	gaaagaaaac tcaactgggca ttttcatatg ggtttccata ttggtcctta 540
atcattcagt	ttgaaagtaa atcaaagagg aatgaanagt taaagnctt tgaaattggg 600
gtgaaaactt	ca 612

<210> 138  
 <211> 478  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)... (478)  
 <223> n = A,T,C or G

<400> 138	
gcaggggctc	ttgcaaatta acacaaaata ataattaaaa atgaaacgaa attgaggata 60
ttcttagaaa	gggtgaagga catgaaatac attactatct gggatttcaa cctttccaaa 120
ggtcaataaa	tccccaaata aaatgtaaat ccaaggctac ctgagaattc catttctgtt 180
gcatctttgt	tcatgatgag catatgtctt ttcattttga ggacttttta aaagagaaga 240
gtgacacaca	atgcaacatg gacaaggaat gaaaattgct ttagacactg cactttgaac 300
atacaaacct	gggagggtgcc agggctctgac actgtatatt tcttcctttg atctgattct 360
tccaaacagg	atccatgtac tggcaaattt ccctagtgtt ccctggtaag catcaaagta 420
aaccactggn	tggcctcggt atttctacat tggctttctc cattggtttt atacataa 478

<210> 139  
 <211> 597  
 <212> DNA  
 <213> Homo sapien

<400> 139	
gttatattgt	agtttttagag atgaggaact aaggaccag ttgctcagt tttcctagct 60
agtgaataga	gactagacac caagtgttct acgtgcagac tttatactgc tcagcctggc 120
acacaaaatg	gcaatggcat agtccccaga ctgtgggtccc aactgtctct ttcctaacag 180
ctccccaggc	accacactt ttctgcctct ttttcaatct gtacccttga ccctcctcct 240
ttttctgctt	tgtcagactc cttaaggcac ttcataaatt aaccatttcc agggatttcc 300
cctcacacat	gagttattcc agtggacagg gcagcctcat ggggtgcctgt ggagggtgaa 360

44

gggtctgcct	ggccgtaggt	gtgatcacac	actcccgttg	taaccctgc	ctcctgtgac	420
acttgctgcc	ccacgattta	gctgctttgt	gttccgtgcc	tcctgtttgc	tggtgaactc	480
ctgagttggg	ggcgctcatt	ccctccactg	tagttcttcc	gcgatgctga	atccaccac	540
ggtcagcacc	actcggaat	acttcacagt	cctgtagagg	aagacaggtc	caggttt	597

&lt;210&gt; 140

&lt;211&gt; 368

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(368)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 140

tttacatcta	gactccacag	acagaaacgt	ttcattttta	ttgagttaat	tttgaaatat	60
atgaatccct	gacccattgt	tatcactagc	tgttactcta	tcaggacagt	tgctgaagtt	120
ttttgtcaat	aaatttaaaa	atcaactatc	aggttgtccc	ttggatgacc	tgagatttct	180
agagacaaaa	gaaatctatt	cttcctgatt	gaagaaagag	tctgagattt	tttttaaacc	240
actgatttgg	ggatcagggt	gtagccagtg	tctcaaactc	tcccctgtcc	cttttttggt	300
ttgctcaagg	agtgggctnt	gaggntcaa	gaattggggg	ngttactggg	ttatttttga	360
ttaggggg						368

&lt;210&gt; 141

&lt;211&gt; 674

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(674)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 141

aatgtcaatc	tttgctcggt	cagtgaggat	gtcgcctggt	gagggaaaaa	tagtagctgt	60
tgccatattc	ctttaactcc	cccccccg	cccccgcaat	atgtccctg	aataaacttt	120
gtgggtagtt	tttcttcatt	cccagaactg	ttatgaggta	agttcagaaa	ttgccagctt	180
cctgatgctc	tatgctttga	acacacaaaa	taatcaaagg	tgctctttag	taggatcctt	240
tccctatcaa	aataacagta	acacccaatc	tgaggcctca	agcccaactc	ttgagcaaaa	300
caaaaaaggg	acagggggaga	gtttgagaca	ctggctacac	cctgatcccc	aaatcagtgg	360
tttaaaaaaa	atctcagact	ctttcttcaa	tcaggaagaa	tagatttctt	ttgtctctag	420
aaatctcagg	tcatccaagg	gacaacctga	tagttgattt	ttaaatttag	tgacaaaaaa	480
actttcagca	actgtcctga	taggagtaac	caggctagnt	ggataaccaa	atggggtnca	540
agggggaatn	tcataatatt	ttcaaaaaat	taaaccctca	attaaaaaaa	tggaaaaaac	600
ggttttctntg	gtcctgggtg	ggaggttctt	aagnatggta	aaaaaaggaa	atttccccac	660
ccaacnacct	tggg					674

&lt;210&gt; 142

&lt;211&gt; 669

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(669)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 142

45

```

gttgaaact tantcctcaa tgcaatagtg ttgagatgtg ggacctttaa gtgataatta    60
gatcatgagg gatttgccctc attcattaat tattgctatt atctcagggtg agttagttat    120
cggagattga aatccctgata aaaagttgag tttgttctct ctgtctctct ctctctctcc    180
actctagaat tgtaaaaaac taatctctat tctgcataaa ttaccagtc tcagggtatc    240
cattatatta gcaggaaatg gactaagaca ctactttata aaattttgca gtttccaatg    300
ttcagctttt ccttgatccg gcttcactca cttttttctt tgcttggtac tgatggtgaa    360
atttctctgt tgtctttcat ttatggctta cactatcaca tgctctctat taattcatgc    420
cttctatttc cttctgttgt ttttggaagc atctcttttc atgggctcat tttagctctg    480
taagacatat cgaaaactca cttgattcct cctgcatgca tagagctctg ctggggaagt    540
ctccttctgc atgctacgcc ttcccaccaa agacaaggct ttgcttattt gcncattctg    600
tttaacgtct gccaaatatg nggtcttgac ncataagaaa actggtttga nccgcaaaan    660
aaaattttg

```

&lt;210&gt; 143

&lt;211&gt; 501

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 143

```

agaccttatt tggtaatctg ctgtcttcca gtgtctctgc attagatacc attactacag    60
tagcaacttg atctctcaca tctattccag aaaatgtgtc tactcatggt tctcagattt    120
ttaatatgat actaaaagaa caatcattag cagcagaaag taaaactgta ctacaggaat    180
tgattaatgt actcaagact gatcttctaa gttcactgga aatgatttta tccccactg    240
tggtgtctat actgaaaatc aatagtcac taaagcatat tttcaagact tcattgacag    300
tgggcgataa gatagaagat caaaaaaagg aactagatgg ctttctcagt atactgtgta    360
acaactcaca tgaactacaa gaaaatccat ttgttccttg gttgagtcac aaaagcaatg    420
tggaacacct actgaagacc tgaagacaat aaagcagacc cattcccagg aactttgcaa    480
gttaaatgaat ctttgacag a

```

&lt;210&gt; 144

&lt;211&gt; 501

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(501)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 144

```

gatatctcag cacctgactt acacatctta catcctcaag caaactcccc agggcacatt    60
tttagttggc cagccatcac cccagacttc tggaaaacaa ctcaccactg ggtcagtggt    120
ccaaggaaca ctgggagtca gcacatcttc tgcacaagga caacaaacgc taaaagtcat    180
ctctggacag aaaaccacat tgtttacaca ggcagcccat ggaggacag catctctaatt    240
gaaaatatcc gatagcacgt tgaagactgt gccagccacc tcacagctct cgaagcctgg    300
aaccacaatg ctgagagtag caggaggggt tatcacaact gccacttccc ctgccgtggc    360
cctctcagca aacggtcctt gccaacagtc tgaaggaatg gctnccgtgt cttcatctac    420
ggncagttc tgtaacgaaa acttctgggc agcaacaaag tgtgtgtgan ocaagccacc    480
cgtggggaac cttgcaaggn t

```

&lt;210&gt; 145

&lt;211&gt; 501

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(501)

&lt;223&gt; n = A,T,C or G



```

<400> 145
ggaatccgag ccggtaccc cctctccgag cgccagcagg tggcccttct catgcagatg      60
acggccgagg agtctgccaa cagcccagtg gacacaacac caaagcacc ctcgccagtct      120
acagtgtgtc agaagggaac gcccaactct gcctcaaaaa ccaagataa agtgaacaag      180
agaaacgagc gtggagagac ccgctgcac cgagccgcca tccgcgggga cgcgcggcgc      240
atcaaagagc tcatcagcga gggggcagac gtcaacgtca aggacttcgc aggctggacg      300
gcgctgcacg aggcctgtaa ccggggctac tacgacgtcg cgaagcaact gctggctgca      360
ggtgcggagg tgaacaccaa gggcctagat gacgacacgc cttttgcacg acgcttgcca      420
acaacgggca ctacaagggt gtgaaactgc ttgttgcggt acnganggaa cccgnacaaa      480
acaacaggaa aagcgaagac c

```

```

<210> 146
<211> 501
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(501)
<223> n = A,T,C or G

```

```

<400> 146
ggccccgaca cggacaggat tgacagattg atagctcttt ctcgattccg tgggtggtgg      60
tgcatggccg ttcttagttg gtggagcgat ttgtctggtt aattccgata acgaacgaga      120
ctctggcatg ctaactagtt acgcgacccc cgagcggtcg gcgtccccc aattcttaga      180
gggacaagtg gcgttcagcc acccgagatt gagcaataac aggtctgtga tgcccttaga      240
tgtccggggc tgcacggccg ctacactgac tggctcagcg tgtgcctacc ctacgccggc      300
agggcggggt aacccgttga accccattcg tgatggggat cggggattgc aattattccc      360
catgaacgan gaattcccag taagtgcggg tcataagctt attccgcact tacctgggga      420
gaagcctttt ggtcttcggg ggacnaaaac agctttgttg ctgaacgcng gcagcaccgg      480
tcgcgcgcgtc cgttggttac c

```

```

<210> 147
<211> 501
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(501)
<223> n = A,T,C or G

```

```

<400> 147
cagcgccgcc gcccgcccc tccagcttcc cggaccatgg ccaacctgga gcgcaccttc      60
atcgccatca agccggacgg cgtgcagcgc ggcctggtgg gcgagatcat caagcgcttc      120
gagcagaagg gattccgcct cgtggccatg aagttcctcc gggcctctga agaacacctg      180
aagcagcact acattgacct gaaagaccga ccattcttcc ctgggctggt gaagtacatg      240
aactcagggc cggttgnggc catggtctgg gaggggctga acgtggtgaa gacaggccga      300
gtgatgcttg gggagaccaa tccagcagat tcaaagccag gcaccattcg tggggacttc      360
tgcattcagg ttggcaggaa catcattcat ggcagtgatt cagtaaaaag tgctgaaaaa      420
gaaatcagcc tatggtttta gcctgaagaa ctggttgact acaagtcttt ggctcatgac      480
tgggtctatn aataagaagg g

```

```

<210> 148
<211> 501
<212> DNA
<213> Homo sapien

```

47

<220>  
 <221> misc\_feature  
 <222> (1)...(501)  
 <223> n = A,T,C or G

<400> 148  
 actcttagct tgtcggggac ggtaaccggg acccgggtgc tgctcctgtc gccttcgcct 60  
 cctaatacct agccactatg cgtgagtga tctccatcca cgttgccag gctgggtgcc 120  
 agattggcaa tgccctgtgg gagctctact gcctggaaca cggcatccag cccgatggcc 180  
 agatgccaa tgacaagacc attgggggag gagatgactc cttcaacacc ttcttcagt 240  
 agacggggcg tggcaagcac gtgcccggg ctgtgtttgt agacttggaa cccacagtca 300  
 ttgatgaagt tcgactggc acctaccgcc agctcttcca ccctgagcag ctcacacag 360  
 gcaaggaaga tgctgccaat aactatgcc gagggcacta caccattggc aaggagatca 420  
 ttgacctgt gttggaccga attcgcaagc tggctgacag tgcaccggc ttcagggctt 480  
 cttggtttn cacagctttg g 501

<210> 149  
 <211> 501  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(501)  
 <223> n = A,T,C or G

<400> 149  
 cgcccgggca ggaatagaag atgaacaaac ccataacacc atcaacatat gtgcgctgcc 60  
 tcaatgttgg actaattagg aagctgtcag attttattga tcctcaagaa ggatggaaga 120  
 agttagctgt agctattaaa aaaccatctg gtgatgatag atacaatcaa gtttcacata 180  
 aggagatttg aagcattctt caaactggaa aaagtccac ttcttgaata ctgtttgact 240  
 gggggcacca caaattggac agttggtgat cttgtggatc ttttgatcca aaatgaattt 300  
 ttgctgctgc gactcttttg ctcccgatg ctcttcgaaa cctgctaata caatgacttc 360  
 taaagaagct ataacagttc agcaaaaaca gatgccttgc tgtgacaaag acaggacatt 420  
 gatgacacct gtgcanaatc ttgaacaaag ctatatgcca cctgactcct caagtccana 480  
 aaataaaagt ttaaaagtta g 501

<210> 150  
 <211> 501  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(501)  
 <223> n = A,T,C or G

<400> 150  
 cagcacagga tactgatatt ctgtcagctg aaaagcatgc ttgatatagt agagcatgat 60  
 ctctcaaac ctcaattgcc ctctgtcact tatttgagat tagatggcag catacctcct 120  
 ggtcagaggc attccattgt ttcccggttt aataatgac catctataga cgttctgtta 180  
 cttaccactc acgttgggtg cctgggactt aatttgacag gcgctgacac agtagtattt 240  
 gtggagcatg actggaantc tatgagagat ctacaagcca tggaccgggc ccatgcatt 300  
 gggcagaaac gtgtggttaa cgtatccgat tgataaccag aggaacattg gaagaaaaa 360  
 taatggggtt gcagaaaatt caagatgaac catagcgaat ctgttattag ccaagagaat 420  
 tcttagtttg canacatggg ggactgatca gctttcttga atctgtttac tcttgataa 480  
 gggatggcaa aagcagaaaa a 501

<210> 151

48

<211> 501  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(501)  
 <223> n = A,T,C or G

<400> 151  
 atggagggggt gtgtgtctaa cctaattggtc tgcaacctgg cctacagccg gaagctggaa 60  
 gagttgaagg agagtattct ggccgataaa tncctgnnta ctacaactga ccaggacagc 120  
 agaactgcat tgcaactggc atgctcagct ggacatacag aaattgttga atttttgttg 180  
 caacttgag tgccagtgaa tgataaagac gatgcagggt ggtctcctct tcatattgag 240  
 gcttctgctg gccgggatga gattgtaaaa gcccttcttg gaaaagggtgc tcaagtgaat 300  
 gctgtcaatc aaaatggctg tactccctta cattatgcag cttcgaaaaa caggcatgag 360  
 atcgctgtca tgttactgga aggcggggct aatccagatg ctaaggacca ttatgaggct 420  
 acagcaatgc accgggcagc agccaagggt aacttgaaga tgattcatat ccttctgtac 480  
 taaaaagcat ccacaaacat c 501

<210> 152  
 <211> 501  
 <212> DNA  
 <213> Homo sapien

<400> 152  
 gcccgccgaa gccgcgccag aactgtactc tccgagaggt cgttttcccg tccccgagag 60  
 caagtttatt tacaaatgtt ggagtaataa agaaggcaga acaaaatgag ctgggctttg 120  
 gaagaatgga aagaaggact gcctacaaga gctcttcaga aaattcaaga gcttgaagga 180  
 cagcttgaca aactgaagaa ggaaaagcag caaaggcagt ttcagcttga cagtctcgag 240  
 gctgcgctgc agaagcaaaa acagaagggt gaaaatgaaa aaaccgaggg taaaaacctg 300  
 aaaagggaga atcaaagatt gatggaaata tgtgaaagtc tggagaaaac taagcagaag 360  
 ttcaggcaaaa aacaaataga aaaactggaa caggaactta aaagtgtaaa tctgacttga 420  
 aagaagcaac aactggcatc t 501

<210> 153  
 <211> 501  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(501)  
 <223> n = A,T,C or G

<400> 153  
 agagagagag agagagagag gagcgagaga gtgtgagcga gaaagaataa aaggaaagaa 60  
 gattttctct atgtatataa agatggccac gttagcaaac ggacaggctg acaacgcaag 120  
 cctcagtacc aacgggctcg gcagcagccc gggcagtgcc gggcacatga acggattaag 180  
 ccacagcccg gggaacccgt cgaccattcc catgaaggac cacgatgcca tcaagctgtt 240  
 cattgggcag atcccccgca cctggatgag aaggacctca agcccctctt cgaggagttt 300  
 ggcaaaatct acgagcttac ggttctgaag gacagggtca caggcatgca caaaggctgc 360  
 gccttcctca cctactgcga gcgtgagtc ggcgtgaagg cccagagcgc gctgcacgag 420  
 cagaagactc tgcccgggat gaaccggcc cgatccnagg tgaagccttg cggacagcga 480  
 gaaccgagga gatagaaact c 501

<210> 154  
 <211> 501

49

<212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(501)  
 <223> n = A,T,C or G

<400> 154  
 ttccttcctg tgtgaggccg gctgagggca cttgctcttg ctgtttctgc ccctggggtta 60  
 acattcaaga tggatcatgc tgaagccttt tctcgtcctt tgagtcggaa tgaagttgtt 120  
 ggtttaattt tccgtttgac aatatttggg gcagtgacat actttactat caaatggatg 180  
 gtagatgcaa ttgatccaac cagaaagcaa aaagtagaag ctcaaaaaca ggcagaaaaa 240  
 ctaatgaagc aaattgggag tgaataatgt gaagctctca gaatatgaaa tgagtattgc 300  
 tgctcatctt gtagaccctc ttaatatgca tgttacttgg agtgatatag cagggttaga 360  
 tgatgtcatt acggatctga aagacacagt catcttacct atcaaaaaga aacatttgtt 420  
 tgagaattcc aggtctctgc agcctccaaa aggtgntctt ctctatgggc ctccagctgt 480  
 ggtaaaacgt tgattgccaa g 501

<210> 155  
 <211> 601  
 <212> DNA  
 <213> Homo sapien  
 <220>  
 <221> misc\_feature  
 <222> (1)...(601)  
 <223> n = A,T,C or G

<400> 155  
 aggaggagga acagcaggag gaggaactca aagtactgct ggccctggag ggatatctca 60  
 gcacctgact tacacatctt acatcctcaa gcaaaactcc cagggcacat ttttagttgg 120  
 actgggagtc agcacatctt ctgcacaagg acaacaaacg ctaaaagtca tctctggaca 240  
 gaaaaccaca ttgtttacac aggcagccca tggaggacag gcattctctaa tgaaaatata 300  
 cgatagcacc ttgaagactg tgccagccac ctacacagctc tcgaagcctg gaaccacaat 360  
 gctgagagta gcaggagggg ttatcacaaac tgccacttcc cctgccgttg ccctctcagc 420  
 aaacggctct gcacaacagt ctgaaggat ggctcccgtg tcttcatcta cggtcagttc 480  
 tgtaacgaaa acttctgggc agcagcaagt gtgtgtgagc caggccaccg tgggaacctg 540  
 caaggntgcc accccccctg cgtcagcgcc acgtncctcg tgctacacca aaccccatct 600  
 c 601

<210> 156  
 <211> 501  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(501)  
 <223> n = A,T,C or G

<400> 156  
 caagaaagga gaaagagagc tcaaaatcgg agacagagta ttggttggtg gcactaaggc 60  
 tgggttagtc cggtttcttg gggagaccga ctttgccaag ggggagtggg gtggcgtgga 120  
 gtttagatgag ccacttgagg agaattgatgg cgtgttgctt ggaacaaggt attttcagtg 180  
 tcaacccaaa tatggcttgt tcgtctctgt ccacaaagtt accaagattg gcttccttc 240  
 cactacacca gccaaagcca aggccaacgc agtgaggcga gtgatggcga ccacgtccgc 300  
 cagcctgaag cgcagccctt ctgcctcttc cctcagctcc atgagctcag tggcctcctc 360

## 50

tgtgagcagc angcccagtc ggacaggact attgactgaa acctcctccc gttacgccag 420  
 gaagatctcc ggtaccactg cctccanga ggcccttgaa ggaaaaacan cagcacattg 480  
 agcancttgc tggcnggaac c 501

<210> 157  
 <211> 501  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(501)  
 <223> n = A,T,C or G

<400> 157  
 caccctcttc gtcgcttcgg ccagtgtgtc gggctgggccc ctgacaagcc acctgaggag 60  
 aggctcggag cggggcccg accccggcga ttgccgccg cttctctcta gtctcacgag 120  
 gggtttcccg cctcgcaccc ccacctctgg acttgccctt cttctcttc tccgcgtgtg 180  
 gaggagcca gcgcttancg cggagcgagc ctgggggccc cccgccgtga agacatcgcg 240  
 gggaccgatt caccatgnag ggccggcg gngcgaacga caagaaaaag ataagtctctg 300  
 aacgtcgaag agaaaagtct cgagatgcag ccanatctcg gcgaagtaaa gaatctgaag 360  
 ttttttatga gcttgctcat cagttgccac ttccacataa tgtgagttcg catcttgata 420  
 angcctcttg tgatgagget taccatcagc tatttgctg tgaggaaact tctggatgct 480  
 ggtgatttgg atattgaaga t 501

<210> 158  
 <211> 501  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(501)  
 <223> n = A,T,C or G

<400> 158  
 acggggtcac ccacacggtg cccatctacg agggctacgc cctccccac gccatcctgc 60  
 gtctggacct ggctggccgg gacctgaccg actacctcat gaagatcctc actgagcgag 120  
 gctacagctt caccaccacg gccgagcggg aaatcgtgog cgacatcaag gagaagctgt 180  
 gctacgtcgc cctggacttc gaggcaggaga tggccacgc cgcatcctcc tcttctctgg 240  
 agaagagcta cgagctgcc gatggccagg tcatcaccat tggcaatgag cggttccggt 300  
 gtccggaggc gctgttccag cttccttcc tgggtatgga atcttgcggn attcacgana 360  
 ccaccttcaa ctccatcatg aagtgtgacg tggacatccg caaagacctg tacgccaaca 420  
 ccgtgctgtc gggcggnacc accatgtacc cgggcattgc cgacaggatg caaaaaggag 480  
 atcaccgcgc cttggcgccc a 501

<210> 159  
 <211> 501  
 <212> DNA  
 <213> Homo sapien

<400> 159  
 cgagcgggac tggctgggtc ggctgggctg ctggtgcgag gagccgcggg gctgtgctcg 60  
 ggggccaagg ggacagcgcg tgggtggccg aggatgctgc ggggcggtag ctccggcgcc 120  
 cctagctggt gactgctgog cctgacctca cacagccga ggcgggctcg gcgcacagtc 180  
 gctgtccgc gcgcgcgccc ggccgcgctc caggtgctga cagcgcgaga gagcgcggcc 240  
 ctccaggagca aggcgaatgt atgacaacat gtccacaatg gtgtacataa aggaagacaa 300  
 gttggagaag ctacacagg atgaaattat ttctaagaca aagcaagtaa ttcaggggct 360  
 ggaagcttgg aagaatgagc acaattccat tttaaaagt ttgctggaga cactgaagt 420

51

tttgaagaaa gatgatgaaa gtaatttggt ggaggagaaa tcaaacaatga tccggaagtc 480  
actggagatg ttggagctcg g 501

&lt;210&gt; 160

&lt;211&gt; 487

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(487)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 160

aagatctcag tctgactctt ttggaacaag tcaaactgcc catgatgttg ctgatcagcc 60  
aaggcctgga tcagagggga gcttctgtgc atcttcaaac tctccaatgc actcccaagg 120  
ccagcagttc tctggtgtct cccaacttcc tggacctgtg ccacttcagg agtaactgat 180  
acacagaata ctgtaaatat ggccaagca gatacagaga aattgagaca gcggcagaag 240  
ttacgtgaaa tcattctcca gcagcaacag cagaagaaga ttgcaggctc acaggagaag 300  
gggtcacagg actcacccgc agtgccttca tccanggcct ctttaacact ggcaaccaag 360  
agaatggtta acccaggctt ttaaccaana acccccacct tccttttccct ggggggaacat 420  
ttaggtcttc ctggttgccc ccttcctttt anggaacctt anaatttgct tggtttttcc 480  
ccnaaaa 487

&lt;210&gt; 161

&lt;211&gt; 501

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(501)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 161

ggttcccggc ccagtcctcg cctgcagcag tctgcctcct ctttcaacat gacagatgcc 60  
gctgtgtcct tcgccaagga cttcctggca ggtggagtgg ccgcagccat ctccaagacg 120  
gcggtagcgc ccacgcagcg ggtcaagctg ctgctgcagg tgcagcatgc cagcaagcag 180  
atcactgcag ataagcaata caaaggcatt atagactgcg tggctcgtat tccaaggag 240  
cagggagtgc tgtccttctg gcgcggtaac ctggccaatg tcatcagata cttccccacc 300  
caggctctta acttcgcctt caaagataaa tacaagcaga tcttcctggg tgggtgtggac 360  
aagagaaccc agttttggcg ctactttgca gggaatctgg catcgggtgg tgccgcangg 420  
gccacatccc tgtgttttgt gtaccctctt gatatttccc gtaccctgct ancantgat 480  
gtggggtaaa agctggagct g 501

&lt;210&gt; 162

&lt;211&gt; 501

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 162

gaaaaagaaa aagaactaca acggcagaaa gaaaaggaaa aagaactaca aaagatgaaa 60  
gaacaagaaa aggaatgtga gctggagaag gaaagggaaa aattagagga gaaaattgaa 120  
cccagagAAC ctAattttaga gcccatggta gaaaaacaag aaagtgaaaa cagctgtaat 180  
aaagaggagg aaccctgttt cactagacaa gacagcaatc gcagtgaaaa ggaagccaca 240  
ccagtgtgtc atgaaacaga accagaatca gggctctaac ctgcggccggc tgtattatct 300  
ggctatttca aacagtttca gaagtcttta cctccacgat tccagcggca gcaggaacag 360  
atgaaacagc agcagtggca gcagcagcaa cagcaagggt tacttccaga ctgttccttc 420  
caaccgtcca gtagtactgt ccctcctccc cacacagacc tcttttcagc ctatgcagcc 480

52

tctcctcagc atttggttc t

501

&lt;210&gt; 163

&lt;211&gt; 501

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(501)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 163

gagctcgacc agttgcctga cgagagctct tcagcaaaag cccttgctcag tttaaaagaa	60
ggaagcttat ctaacacgtg gaatgaaaag tacagttctt tacagaaaac acctgttttg	120
aaaggcagga atacaagctc tgctgtggaa atgccttttc agaaattcaa aacgaagtcg	180
acttttttct gatgaagatg ataggcaaat aaatacaagg tcacctaaaa gaaaccagag	240
ggttgcaatg gttccacaga aatttacagc aacaatgtca acaccagata agaaagcttc	300
acagaagatt ggttttcgat tacgtaatct gctcaagctt cctaaagcac ataaatggtg	360
tatatacgag tggttctatt caaatataga taaaccactt tttgaaggty ataagactt	420
ttgtgtatgt ctaaagggaat cttttctaatt ttgaaaacaa gaaagttaac aagagtagaa	480
tggggaaaaa ttcngcggct t	501

&lt;210&gt; 164

&lt;211&gt; 501

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(501)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 164

cgggtgcgcy cccacgaccy ccagactcga gcagtctctg gaacacgctg cggggtcccc	60
gggctgagc caggtctgtt ctccacgcag gtgttcgcg cyccccgttc agccatgtcg	120
tccggcatcc atgtagcgtt ggtgactgga ggcaacaagg ggcacggtt tggccatcgt	180
gcgcgacctg tgccggctgt tctcggggga cgtggtgctc acggcgcggy acgtgacgcy	240
gggccaggcy gccgtacagc agctgcaggc ggagggcctg agcccgctt tccaccagct	300
ggacatcgac gatctgcaga gcacccgcgc cctgcgcgac ttcttgcgca aggagtacgy	360
gggctggac gtgctggtca acaacgcggy catcgccctc aaggttgctg atcccacacc	420
ctttcatatt caagctgaag tgacgatgaa aacaaatttc tttggtaccc ganatgtgtg	480
cacagaatta ctccctctaa t	501

&lt;210&gt; 165

&lt;211&gt; 501

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(501)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 165

ccggtgaagg accgcgaggy cttccagaggy ctcaacttcc tgtaccaggt gagtctgcga	60
caaggggcccc acggggagcy tgctcggcgt ccagagtgta ctgctccctt cccgcaggcc	120
gccattgtg tccttgccca ggaccccgag aaccangcgc tggcgagggt ttactgctac	180
actgagagga ccattgcgaa gcggctcgtc ttgcggcggy atccctcgggt gaagaggact	240

53

```

ctctgtcgag gctgctcttc cctcctcgtc cggggcctca cctgcaccca ccgccagaga 300
cgctgcaggg gacagcgctg gaccgtacag acctgcctaa catgccagcg cagccaacgc 360
ttnctcaatg atcccnngca ttactntgg ggagacnggn ctgaggccca actcggggagc 420
caagcagatt ccaaaccact acaacccttg ccaaacacag cccactccat ttcagaccgc 480
cttctcgagg agaaaaatgca g 501

```

&lt;210&gt; 166

&lt;211&gt; 412

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(412)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 166

```

atgtccaagc cgggtggacca cgtcaagcgg cccatgaacg ccttcatggt gtggtcgcgg 60
gctcagcggc gcaagatggc ccaggagaac cccaagatgc acaactcgga gatcagcaag 120
cgcttggggc cggagtggaa actgctcaca gctcgggaga agcggccgtt catcgacgag 180
gccaagcgtc tacgcgccat gcacatgaag gagcaccgg actacaagta ccggccgcgg 240
cgcaagccca agacgctgct caagaaggac aagttcgct tcccgggtgcc ctacggcctg 300
ggcggcgctg cggacgccga gcaccctgcg ctcaaggcgg gcgcggggct gcacgcgggg 360
gcggggcggc gnetggtgcc tgagtcgctg ctgcaccaat ccgagaaggc gg 412

```

&lt;210&gt; 167

&lt;211&gt; 501

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 167

```

aaatgcaagt tgatctggag aaagaattac aatctgcttt taatgagata acaaaactca 60
ctctcctctc agatggcaac gttccacacg atttgccttg taatttggcc ttggaaggag 120
agattactga tcttcagaaa gaactaaata aagaaaagtg aagaaaaatg aagctttgcg 180
ggaagaagtc attttgcttt cagaattgaa atctttacct tctgaagtag aaaggctgag 240
gaaagagata caagacaaat ctgaagagct ccatataata acatcagaaa aagataaatt 300
gttttctgaa gtagttcata aggagagtag agttcaaggt ttacttgaag aaattgggaa 360
aacaaaagat gacctagcaa ctacacagtc gaattataaa agcactgatc aagaattcca 420
aaatttcaaa acccttcata tggactttga gcaaaagtat aagatggtcc ttgaggagaa 480
tgagagaatg aatcaggaaa t 501

```

&lt;210&gt; 168

&lt;211&gt; 501

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(501)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 168

```

ggggcccgcg gagctcgcgc caggctcctg ggaaaggacg gggagtgtta ccggggagca 60
gctgctccat tgtgcctcga ggccccgacg gggctaggcc gacggcctcc ctcccttcac 120
ctttcctctc ctggcggggg tgcggcgcgg gcgagtgaat tgcggccacg cctgaaaggc 180
gactctcctg attcaagatg accaacgaag aacctcttcc caagaagggt cgattgagtg 240
aaacagactt caaagttatg gcaagagatg agttaattct aagatggaaa caatatgaag 300
catatgtaca agctttggag ggcaagtaca cagattctaa ctctaagat gtaactggcc 360
taagagagtc tgaagaaaaa ctaaagcaac aacagcagga gtctgcacgc agggaaaaca 420

```



54

tccttgtaat ggcactagca accaaggaac aagagatgca agagtgtact acttaaatcc 480  
 agtacctcaa gcaagtcacn c 501

<210> 169  
 <211> 501  
 <212> DNA  
 <213> Homo sapien

<400> 169  
 gctgtgcggc ggtcccgcg cccggcgatgt tcccgggcac tccctgagta gcggcagctt 60  
 atcccccgcc cgctagcccc ccctgggtccc cggtcgcctc gctggctggc gcggccccgg 120  
 ccccgctctg cgtcggcccc gccgcggtgg aggcgcgcga gggggacgcg gccggggatg 180  
 agcggattgc ggtggaactc gccgccccgg ggccccgcga agccgtgagc cgctgctttt 240  
 ctccgagtgc ccgccctgcc cttggatttg agatcatgtc catccacatc gtggcgctgg 300  
 ggaacgaggg ggacacattc caccaggaca accggccgctc ggggcttata cgcaattacc 360  
 tggggagaag ccctctggtc tccggggacg agagcagctt gttgctgaac gcggccagca 420  
 cggtcgcgcg tccggtgttc accgagtatc aggcagctgc gtttgggaat gtcaaagctg 480  
 gtggtccacg actgtccccg c 501

<210> 170  
 <211> 501  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(501)  
 <223> n = A,T,C or G

<400> 170  
 gcacccctctt gccgttcccg gtgtttgggc cttgcctgtg acggtgggaa aagaaaatgg 60  
 ccttgctgtg ctacaaccgg ggctgcggtc agcgttcga tccctgagacc aattccgacg 120  
 gctgtaagag aagaacaact gatttttctg atttcttaag cattgtaggc tgtacaaaag 180  
 gtagacataa tagtgagaag ccacctgagc cagtcaaac tgaagtcaag actactgaga 240  
 agaaggagct atgtgaatta aaacccaaat ttcangaaca catcattcaa gccctaagc 300  
 cagtagaagc aataaaaaga ccaagcccag atgaaccaat gacaaatttg gaattaaaaa 360  
 tatctgcctc cctaaaacaa gcacttgata aacttaaact gtcatcaggg aatgaagaaa 420  
 atnagaaaga agaagacnat g 501

<210> 171  
 <211> 601  
 <212> DNA  
 <213> Homo sapien

<400> 171  
 agcgacctat cttgaactcc acagccttga tgacttctac ataggaaagt attttgaggg 60  
 agtggttgag tattttatga ttcaagcctt aaatcagaag acaagtgaag aaatgaagaa 120  
 aagaaaaatg agcaactcct ttcatggaat tagaccacct caacttgaac aaccagaaaa 180  
 aatgcctgtc ttaaaggctg aagcgtcaca ttataactct gacttaataa acttgctgtt 240  
 ctgctgccag tgtgtggacg tggatattta caacccaat ttaaagaaag ttgtagaggc 300  
 ccacaagatc gttctctgct ctgtaagcca tgttttcatg ctgcttttca atgtgaagag 360  
 tcccactgac attcaggatt ccagtatcat ccgaactacc caggatcttt ttgtataaaa 420  
 cagagatact gcatttccag gtgctagcca tgaatcttca ggcaaccac cattacgagt 480  
 cattgttaa gacgccctct tctgttcttg tttatcagac atccttcgct tcatttattc 540  
 aggtgctttt cagtgggaag aattggaaga agatatcagg aagaagtga aagattctgg 600  
 g 601

<210> 172

55

<211> 501  
<212> DNA  
<213> Homo sapien

<400> 172

gaccgtttta	aaaactggta	tccagctcac	atagaagaca	ttgactacga	ggaaggaaaa	60
gtactcatcc	atttcaagcg	ttggaaccat	cgttatgatg	agtggttctg	ctgggacagt	120
ccttattttac	gccctttaga	gaaaatacag	ctgaggaaaag	agggccttgca	tgaagaggat	180
ggatctttctg	aatttcaaat	aaatgagcag	gtccttgctt	gctggctctga	ttgtcgtttt	240
taccgggcca	aagtcactgc	tgtaacaag	gatggactct	acactgtgaa	attttatgat	300
ggagtagttc	agactgtcaa	acatattcat	gtcaaagctt	tttccaaaga	tcagaatatt	360
gtgggtaatg	ctaggcctaa	agaaacagat	cacaaaagtc	tttcatcatc	tcctgataaa	420
cgagagaagt	ttaaagaaca	gagaaaagca	acagtgaatg	tgaagaaaga	caaagaagat	480
aaacccttaa	agacagaaaa	g				501

<210> 173  
<211> 501  
<212> DNA  
<213> Homo sapien

<400> 173

gcgacctatc	ttgaactcca	cagccttgat	gactttctaca	taggaaagta	ttttggagga	60
gtgttggagt	attttatgat	tcaagcctta	aatcagaaga	caagtgaaaa	aatgaagaaa	120
agaaaaatga	gcaactcctt	tcatggaatt	agaccacctc	aacttgaaca	accagaaaaa	180
atgcctgtct	taaaggctga	agcgtcacat	tataactctg	acttaaaata	cttgctgttc	240
tgctgccagt	gtgtggacgt	ggtattttac	aaccccaatt	taaagaaagt	tgtagaggcc	300
cacaagatcg	ttctctgcgc	tgtaagccat	gttttcatgc	tgcttttcaa	tgtgaagagt	360
cccactgaca	ttcaggattc	cagtatcatc	cgaactaccc	aggatctttt	tgctataaac	420
agagatactg	catttccagg	tgctagccat	gaatcttcag	gcaaccacc	attacagatc	480
attgttaaag	acgccctctt	c				501

<210> 174  
<211> 501  
<212> DNA  
<213> Homo sapien

<400> 174

ccccgggagg	cgggccgctg	ggcgagccg	cgaagatgcc	gttggaaactg	acgcagagcc	60
gagtgacaga	gatctgggtg	cccgaggacc	acaggccctc	gttgccaga	tcctgtgggc	120
caaagctgac	caactcccc	accgtcatcg	tcatggtggg	cctccccgcc	cggggcaaga	180
cctacatctc	caagaagctg	actcgctacc	tcaactggat	tggtcgtccc	acaaaagtgt	240
tcaacgtcgg	ggagtatcgc	cgggaggctg	tgaagcagta	cagctcctac	aacttcttcc	300
gccccgacaa	tgaggaagcc	atgaaagtcc	ggaagcaatg	tgcttagct	gccttgagag	360
atgtcaaaaag	ctacctggcg	aaagaagggg	gacaaattgc	ggttttcgat	gccaccaata	420
ctactagaga	gaggagacac	atgatccttc	attttgccaa	agaaaatgac	tttaaggcgt	480
ttttcatcga	gtcgggtgtc	g				501

<210> 175  
<211> 501  
<212> DNA  
<213> Homo sapien

<220>  
<221> misc\_feature  
<222> (1)... (501)  
<223> n = A,T,C or G

<400> 175  
ccaacatgac cgaacgaaga agggacgagc tctctgaaga gatcaacaac ttaagagaga 60

56

aggatcatgaa	gcagtcggag	gagaacaaca	acctgcagag	ccaggtgcag	aagctcacag	120
aggagaacac	cacccttcga	gagcaagtgg	aaccaccccc	tgaggatgag	gatgatgaca	180
tcgagctccg	cggtgctgca	gcagctgctg	ccccaccccc	tccaatagag	gaagagtgcc	240
cagaagacct	cccagagaag	ttcgatggca	accagacat	gctggctcct	ttcatggccc	300
agtgccagat	cttcatggaa	aagagcacca	gggattttct	agttgatcgt	gtccgtgtct	360
gttctgtgac	aagcatgatg	accggccgtg	ctgccgttgg	gcctcagcaa	agctggagcg	420
ctccactacc	tgatgcacaa	ctaccactt	tcatgatgga	aatgaagcat	gtctttgaag	480
accctcanag	gcgagaggtt	g				501

&lt;210&gt; 176

&lt;211&gt; 378

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 176

ggcgggaagag	gtgattttatt	atatggttgt	tacactcggc	cacaaataaa	cacagaaata	60
gtccagaatg	tcacaggtcc	agggcagagg	accaacatgg	gcattttgtt	tatgagcaag	120
gtgggtctca	gaggtgatcg	gcgatcagag	ggcgatgaag	ttctagatcc	attgagacaa	180
gctctagaca	gtagcatgca	gtcccacaac	ttgtaccagc	atccccagcg	tctggcattc	240
catgtttctg	ctcctgtggc	ctccacgggt	caacaagcta	gcggtttact	tggacctctg	300
ctcatctttt	cttcttttgc	gcttcagcct	gcgcattcgc	ttcttctctc	acttggctct	360
catggcgag	aggtttcc					378

&lt;210&gt; 177

&lt;211&gt; 501

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 177

ggcaggagagc	tggacctgga	ggcgccggcg	cgacagcagc	agccatggag	gacgagatgc	60
ccaagactct	atacgtcggg	aacctttcca	gagatgtgac	agaagctcta	attctgcaac	120
tcttttagcca	gattggacct	tgtaaaaact	gcaaaatgat	tatggataca	gctggaaatg	180
atccctatgg	tcttggggag	tttcatgggc	atgtctatgc	agctggcgag	ttagctgcta	240
tgaatggagc	gaagataatg	ggtaaggaag	tcaaagtga	ttgggcaaca	acctctagca	300
gtcaaaagaa	agatacaagc	aatcattttc	atgtctttgt	tggatgatct	agcccagaaa	360
ttacaactga	agatatataa	gctgcttttg	caccatttgg	aagaatatca	gatgcccgag	420
tggtaaaaga	catggcaaca	ggaaagtcta	agggatatgg	ctttgtctcc	tttttcaaca	480
aatgggatgc	tgaaaacgcc	a				501

&lt;210&gt; 178

&lt;211&gt; 501

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 178

agccccgggc	caggccgcgg	ccggggcagg	agcgcagggg	ctttgttatg	cacctaaagc	60
catattggaa	gctocagaag	aaagagcacc	ccccggaagt	cagcagggaa	acgcagagaa	120
ctcctatgaa	ccaccaaag	gctgtaaatg	atgaaacatg	caaagctagc	cacataacat	180
caagtgtctt	tccttcagcc	tctctcggta	aagcatcatc	tcgaaagcca	tttgggatcc	240
tttctccaaa	tgttctgtgc	agtatgagt	ggaagagtc	tgtagagagc	agcttgaatg	300
ttaaaaccaa	aaagaatgca	ccatctgcaa	cgatccacca	gggcgaagaa	gaaggaccac	360
ttgatattct	ggctgttgtg	aaacctggaa	ataccaagga	aaaaattgca	ttctttgcat	420
cccaccagt	tagtaacagg	ataggatcta	tgaaaataaa	aagttcctgg	gatattgatg	480
ggagagctac	taagagaagg	a				501

&lt;210&gt; 179

&lt;211&gt; 501

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 179

cgggactagg	agcgcggcgg	ggccggcggc	agagctgtcc	ggctgcgcgg	tggcccgggg	60
ggcccgggcg	gcagggcaag	cagcggggcc	tcggcctatg	cgaccgggtg	cgccggcgcg	120
gcttctgcct	ggagaggatt	caagatgacc	aacgaagaac	ctcttcccaa	gaaggttcga	180
ttgagtgaag	cagacttcaa	agttatggca	agagatgagt	taattctaag	atggaaacaa	240
tatgaagcat	atgtacaagc	tttggagggc	aagtacacag	atcttaactc	taatgatgta	300
actggcctaa	gagagtctga	agaaaaacta	aagcaacaac	agcaggagtc	tgacgcagg	360
gaaaacatcc	ttgtaatgcg	actagcaacc	aaggaacaag	agatgcaaga	gtgtactact	420
caaatccagt	acctcaagca	agtccagcag	cccgagcggt	gccaaactgag	atcaacaatg	480
gtagaccag	cgtacaactt	t				501

&lt;210&gt; 180

&lt;211&gt; 571

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(571)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 180

gagcgtaccg	ggttttctcc	atgctgtttc	ttactctcct	cttttgcacc	cctcccattt	60
ccctcgtttt	tctttgaaaa	tttctccccc	ctccagttcg	ctgtccggcc	ctcacatgtg	120
tganaggggc	agtgtgccgt	taatggccgt	gccgggcacc	gggcccgtct	ggtagtgctg	180
ggacatgtga	agtctgctgg	gggcccgggg	ttccggcacc	tcggcgccgg	ggagatacat	240
gctgatcatg	tcccggaggt	ccccggcctg	gcagggcgcc	ctggagtggt	aggaagaggt	300
aaccacaggg	gggctggagc	tggcctcgga	cttgaccacc	gaacccatgg	agccaanagc	360
catgccaggg	gtgccctgct	gcgagtagga	catgctgtag	gtgggcgagc	cgttcattgta	420
ggtctgcgag	ctggatcatg	agttgtactg	cagggcgctc	acgtcgtaac	gggtcatggg	480
ctgcatctgc	gctgcgcctg	gcgcattgag	gcccggtg	tgngggtagc	ccaactggtc	540
ctgcatctgc	ctgcatctgc	ctgcatctgc	ctgcatctgc	ctgcatctgc	ctgcatctgc	571

&lt;210&gt; 181

&lt;211&gt; 501

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 181

tgagaccgcc	aagatgggtg	tgggcgcggt	ccctatggcg	aagctgctat	acttgggcat	60
ccggcaggtc	agcaagccgc	ttgccaaccg	tattaaggag	gccgcccggc	gaagcgagtt	120
cttcaagacc	tatatctgcc	tcccgcggcg	tcaactgtat	cactgggtgg	agatgcggac	180
caagatgcgc	atcatgggct	tccggggcac	ggtcatcaag	ccgctgaacg	aggaggcggc	240
agccgagctg	ggcgagagc	tgctggggca	agccaccatc	ttcatcgtgg	gcggcggtcg	300
cctagtgtcg	gagtactggc	gccaccaggc	gcagcagcgc	cacaaggagg	aggagcagcg	360
tgctgcctgg	aacgcgctgc	gggacgaggt	gggccacctg	gcgctggcgc	tggaagcgct	420
gcaggcgag	gtgcaggcgg	cgccgccaca	gggcgcctcg	gaggaactgc	gcacagaact	480
gcaagaggtg	cgcgccact	c				501

&lt;210&gt; 182

&lt;211&gt; 501

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 182

ccccagcaga	catgtttgcc	aaggcctttc	gggtcaagtc	caacacggcc	atcaaggggt	60
cggacaggag	aaagcttcga	gctgatgtga	caactgcttt	ccccaccctt	ggaactgatc	120
aagtctctga	gttagtacct	ggaaaggagg	agctcaacat	tgtgaagttg	tatgctcaca	180

58

```

aaggggatgc agtgactgtg tacgtgagtg gtggtaaccc catcctcttt gaactggaga 240
aaaatctgta tccaacagtg tacacgctgt ggctctatcc tgatcttctg ccaaccttta 300
caacatggcc tctggtgctc gagaactgg tagggggagc agatttgatg ctgcctggac 360
tggtgatgcc ccctgctggt ctgcctcagg tacagaaggg cgacctctgt gccatttctt 420
tggtggggaa cagagccctt gtagccattg gagttgcagc catgtccaca gctgagatgc 480
tcacgtcagg cctgaaggga a

```

&lt;210&gt; 183

&lt;211&gt; 501

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 183

```

atctgctcac tttagcactc tggcaattaa acagaacccc cttctggcag aagcttattc 60
gaatttgggg aatgtgtaca aggaagagg gcagttgcag gaggcaattg agcattatcg 120
acatgcattg cgtctcaaac ctgatttcat cgatggttat attaacctgg cagccgcctt 180
ggtagcagcg ggtgacatgg aaggggcagt acaagcttac gtctctgctc ttcagtacaa 240
tcctgatttg tactgtgttc gcagtgcctt ggggaacctg ctcaaagccc tgggtcgctt 300
ggaagaagcc aaggcatggt atttgaaagc aattgagacg caaccgaact ttgcagtagc 360
ttggagtaat cttggctgtg ttttcaatgc acaaggggaa atttggcttg caattcatca 420
ctttgaaaag ctgtcaccct tgacccaaac tttctggatg cttatatcaa tttaggaaat 480
gtcttgaaag agcacgcatt t

```

&lt;210&gt; 184

&lt;211&gt; 501

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 184

```

agttctccca ggagaaagcc atgttcagtt cgagcgccaa gatcgtgaag cccaatggcg 60
agaagccgga cgagttcgag tccggcatct cccaggctct tctggagctg gagatgaact 120
cggacctcaa ggctcagctc agggagctga atattacggc agctaaggaa attgaagttg 180
ggtgtggtgc gaaagctatc ataacttttg ttcgggttc tccactgaa tctttcaga 240
aaatccaagt ccggtagta cgcgattgg agaaaaagtt cagtgggaag catgtcgtct 300
ttatcgctca gaggagaatt ctgcctaagc caactcgaaa aagccgtaca aaaaataagc 360
aaaagcgtcc caggagccgt actctgacag ctgtgcacga tgccatcctt gaggacttgg 420
tcttcccaag cgaaattgtg ggcaagagaa tccgcgtcaa actagatggc agccggctca 480
taaaggttca tttggacaaa g

```

&lt;210&gt; 185

&lt;211&gt; 460

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(460)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 185

```

gcacaaaatg gcggcggcgg cgggcggcggc tgggtgctgca gggtcggcag ctcccggcgc 60
agcggccggc gccccgggat ctgggggcgc accctcaggg tcgcaggggg tgctgatcgg 120
ggacaggctg tactccgggg tgctcatcac cttggagaac tgctcctgc ctgacgacaa 180
gtcccgtttc acgcggtcca tgtcgagcgg cctcgacacc gacacagaga ccgacctccg 240
cgtggtgggc tgcgagctca tccaggcggc cggtatcctg ctcccctgc cgcagggtggc 300
catggctacc gggcaggtgt tgttccagcg gttcttttat accaagtcct tcgtgaagca 360
ctccatggag catgtgtcaa tggcctgtgt ccacctggt tccaagatag aagangcccc 420
aagaccatac gggacgtcat caatgtgttt caccgccttc

```

59

<210> 186  
 <211> 401  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(401)  
 <223> n = A,T,C or G

<400> 186  
 cgtgttttgg gccggttctg gagggtgctg cgccggggcc tgggtgtccg cccagtgcc 60  
 gaggacgcag gctttggcac cgaagcccg catcagaggc aaccccgcg ctccctgcaa 120  
 cggctcggggc ccctcgggga ccagcccttc gcggggctgc tgccaaaaa cctcagtcgg 180  
 gaggagctgg ttgatgcgct gcgggcagcc gtggtggacc ggaaaggacc tctagtgcg 240  
 ttgaacaagc cacagggctc accagtgcac ggaaaaccag gagagctgac gttgttctca 300  
 gtgctgccag agctgagcca gtccctangg ctccaggagc aggagcttca ggtgtgccga 360  
 ncatctggga agtaagtgg anggtgaca ggaagctang a 401

<210> 187  
 <211> 376  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(376)  
 <223> n = A,T,C or G

<400> 187  
 gcatccgccc tgtctgggag gtggggggcg cgcctctgnc cagccgccac gtctgggaag 60  
 tggggagccc cactgcccgg ctgccacccc gtctgggagg tgtaccaac agctcattga 120  
 gaaaggggaa agagagagac ggcggttttg tcgataagaa aggggggaaa tctgggggaa 180  
 agaaagagag atcagattgt tactgtgtct gtgtagaaag aagtagacat aggagactcc 240  
 attttgttct gtactaagaa aaattcttct tccttgggat gctgttaatc tataacctta 300  
 cccccaacc cgtgctctct gaaacatatg ctgtgtcaac tcagggttaa atggattaag 360  
 ggcggtgcaa gatgtg 376

<210> 188  
 <211> 376  
 <212> DNA  
 <213> Homo sapien

<400> 188  
 aacctggagc gcaccttcac gccatcaag ccggacggcg tgcagcgagg cctggtgggc 60  
 gagatcatca agcgcttcga gcagaaggga ttccgcctcg tggccatgaa gttcctccgg 120  
 gcctctgaag aacacctgaa gcagcactac attgacctga aagaccgacc attcttcct 180  
 gggctggtga agtacatgaa ctccgggccc gttgtggcca tgggtctgga ggggctgaac 240  
 gtggtgaaga caggccgagt gatgcttggg gagaccaatc cagcagattc aaagccaggc 300  
 accattcgtg gggacttctg cattcaggtt ggcaggaaca tcattcatgg cagtattca 360  
 gtaaaaagtg ctgaaa 376

<210> 189  
 <211> 501  
 <212> DNA  
 <213> Homo sapien

<400> 189  
 cccctaccgc ggagcagcac catgtcggcg ccggcgccca aagtcagtaa aaaggagctc 60

60

```

aactccaacc acgacggggc cgacgagacc tcagaaaaag aacagcaaga agcgattgaa 120
cacattgatg aagtacaaaa tgaatagac agacttaatg aacaagccag tgaggagatt 180
ttgaaagtag aacagaaaata taacaaactc cgccaaccat tttttcagaa gaggtcagaa 240
ttgatcgcca aaatcccaaa tttttgggta acaacatttg toaaccatcc acaagtgtct 300
gcaactgctg gggaggaaga tgaagaggca ctgcattatt tgaccagagt tgaagtgaca 360
gaatttgaa atattaaatc aggttacaga atagattttt attttgatga aaatccttac 420
tttgaaaata aagtctcttc caaagaattt catctgaatg agagtgggtga tccatcttcg 480
aagtcaccgc aaatcaaatg g 501

```

```

<210> 190
<211> 501
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(501)
<223> n = A,T,C or G

```

```

<400> 190
aagttctgaa gattcatttt tgtctgccat tataaattat actaatagct ctacagtcca 60
ctttaagttg tcccctacat atgtattata tatggcatgc cggtatgtat tgtccaacca 120
gtacagacct gacctcagcc ctacagagcg cacacataaa gtcattgcag tcgtcaacaa 180
gatggtgagc atgatggagg gtgtcatcca gaaacagaag aatattgcag gggcacttgc 240
cttctggatg gcaaatgcat ctgaacttct caacttcatt aagcaagacc gagaccttag 300
tcggatcaca ctggatgctc aagatgtttt agcacatttg gttcaaatgg catttaaata 360
cttggttcac tgtcttcaat cagaacttaa taattacatg ccagccttc tagatgacct 420
tgaagagaac agtctgcaac gacaaaaat agatgatgtg ctgcacacgc tcacaggagc 480
catgtntctg ctacgacgct g 501

```

```

<210> 191
<211> 501
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(501)
<223> n = A,T,C or G

```

```

<400> 191
ttgtgcgtgc tcagccacta ccctttcttn gnccactttc cganagtgtt tgtatactct 60
caagcgctcg gnggactgct gtagtgagcg cttctctggc aagaaactgg gcatccctcg 120
aggcgtagaa agggacacca tgtggcggtt ctttactgga tcgctgctgg tagaggagaa 180
gtcaagtgcc cttctgcatg accttcgaga gattgaggcc tggatctatc gattgctgcg 240
ctccccagta cccgtctctg ggcagaagcg agtagacatc gaggtcctac cccaagagct 300
ccagccagct ctgacctttg ctcttcagaa cccatctcga ttcaacctag tggatttccc 360
actgcacctt cccttggaac ttgtaggtgt ggacgcctgt ctccagntgc taacctgcat 420
tctggtagag cacaaggcgg cgctacagtc ccgagactac aatgcactct ccatgtctgt 480
gatggcatnc atggcaatga t 501

```

```

<210> 192
<211> 501
<212> DNA
<213> Homo sapien

```

```

<220>
<221> misc_feature
<222> (1)...(501)

```

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 192

tttganttga accagaagct ccaggaagaa aaacataaaa gcataactga ggcacttagg	60
agacaggagc agaataataa gagttttgag gagacctatg accgaaagct caagaatgaa	120
cttctaaact tccacaggct gcatgggtgc tgcctggctt tgggaatcct catatgactt	180
tggcaggtgt tggagtttgg aggtctcttcg ccacaggagt gcttctattt ccttttggaa	240
ccaaaagggc agctggtaac agctgggaaa gggaagtga actgtgaaaa tgtgcctttt	300
ggtattgcta atccggatat aatgctcttg gcagttggct ctcaggactg tgcctagtcc	360
ctgagcaciaa aagttcttac cttgggtggg ggtgggcaga tggtagaggt ggattggaag	420
tgaccgtctg attatcattt gggattgagt ctgttgtgtg ctgtgtaaat ttaatttacc	480
ccttgcctct ttgtgtcagt t	501

&lt;210&gt; 193

&lt;211&gt; 501

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)... (501)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 193

agntttctgc tctcgctgc ctgcccgtc ccttgcttgc tgcgccttc gctcgcctc	60
tcctcgagga tcgaggggac tctgaccaca gcctgtgctt gggaaaggag acagaggcgg	120
cgccggctca ggggaaacga ggctgcagtg gtggtagtag gaagatgtcg ggcgaggacg	180
agcaacagga gcaaaactatc gctgaggacc tggctcgtgac caagtataag atggggggcg	240
acatcgccaa cagggtactt cggctccttg tggaagcatc tagctcaggt gtgtcggtag	300
tgagcctgtg tgagaaagggt gatgccatga ttatggaaga aacagggaaa atcttcaaga	360
aagaaaagga aatgaagaaa ggtattgctt tccccaccag catttcggta aataactgtg	420
tatgtcactt ctcccctttg aagagcgacc aggtattat tctcaaggaa ggtgacttgg	480
tataaattga ccttggggtc c	501

&lt;210&gt; 194

&lt;211&gt; 560

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)... (560)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 194

ggcttcactc tcacaaactc cttgaatttc ttctctttat tcttttcctt gtcttttgta	60
gttggggaac tggcanagac ccgttcctg gtcagggtct cctggctggg cttgtctgaa	120
gctgaagggc ccttggtttg gacatgcctc tttccgggc tctcttctgg ctccagtgc	180
ttctccattc catggaataa cttcatgtga tagtgcaaca gtttggttt gcggaaaaat	240
tttaaacagt ccacaacttt gcatctaaac ttatgggtcta ggtcgacagc tggtagcata	300
natgacccaa aatcatctgt tttcttaaaa gtatttgta cttccacagt cgaaatctct	360
tgtaattcca caaggggaga agtcgggtct gttttcatcg tgttttctcc cattgatggg	420
cagttcaact ccaagcctgc agccccgat ccatcccaa aggagnggca agtcagtga	480
natganacct ggccagcttc caaagcagac ttcaactgac cttcttcaga ttccttggtg	540
ctanacaacg tgtcttgcaa	560

&lt;210&gt; 195

&lt;211&gt; 582

&lt;212&gt; DNA



62

&lt;213&gt; Homo sapien

&lt;400&gt; 195

ggcacctggg	gagaaatgga	tggagaaggg	acctggctgg	aaagcctttg	ccccgctgct	60
ctgctccgcc	cataagagga	cccctgaaat	gtcccgtgca	gtttgttcaa	gtcccctgtg	120
tgatgaaatg	tgctctcgc	cttaccctgt	tgagaatacc	tgtggtgtgg	cagcgagtat	180
tttggtat	gacctgtcca	aagacgactt	gatacctcta	taatgtaaca	gaaaagggtca	240
gaaaatatta	agcaagtaga	agtgtggagc	atattaagca	agatgaacat	ctcggaagc	300
agctgtggaa	gccctaactc	tgagataca	tctagtact	ttaaggacct	ttggacaaaa	360
ctaaaaaat	gtcatgatag	agaagtacaa	ggtttacaag	taaaagtaac	caagctaaaa	420
caggaacgaa	tcttagatgc	acaaagacta	gaagaattct	tcacaaaaaa	tcaacagctg	480
agggaaacagc	agaaagtcct	tcatgaaacc	attaaagttt	tagaagatcg	gttaagagca	540
ggcttatgtg	atcgctgtgc	agtaactgaa	gaacatatgc	gg		582

&lt;210&gt; 196

&lt;211&gt; 401

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(401)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 196

aaaccaaaga	atggattgaa	gagaagaatc	aagctctaaa	cacagacaat	tatggacatg	60
atctcgccag	tgtccaggcc	ctgcaacgca	agcatgaggg	cttcgagagg	gaccttgccg	120
ctctcgggtga	caaggtaaac	tcccttggtg	aaacagcaga	gcgcctgatc	cagtcccatc	180
ccgagtcagc	agaagacctg	caggaaaagt	gcacagagtt	aaaccaggcc	tggagcagcc	240
tggggaaacg	tgacagatcg	cgcaaggcaa	agttgggtga	ctcccacgac	ctgcagcgt	300
tccttagcga	tttccgggac	ctcatgtctt	ggatcaatgg	aatacggggg	ttggtgtcct	360
cagatgagct	anccaaggat	gtcaccggag	ctgangcatt	g		401

&lt;210&gt; 197

&lt;211&gt; 457

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(457)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 197

agtttcccgg	accatggcca	acctggagcg	caccttcatt	gccatcaagc	cggacggngt	60
gcancgcggc	ctggtgggcg	agatcatcaa	gcgcttngan	cagaagggat	tccgcctcnt	120
ggccatgaan	ttctccggg	cctctgaana	acacctgaag	cagcactaca	ttgacctgaa	180
agaccgacca	ttctccctg	ggctggtgaa	ntacatgaac	tcagggccgg	ttgtggccat	240
ggtctgggag	gggctgaacg	tggtgaagac	aggccgagtg	atgcttgggg	agaccaatcc	300
agnagattca	aagccaggca	ccattcntgg	ggacttctgc	attcaggttg	gnangaacat	360
nattcatggn	agtgattcan	taaaaagtgc	tgaaaaanaa	atcancctat	ggnttaagcc	420
tgaagaactg	gttgactaca	agtcttgngc	tcatgac			457

&lt;210&gt; 198

&lt;211&gt; 474

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 198

63

aggctgaacc	cgaggagatg	aacccttta	ctaagggtgaa	gctgatcaac	gagctgaatg	60
aacgagaggt	ccagcttggg	gtggccgata	aggtgtcctg	gcactccgag	tacaaggaca	120
gcgcttgat	cttcctggga	gggcttcctt	atgaactgac	tgaaggggac	atcatctgtg	180
tggtctcaca	atatggggag	attgttaaca	ttaatctcgt	gcgggacaag	aaaactggga	240
aatccaaagg	attctgtttc	ctctgctatg	aagaccagag	gagcacaatt	ctggccgtcg	300
acaattttta	tgggatcaag	atcaaaggaa	gaactatccg	agtggatcat	gtgtctaact	360
atcgggctcc	taaggactca	gaagaaatag	atgatgtgac	cagacaactc	caggagaagg	420
gctgtggggc	tcgtaccccc	tcaccaagtt	tgtctgagag	ctctgaagat	gaaa	474

&lt;210&gt; 199

&lt;211&gt; 574

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)... (574)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 199

gagaagaaac	aggaagaaga	agaaacgatg	cagcaagcga	catgggtaaa	atacacattt	60
ccagttaagc	atcaggtttg	gaaacaaaa	ggtgaagagt	acagagtgc	aggatatggt	120
ggttgagct	ggattagtaa	aactcatgtt	tataggtttg	ttcctaaatt	gccaggcaat	180
actaatgtga	attacagaaa	gtcgttagaa	ggaaatgtga	aggagctctt	agattctgac	240
agtgataaac	cctgcaagga	agaaccaatg	gaagtagacg	atgacatgaa	aacagagtca	300
catgtaaatt	gtcaggagag	ttctcaagta	gatgtggtca	atgttagtga	gggttttcat	360
ctaaggacta	gttacaaaaa	gaaaacaaaa	tcattcaaac	tagatggact	tcttgaaagg	420
agaattaaac	agtttacact	ggaagaaaaa	cagcgactcg	aaaaaatcaa	gttgaggagg	480
ggaattaaag	gtataaggaa	agacttctac	aaattcttca	aaaaatctct	ctgaatcacc	540
agtaataacc	gaaagcaaaa	gaanggtgtc	agag			574

&lt;210&gt; 200

&lt;211&gt; 522

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 200

tccataacct	tatggagaga	aaggactttg	agacatggct	tgataacatt	tctgttacat	60
ttctttctct	gacggacttg	cagaaaaatg	aaactctgga	tcacctgatt	agtctgagtg	120
gggcagtcga	gctcaggcat	ctctccaata	acctagagac	tctcctcaag	cgggacttcc	180
tcaaaactcct	tcccctggag	ctcagttttt	atttggttaa	atggctcgat	cctcagactt	240
tactcacatg	ctgcctcgtc	tctaaacagt	ggaataaggt	gataagtgcc	tgtacagagg	300
tgtggcagac	tgcatgtaaa	aatttgggct	ggcagataga	tgattctgtt	caggacgctt	360
tgcaactggaa	gaaggtttat	ttgaaggcta	ttttgagaat	gaagcaactg	gaggaccatg	420
aagcctttga	aacctcgtca	ttaattggac	acagtgccag	agtgtatgca	ctttactaca	480
aagatggact	tctctgtaca	gggtcagatg	acttgcgtga	aa		522

&lt;210&gt; 201

&lt;211&gt; 501

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)... (501)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 201

atctccgcct	ggttcggccc	gcctgcctcc	actcctgcct	ctaccatgtc	catcagggtg	60
------------	------------	------------	------------	------------	------------	----

64

accagaagt	cctacaaggt	gtccacctct	ggcccccg	ccttcagcag	cgctcctac	120
acgagtggc	ccggttcccg	catcagctcc	tcgagcttct	cccagtgagg	cagcagcaac	180
tttcgcggtg	gcctggggcg	cggtatggt	ggggccagcg	gcagggagg	catcaccgca	240
gttacgggtca	accagagcct	gctgagcccc	cttgtcctgg	aggtggaccc	caacatccag	300
gccgtgcgca	cccaggagaa	ggagcagatc	aagacctca	acaacaagtt	tgctccttc	360
atagacaagg	tacggttcct	ggagcancag	aacaagatgc	tggagaccaa	gtggagcctt	420
cttgacagcag	cagaagacgg	ctcgaagcaa	catggacaac	atgttcnaaa	gctacatcaa	480
caaccttagg	cgnagcttga	a				501

&lt;210&gt; 202

&lt;211&gt; 501

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 202

gcgttctgtg	gagagagtgc	gaggtcaggc	catgaacttg	ggagatggtt	taaagcttga	60
aactaaatta	ctggatggaa	aaaccaagct	aatattgtct	ccatatgaac	ataaatcaaa	120
aatttctgtg	aagatgggaa	ataaggccaa	gattgcaaaa	tgtcctttaa	gaacaaaaac	180
tgggcacatt	ctaaaaatcaa	cacaagatac	ttgtattggg	agtgaataac	ttttgcaaaa	240
gaagccagtt	ggttcagaaa	catcacaggc	aaaaggtgaa	aaaaatggaa	tgactttttc	300
atccactaag	gatttatgta	aacaatgtat	agataaagac	tgtcttcata	tccagaaaga	360
gattttcacct	gcaactccta	atatgcagaa	gactagaaac	accgtaaata	catctctagt	420
aggtaaacag	aagcctcaca	aaaaacacat	cacagctgaa	aacatgaaga	gcagtttggg	480
gtgtctaaca	caagaccaac	t				501

&lt;210&gt; 203

&lt;211&gt; 395

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 203

cttcattcatt	gcagactcct	tctacatcaa	tgcttatcgt	tttcattata	cactttgtgc	60
ctctttgtct	ctcagcttca	agggattgca	cagctacttc	attacagtac	cagaagagat	120
tcttcttctg	cagaaactag	aactggccaa	ggccaacatg	cagctcctat	atgagcgtct	180
tctcagaaga	aaacagctac	gaacacagaa	agacaaccat	ctagaggaaa	tggatgtaga	240
agctcgactt	actgaactat	gtgaagaagt	taagaaaata	gagaatcctg	atgaactggc	300
agaacttata	aatatgaatc	ttgcgcaact	ttgctcactt	ttgatggctt	tatggggaca	360
gtttctggaa	gttataacgc	tacacgaaga	actaa			395

&lt;210&gt; 204

&lt;211&gt; 501

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 204

aggtcaggca	gaaattggag	agggggctca	aaagctgctg	cggcccaaca	gottgagact	60
ggcaagtgc	tcagatgcag	agtcagactc	tcgggcaagc	tctcccaact	ccaccgtctc	120
caacaccagc	accgagggct	tcgggggcat	catgtctttt	gccagcagcc	tctatcggaa	180
ccacagtacc	agcttcagtc	tttcaaacct	cacactgccc	accaaagggtg	cccagagaaa	240
ggccacgccc	ttccccagtc	tgaaaggaaa	caggaggcg	ttagtggatc	agaagtcac	300
tgctattaaa	cacagcccaa	cagtgaagag	agaacctcca	tcaccccagg	gtcgatccag	360
caattctagt	gagaaccagc	agttcctgaa	ggaggtggtg	cacagcgtgc	tggacggcca	420
gggagttggc	tggtcaaca	tgaaaaagg	gcgccggctg	ctggagagcg	agcagctgcg	480
agtctttgtc	ctgagcaagc	t				501

&lt;210&gt; 205

&lt;211&gt; 501

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

65

<220>  
 <221> misc\_feature  
 <222> (1)...(501)  
 <223> n = A,T,C or G

<400> 205  
 cagaagtgc gcggtggcgc cggttggttg cgggccggcg gcgggctggc ggagatggag 60  
 gatcttggtc aagatggggt ggcttcacca gctacccttg ggaccgggaa atctaagaat 120  
 tggagaaaga aattgaagaa ctcagatcaa aacctgttac tgaaggaaact ggtgatatta 180  
 ttaaggcatt aactgaacgt ctggatgctc ttcttctgga aaaagcagag actgagcaac 240  
 agtgtctttc tctgaaaaag gaaaatataa aaatgaagca agaggttgag gattctgtaa 300  
 caaagatggg agatgcacat aaggagttgg aacaatcaca tataaactat gtgaaagaaa 360  
 ttgaaaattt gaaaaatgag ttgatggcag tacgttccaa atacagtga gacaaagcta 420  
 acttacaaaa ncagctggaa naagcaatga atacncaatt agaactttca naacaactta 480  
 aatttcanaa caactctgaa g 501

<210> 206  
 <211> 599  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(599)  
 <223> n = A,T,C or G

<400> 206  
 tggtcgcacc agctctctgc tctcccagcg cagcgccgcc gcccgcccc tccagcttcc 60  
 cggaccatgg ocaacctgga gcgcaccttc atcgccatca agccggacgg cgtgcagcgc 120  
 ggcctgggtg gcgagatcat caagcgcttc gagcagaagg gattccgcct cgtggccatg 180  
 aagttcctcc gggcctctga agaacacctg aagcagcact acattgacct gaaagaccga 240  
 cagttctctc ctgggtggtg gtagtacatg aactcagggc aggttctggc catggtctgg 300  
 gaggggctga acgtggtgaa gacaggccga gtgatgcttg gggagaccaa tccagcagat 360  
 tcaaagccag gcaccattcg tggggacttc tgcattcag ttggcaggaa catcattcat 420  
 ggcagtgatt cagtaaaaag tgctgaaaaa gaaatcagcc tatggtttaa gcctgaagaa 480  
 ctggttgact acaagtcttg tgctcatgac tgggtctatg aataagaggt ggacacaaca 540  
 gcagtctcct tcacacggcg tgggtgtgtcc tggacacagt nttattcttg acttaaagc 599

<210> 207  
 <211> 395  
 <212> DNA  
 <213> Homo sapien

<400> 207  
 ccggccgggc cgagggtcgg cggccgcccgc cgggccgggc ccgcgcacag cggccgcattg 60  
 tacaacatga tggagacgga gctgaagccg ccgggcccgc agcaaacttc ggggggcggc 120  
 ggcggcaact ccaccgcggc ggcggccggc ggcaaccaga aaaacagccc ggaccgcgtc 180  
 aagcggccca tgaatgcctt catggtgttg tcccgcgggc agcggcgcaa gatggcccag 240  
 gagaacccca agatgcacaa ctcgagatc agcaagcgc tgggcgccga gtggaactt 300  
 ttgtcggaga cggagaagcg gccgttcac gacgaggcta agcggctgcg agcgtgcac 360  
 atgaaggagc acccggatta taaataccgg ccccg 395

<210> 208  
 <211> 398  
 <212> DNA  
 <213> Homo sapien

<400> 208

## 66

aggetctcca	agccctgctg	ttatatTTTT	ccaggaggga	ggggcgattc	tgccttggtt	60
gcagtgaatg	gtttcaatat	gctcatcaat	ggcggatcag	agagaaaatc	ctgcttctgg	120
aagctcatcc	gacacttaga	ccgagtggac	tccatcctgc	tcacccacat	tggggatgac	180
aatttgctcg	gaataaacag	catgttacag	cggaattg	cagagctcga	ggaagaacag	240
tcccagggtc	ccaccacaaa	tagtgactgg	atgaaaaacc	tcatctcccc	tgacttagga	300
gttgtatttc	tcaatgtacc	tgaaaatctc	aaaaatccag	agccaaacat	caagatgaag	360
agaagcatag	aagaagcctg	cttcactctc	cagtacct			398

&lt;210&gt; 209

&lt;211&gt; 501

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 209

gcgcagcctc	ctgggagttg	tagtcgcgat	cctgaggtaa	cggataagtt	tataccatgg	60
atagcaca	ggagaagtgt	gacagttaca	aagatgatct	tctgcttagg	atgggactta	120
atgataataa	agcaggaatg	gaaggattag	ataaagagaa	aattaacaaa	attataatgg	180
aagccacgaa	ggggtccaga	ttttatggaa	atgagctcaa	gaaagaaaag	caagtcaacc	240
aacgaattga	aaatatgatg	caacaaaaag	ctcaaatcac	cagccaacag	ctaagaaaag	300
cacaattaca	ggttgacaga	tttgcaatgg	aattagaaca	aagccgaaat	ttgagcaata	360
ccatagtgc	cattgacatg	gatgctttct	atgcagctgt	agaaatgagg	gacaatccag	420
aattgaagga	taaaccatt	gctgtaggat	caatgagtat	gctgtctact	tcaaattacc	480
atgcaaggag	atttggtgtt	c				501

&lt;210&gt; 210

&lt;211&gt; 450

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(450)

&lt;223&gt; n = 2, 7, 10, 13, 16, 19, 22, 25, 28, 31, 34, 37, 40, 43, 46, 49, 52, 55, 58, 61, 64, 67, 70, 73, 76, 79, 82, 85, 88, 91, 94, 97, 100, 103, 106, 109, 112, 115, 118, 121, 124, 127, 130, 133, 136, 139, 142, 145, 148, 151, 154, 157, 160, 163, 166, 169, 172, 175, 178, 181, 184, 187, 190, 193, 196, 199, 202, 205, 208, 211, 214, 217, 220, 223, 226, 229, 232, 235, 238, 241, 244, 247, 250, 253, 256, 259, 262, 265, 268, 271, 274, 277, 280, 283, 286, 289, 292, 295, 298, 301, 304, 307, 310, 313, 316, 319, 322, 325, 328, 331, 334, 337, 340, 343, 346, 349, 352, 355, 358, 361, 364, 367, 370, 373, 376, 379, 382, 385, 388, 391, 394, 397, 400, 403, 406, 409, 412, 415, 418, 421, 424, 427, 430, 433, 436, 439, 442, 445, 448, 451, 454, 457, 460, 463, 466, 469, 472, 475, 478, 481, 484, 487, 490, 493, 496, 499, 502, 505, 508, 511, 514, 517, 520, 523, 526, 529, 532, 535, 538, 541, 544, 547, 550, 553, 556, 559, 562, 565, 568, 571, 574, 577, 580, 583, 586, 589, 592, 595, 598, 601, 604, 607, 610, 613, 616, 619, 622, 625, 628, 631, 634, 637, 640, 643, 646, 649, 652, 655, 658, 661, 664, 667, 670, 673, 676, 679, 682, 685, 688, 691, 694, 697, 700, 703, 706, 709, 712, 715, 718, 721, 724, 727, 730, 733, 736, 739, 742, 745, 748, 751, 754, 757, 760, 763, 766, 769, 772, 775, 778, 781, 784, 787, 790, 793, 796, 799, 802, 805, 808, 811, 814, 817, 820, 823, 826, 829, 832, 835, 838, 841, 844, 847, 850, 853, 856, 859, 862, 865, 868, 871, 874, 877, 880, 883, 886, 889, 892, 895, 898, 901, 904, 907, 910, 913, 916, 919, 922, 925, 928, 931, 934, 937, 940, 943, 946, 949, 952, 955, 958, 961, 964, 967, 970, 973, 976, 979, 982, 985, 988, 991, 994, 997, 1000, 1003, 1006, 1009, 1012, 1015, 1018, 1021, 1024, 1027, 1030, 1033, 1036, 1039, 1042, 1045, 1048, 1051, 1054, 1057, 1060, 1063, 1066, 1069, 1072, 1075, 1078, 1081, 1084, 1087, 1090, 1093, 1096, 1099, 1102, 1105, 1108, 1111, 1114, 1117, 1120, 1123, 1126, 1129, 1132, 1135, 1138, 1141, 1144, 1147, 1150, 1153, 1156, 1159, 1162, 1165, 1168, 1171, 1174, 1177, 1180, 1183, 1186, 1189, 1192, 1195, 1198, 1201, 1204, 1207, 1210, 1213, 1216, 1219, 1222, 1225, 1228, 1231, 1234, 1237, 1240, 1243, 1246, 1249, 1252, 1255, 1258, 1261, 1264, 1267, 1270, 1273, 1276, 1279, 1282, 1285, 1288, 1291, 1294, 1297, 1300, 1303, 1306, 1309, 1312, 1315, 1318, 1321, 1324, 1327, 1330, 1333, 1336, 1339, 1342, 1345, 1348, 1351, 1354, 1357, 1360, 1363, 1366, 1369, 1372, 1375, 1378, 1381, 1384, 1387, 1390, 1393, 1396, 1399, 1402, 1405, 1408, 1411, 1414, 1417, 1420, 1423, 1426, 1429, 1432, 1435, 1438, 1441, 1444, 1447, 1450, 1453, 1456, 1459, 1462, 1465, 1468, 1471, 1474, 1477, 1480, 1483, 1486, 1489, 1492, 1495, 1498, 1501, 1504, 1507, 1510, 1513, 1516, 1519, 1522, 1525, 1528, 1531, 1534, 1537, 1540, 1543, 1546, 1549, 1552, 1555, 1558, 1561, 1564, 1567, 1570, 1573, 1576, 1579, 1582, 1585, 1588, 1591, 1594, 1597, 1600, 1603, 1606, 1609, 1612, 1615, 1618, 1621, 1624, 1627, 1630, 1633, 1636, 1639, 1642, 1645, 1648, 1651, 1654, 1657, 1660, 1663, 1666, 1669, 1672, 1675, 1678, 1681, 1684, 1687, 1690, 1693, 1696, 1699, 1702, 1705, 1708, 1711, 1714, 1717, 1720, 1723, 1726, 1729, 1732, 1735, 1738, 1741, 1744, 1747, 1750, 1753, 1756, 1759, 1762, 1765, 1768, 1771, 1774, 1777, 1780, 1783, 1786, 1789, 1792, 1795, 1798, 1801, 1804, 1807, 1810, 1813, 1816, 1819, 1822, 1825, 1828, 1831, 1834, 1837, 1840, 1843, 1846, 1849, 1852, 1855, 1858, 1861, 1864, 1867, 1870, 1873, 1876, 1879, 1882, 1885, 1888, 1891, 1894, 1897, 1900, 1903, 1906, 1909, 1912, 1915, 1918, 1921, 1924, 1927, 1930, 1933, 1936, 1939, 1942, 1945, 1948, 1951, 1954, 1957, 1960, 1963, 1966, 1969, 1972, 1975, 1978, 1981, 1984, 1987, 1990, 1993, 1996, 1999, 2002, 2005, 2008, 2011, 2014, 2017, 2020, 2023, 2026, 2029, 2032, 2035, 2038, 2041, 2044, 2047, 2050, 2053, 2056, 2059, 2062, 2065, 2068, 2071, 2074, 2077, 2080, 2083, 2086, 2089, 2092, 2095, 2098, 2101, 2104, 2107, 2110, 2113, 2116, 2119, 2122, 2125, 2128, 2131, 2134, 2137, 2140, 2143, 2146, 2149, 2152, 2155, 2158, 2161, 2164, 2167, 2170, 2173, 2176, 2179, 2182, 2185, 2188, 2191, 2194, 2197, 2200, 2203, 2206, 2209, 2212, 2215, 2218, 2221, 2224, 2227, 2230, 2233, 2236, 2239, 2242, 2245, 2248, 2251, 2254, 2257, 2260, 2263, 2266, 2269, 2272, 2275, 2278, 2281, 2284, 2287, 2290, 2293, 2296, 2299, 2302, 2305, 2308, 2311, 2314, 2317, 2320, 2323, 2326, 2329, 2332, 2335, 2338, 2341, 2344, 2347, 2350, 2353, 2356, 2359, 2362, 2365, 2368, 2371, 2374, 2377, 2380, 2383, 2386, 2389, 2392, 2395, 2398, 2401, 2404, 2407, 2410, 2413, 2416, 2419, 2422, 2425, 2428, 2431, 2434, 2437, 2440, 2443, 2446, 2449, 2452, 2455, 2458, 2461, 2464, 2467, 2470, 2473, 2476, 2479, 2482, 2485, 2488, 2491, 2494, 2497, 2500, 2503, 2506, 2509, 2512, 2515, 2518, 2521, 2524, 2527, 2530, 2533, 2536, 2539, 2542, 2545, 2548, 2551, 2554, 2557, 2560, 2563, 2566, 2569, 2572, 2575, 2578, 2581, 2584, 2587, 2590, 2593, 2596, 2599, 2602, 2605, 2608, 2611, 2614, 2617, 2620, 2623, 2626, 2629, 2632, 2635, 2638, 2641, 2644, 2647, 2650, 2653, 2656, 2659, 2662, 2665, 2668, 2671, 2674, 2677, 2680, 2683, 2686, 2689, 2692, 2695, 2698, 2701, 2704, 2707, 2710, 2713, 2716, 2719, 2722, 2725, 2728, 2731, 2734, 2737, 2740, 2743, 2746, 2749, 2752, 2755, 2758, 2761, 2764, 2767, 2770, 2773, 2776, 2779, 2782, 2785, 2788, 2791, 2794, 2797, 2800, 2803, 2806, 2809, 2812, 2815, 2818, 2821, 2824, 2827, 2830, 2833, 2836, 2839, 2842, 2845, 2848, 2851, 2854, 2857, 2860, 2863, 2866, 2869, 2872, 2875, 2878, 2881, 2884, 2887, 2890, 2893, 2896, 2899, 2902, 2905, 2908, 2911, 2914, 2917, 2920, 2923, 2926, 2929, 2932, 2935, 2938, 2941, 2944, 2947, 2950, 2953, 2956, 2959, 2962, 2965, 2968, 2971, 2974, 2977, 2980, 2983, 2986, 2989, 2992, 2995, 2998, 3001, 3004, 3007, 3010, 3013, 3016, 3019, 3022, 3025, 3028, 3031, 3034, 3037, 3040, 3043, 3046, 3049, 3052, 3055, 3058, 3061, 3064, 3067, 3070, 3073, 3076, 3079, 3082, 3085, 3088, 3091, 3094, 3097, 3100, 3103, 3106, 3109, 3112, 3115, 3118, 3121, 3124, 3127, 3130, 3133, 3136, 3139, 3142, 3145, 3148, 3151, 3154, 3157, 3160, 3163, 3166, 3169, 3172, 3175, 3178, 3181, 3184, 3187, 3190, 3193, 3196, 3199, 3202, 3205, 3208, 3211, 3214, 3217, 3220, 3223, 3226, 3229, 3232, 3235, 3238, 3241, 3244, 3247, 3250, 3253, 3256, 3259, 3262, 3265, 3268, 3271, 3274, 3277, 3280, 3283, 3286, 3289, 3292, 3295, 3298, 3301, 3304, 3307, 3310, 3313, 3316, 3319, 3322, 3325, 3328, 3331, 3334, 3337, 3340, 3343, 3346, 3349, 3352, 3355, 3358, 3361, 3364, 3367, 3370, 3373, 3376, 3379, 3382, 3385, 3388, 3391, 3394, 3397, 3400, 3403, 3406, 3409, 3412, 3415, 3418, 3421, 3424, 3427, 3430, 3433, 3436, 3439, 3442, 3445, 3448, 3451, 3454, 3457, 3460, 3463, 3466, 3469, 3472, 3475, 3478, 3481, 3484, 3487, 3490, 3493, 3496, 3499, 3502, 3505, 3508, 3511, 3514, 3517, 3520, 3523, 3526, 3529, 3532, 3535, 3538, 3541, 3544, 3547, 3550, 3553, 3556, 3559, 3562, 3565, 3568, 3571, 3574, 3577, 3580, 3583, 3586, 3589, 3592, 3595, 3598, 3601, 3604, 3607, 3610, 3613, 3616, 3619, 3622, 3625, 3628, 3631, 3634, 3637, 3640, 3643, 3646, 3649, 3652, 3655, 3658, 3661, 3664, 3667, 3670, 3673, 3676, 3679, 3682, 3685, 3688, 3691, 3694, 3697, 3700, 3703, 3706, 3709, 3712, 3715, 3718, 3721, 3724, 3727, 3730, 3733, 3736, 3739, 3742, 3745, 3748, 3751, 3754, 3757, 3760, 3763, 3766, 3769, 3772, 3775, 3778, 3781, 3784, 3787, 3790, 3793, 3796, 3799, 3802, 3805, 3808, 3811, 3814, 3817, 3820, 3823, 3826, 3829, 3832, 3835, 3838, 3841, 3844, 3847, 3850, 3853, 3856, 3859, 3862, 3865, 3868, 3871, 3874, 3877, 3880, 3883, 3886, 3889, 3892, 3895, 3898, 3901, 3904, 3907, 3910, 3913, 3916, 3919, 3922, 3925, 3928, 3931, 3934, 3937, 3940, 3943, 3946, 3949, 3952, 3955, 3958, 3961, 3964, 3967, 3970, 3973, 3976, 3979, 3982, 3985, 3988, 3991, 3994, 3997, 4000, 4003, 4006, 4009, 4012, 4015, 4018, 4021, 4024, 4027, 4030, 4033, 4036, 4039, 4042, 4045, 4048, 4051, 4054, 4057, 4060, 4063, 4066, 4069, 4072, 4075, 4078, 4081, 4084, 4087, 4090, 4093, 4096, 4099, 4102, 4105, 4108, 4111, 4114, 4117, 4120, 4123, 4126, 4129, 4132, 4135, 4138, 4141, 4144, 4147, 4150, 4153, 4156, 4159, 4162, 4165, 4168, 4171, 4174, 4177, 4180, 4183, 4186, 4189, 4192, 4195, 4198, 4201, 4204, 4207, 4210, 4213, 4216, 4219, 4222, 4225, 4228, 4231, 4234, 4237, 4240, 4243, 4246, 4249, 4252, 4255, 4258, 4261, 4264, 4267, 4270, 4273, 4276, 4279, 4282, 4285, 4288, 4291, 4294, 4297, 4300, 4303, 4306, 4309, 4312, 4315, 4318, 4321, 4324, 4327, 4330, 4333, 4336, 4339, 4342, 4345, 4348, 4351, 4354, 4357, 4360, 4363, 4366, 4369, 4372, 4375, 4378, 4381, 4384, 4387, 4390, 4393, 4396, 4399, 4402, 4405, 4408, 4411, 4414, 4417, 4420, 4423, 4426, 4429, 4432, 4435, 4438, 4441, 4444, 4447, 4450, 4453, 4456, 4459, 4462, 4465, 4468, 4471, 4474, 4477, 4480, 4483, 4486, 4489, 4492, 4495, 4498, 4501, 4504, 4507, 4510, 4513, 4516, 4519, 4522, 4525, 4528, 4531, 4534, 4537, 4540, 4543, 4546, 4549, 4552, 4555, 4558, 4561, 4564, 4567, 4570, 4573, 4576, 4579, 4582, 4585, 4588, 4591, 4594, 4597, 4600, 4603, 4606, 4609, 4612, 4615, 4618, 4621, 4624, 4627, 4630, 4633, 4636, 4639, 4642, 4645, 4648, 4651, 4654, 4657, 4660, 4663, 4666, 4669, 4672, 4675, 4678, 4681, 4684, 4687, 4690, 4693, 4696, 4699, 4702, 4705, 4708, 4711, 4714, 4717, 4720, 4723, 4726, 4729, 4732, 4735, 4738, 4741, 4744, 4747, 4750, 4753, 4756, 4759, 4762, 4765, 4768, 4771, 4774, 4777, 4780, 4783, 4786, 4789, 4792, 4795, 4798, 4801, 4804, 4807, 4810, 4813, 4816, 4819, 4822, 4825, 4828, 4831, 4834, 4837, 4840, 4843, 4846, 4849, 4852, 4855, 4858, 4861, 4864, 4867, 4870, 4873, 4876, 4879, 4882, 4885, 4888, 4891, 4894, 4897, 4900, 4903, 4906, 4909, 4912, 4915, 4918, 4921, 4924, 4927, 4930, 4933, 4936, 4939, 4942, 4945, 4948, 4951, 4954, 4957, 4960, 4963, 4966, 4969, 4972, 4975, 4978, 4981, 4984, 4987, 4990, 4993, 4996, 5000, 5003, 5006, 5009, 5012, 5015, 5018, 5021, 5024, 5027, 5030, 5033, 5036, 5039, 5042, 5045, 5048, 5051, 5054, 5057, 5060, 5063, 5066, 5069, 5072, 5075, 5078, 5081, 5084, 5087, 5090, 5093, 5096, 5099, 5102, 5105, 5108, 5111, 5114, 5117, 5120, 5123, 5126, 5129, 5132, 5135, 5138, 5141, 5144, 5147, 5150, 5153, 5156, 5159, 5162, 5165, 5168, 5171, 5174, 5177, 5180, 5183, 5186, 5189, 5192, 5195, 5198, 5201, 5204, 5207, 5210, 5213, 5216, 5219, 5222, 5225, 5228, 5231, 5234, 5237, 5240, 5243, 5246, 5249, 5252, 5255, 5258, 5261, 5264, 5267, 5270, 5273, 5276, 5279, 5282, 5285, 5288, 5291, 5294, 5297, 5300, 5303, 5306, 5309, 5312, 5315, 5318, 5321, 5324, 5327, 5330, 5333, 5336, 5339, 5342, 5345, 5348, 5351, 5354, 5357, 5360, 5363, 5366, 5369, 5372, 5375, 5378, 5381, 5384, 5387, 5390, 5393, 5396, 5399, 5402, 5405, 54

67

aagtcttgga agaagccaag aagaacttct gaaggacgag gaggcctga gccaacgcct 600  
g 601

<210> 212

<211> 498

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(498)

<223> n = A,T,C or G

<400> 212

atgacaaata	ttccacatct	gtgattctct	ccagtcacaa	gttctttgag	acgatgccat	60
cgcccttgcc	caatcggaga	atggaatcat	ctgactcacc	catcctacga	atggcccgc	120
agatagcata	agttttaaac	tggccattaa	acctgcctgt	gaccttgta	acctcggcca	180
cgttcacatg	gatggatgag	tggctccttg	caccgatgat	gcgattgcta	gcggagcatt	240
tccggggcac	gtacaggtcc	acgaactcgc	cgccgtcgtt	ctgcatttcg	aggctgggct	300
gcgcctgctg	ccactcgtgc	cgaattcttt	ggatccacta	gtgtcgacct	gcaggcgcgc	360
gagctccagc	ttttgtccct	ttagtgaggg	ttaatttcga	gcttggcgta	atcaanggca	420
tagctgggtc	ctgmnggaaa	ttggtatccg	tcacaattcc	ncncaatata	cgagccggaa	480
gtataaagg	naaagcct					498

<210> 213

<211> 601

<212> DNA

<213> Homo sapien

<400> 213

actaccagac	aaccttagcc	aaaccattta	cccaaataaa	gtataggcga	tagaaattga	60
aacctggcgc	aatagatata	gtaccgcaag	ggaaagatga	aaaattataa	ccaagcataa	120
tttagcagga	agtagcccat	ctacattctg	ctaatgaat	ttactagaaa	taactcttgc	180
aggagagcca	aagctaagac	ccccgaaacc	agacgagcta	cttaagaaca	gctaaaagag	240
cacacccgtc	tatgtagcaa	aatagtggga	agatttatag	gtagaggcga	caaacctacc	300
gagcctgggt	atagctgggt	gtccaagata	gaatcttagt	tcaactttta	atttgccac	360
agaaccctct	aaatcccctt	gtaaatttaa	ctgttagtcc	aaagaggaa	agctctttgg	420
acactaggaa	aaaaccttgt	agagagagta	aaaaatttaa	caccatagat	aggcctaaaa	480
gcagccacca	attaagaaag	ogttcaagct	caacaccac	tacctaaaaa	atcccaaaca	540
tatactgaac	tcctcaaccc	aattggccaa	tctatcccct	atagaagact	aatggtagta	600
t						601

<210> 214

<211> 500

<212> DNA

<213> Homo sapien

<220>

<221> misc\_feature

<222> (1)...(500)

<223> n = A,T,C or G

<400> 214

aggctgcatt	tacggggtct	cccggagggc	cagagtcgtg	gcttacagaa	gagacgaaat	60
gtggctctgag	ggacgatatg	aatatgaaag	aattccgaga	gaacgagcac	ctcctcgaag	120
tcattccagt	gatgaatctg	gttatagatg	gacaagagac	gatcattctg	caagcaggca	180
acctgaatac	agggacatga	gagatggcct	tagaagaaaa	agtttctact	cttcccatta	240
tgcgagagag	cggtctcctt	ataaaaggga	caatactttt	ttcagagaat	cacctgttgg	300
ccgaaaggat	tctccacaca	gcanatctgg	ttccagtgtc	agtagcanaa	gctctctcca	360

68

gaaaggagca	aatcatactc	tttccatcag	tctcaacata	gaaataaaga	gaggcctgtc	420
agtctttttaa	aacatcaaga	gatacttccc	ctcaagtggg	tcacagttct	tctcaaagg	480
gtagacaaac	ccagtaggta					500

&lt;210&gt; 215

&lt;211&gt; 501

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(501)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 215

gcctgtggga	gcccgtggcc	tttaaagtgc	cggttcagcct	tttcctccag	gggtgctttg	60
taaacacggc	tgtgtctcagg	gctcgcgggt	gaccgaaagg	atcatgaact	agtgacctgg	120
aaagggtaact	agatggaaac	ttgagaaagg	actgcttatt	gataacagct	aaggatttcc	180
tggaagcaga	gtaaataaag	ctcatggccc	accagctaga	aagtattctt	gccatgagaa	240
aaagaatgtg	ataaatttatt	caacttatga	aattcaagtt	acatgtgaat	tctgccaggc	300
aatacaagga	cctgtggaat	atgagtgatg	acaaaccctt	tctatgtact	gcgcctggat	360
gtggccagcg	ttttaccaac	gaggatcatt	tggctgtcca	taaacataaa	catgagatga	420
cactgaaatt	tggtccanca	cgtaatgaca	gtgtcattgt	ggctgatcag	acccaacac	480
caacaagatt	cttgaaaaac	t				501

&lt;210&gt; 216

&lt;211&gt; 501

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 216

aggcggcctt	gggggcatct	gcattggagt	tgggggtgcc	gatgctgtgg	atgtcatggc	60
ctccggttgg	tcctcaccca	aagatgtgat	cctgaagggtg	gcaggcatcc	tcacggtgaa	120
aggtggcaca	ggtgcaatcg	tggaatacca	cgggcctggg	gtagactcca	tctcctgcac	180
tgccatggcg	acaatctgca	acatgggtgc	agaaattggg	gccaccactt	ccgtgttccc	240
ttacaaccac	aggatgaaga	agtacctgag	caagaccggc	cggaagaca	ttgccaatct	300
agctgatgaa	ttcaaggatc	acttggtgcc	tgacctggc	tgccattatg	accaactaat	360
tgaaattaac	ctcagtggac	tgaagccaca	catcaatggg	cccttcaccc	ctgacctgct	420
caccctgtgg	cagaagtggg	c				480
						501

&lt;210&gt; 217

&lt;211&gt; 408

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(408)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 217

gtacacctg	gacgtgacgt	ggggctggga	gcactggggc	gggatcctgc	cacagtgcgt	60
ggacctgttg	ctctgcatca	acatggccca	tgctagcccc	ctgcgctgca	cggaggaacc	120
cagaatgggg	gcttcgggac	acagccctcc	tggaggacct	gggaaaggcc	agtggcctgc	180
tcttgagag	gatggtggac	atgccagcca	acaacaaatg	cctgatcttc	cggaaaaact	240
aagccctcc	ttcacccccc	cacacctgca	tccttgccgg	angctctgtg	aggcacgaac	300
cctgcctccc	taggcgggac	cttgtggacg	acagcccccac	ccagtctgtg	ctctcagccg	360
ntggccgaag	ggccancct	gctcagaata	aacatgtcct	gctgccgg		408

69

<210> 218  
 <211> 402  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(402)  
 <223> n = A,T,C or G

<400> 218  
 tgcttgctc aaagattaag ccatgcatgt ctaagtacgc acggccggta tcctgctccg 60  
 cctgccgcag gnggccatgg ntaccgggca gnggttggtc cagcgggttct tttataccaa 120  
 gtccttcgtg aagcactcca tggagcatgt gtcaatggcc tgtgtccacc tggctttcaa 180  
 gatagaagag gccccaagac gcatacggga cgtcatcaat gtgtttcacc cgccttcgac 240  
 agctgagaga caaaaagaag cccgtgcctc tactactgga tcaagattat gtttaatttaa 300  
 agaacccaat tataaaggcg ggnaagacna ttcttcaaaa agatgggntt ctgcgnccat 360  
 gtgaagcatn ctcataagan aatcgntatg taccttcagg gg 402

<210> 219  
 <211> 486  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(486)  
 <223> n = A,T,C or G

<400> 219  
 aatgctgcgg agattgaggt gtcggttcgt gctgctgagc tgcccaggct tcacggagcg 60  
 gctgaggaa tcaatggcga ttataggctt tcaattgttt aatataata gtgtcattgg 120  
 actaagatgt tcctgatgcc aacctcttca gagttaaaca gtgggcagaa cttcctaacc 180  
 cagtggatga ccaatccttc tcgggctggg gtcatattaa atcgtggatt tcctattttg 240  
 gaagcagaca aagagaagcg agcagcttgt ggacatttct accagctttt nctattaaaa 300  
 ggcacacatt tttctgatag cttcagcttt tataaatgaa gaaaaattca cttcttgaag 360  
 aacagaagtt ggagtcaaac aacacttaca aaccacagtc agataaatct gaaaccata 420  
 cagccttttc ttgcattaaa aagggaccnc agtngcggg atggtccagt gctcctggac 480  
 ncccgg 486

<210> 220  
 <211> 380  
 <212> DNA  
 <213> Homo sapien

<400> 220  
 ggcggattag ccttcgcggg gcaaaatgga gctcgaggcc atgagcagat ataccagccc 60  
 agtgaacca gctgtcttcc cccatctgac cgtggtgctt ttggccattg gcatgttctt 120  
 caccgcctgg ttcttcgttt acgaggcac ctctaccaag tacactcgtg atatctataa 180  
 agagctctc atctccttag tggcctcact cttcatgggc tttggagtcc tcttcctgct 240  
 gctctgggtt ggcactacg tgtgagcacc caagggtaac aaccagatgg cttcactgaa 300  
 acctgctttt gtaaattact tttttttact gttgctggaa gtgtccacc tgctgctcat 360  
 aataaatgca gatgtatagc 380

<210> 221  
 <211> 406  
 <212> DNA  
 <213> Homo sapien



<220>  
 <221> misc\_feature  
 <222> (1)...(406)  
 <223> n = A,T,C or G

<400> 221  
 gcggattagc cttcgcgggg caaatggag ctcgaggcca tgagcagata taccagccca 60  
 gtgaaccag ctgtcttccc ccatctgacc gtggtgcttt tggccattgg catgttcttc 120  
 accgcctggt tcttcgttta cgangtcacc tctaccaagt acactcgtga tatctataaa 180  
 gagctcctca tctccttagt ggccctcactc ttcattgggt ttggagtcct cttcctgctg 240  
 ctctgggttg gcatctacgt gtgagcacc aagggttaaca accagatggc ttcactgaaa 300  
 cctgcttttg taaattactt ttttttactg ttgctggaag tgtcccacct gctgctcata 360  
 ataatgcag atgtatagcc ctatagnag cgtattacaa ttcact 406

<210> 222  
 <211> 501  
 <212> DNA  
 <213> Homo sapien

<400> 222  
 aatggcggta gttggtgtgt cctcggtttc teggctgctg ggtcgggtccc gccacagct 60  
 ggggcggcct atgtcgagt ggcgccatgg cgaagagggc tcagctcgca tgtggaagac 120  
 tctcaccttc ttcgtcgcgc tccccggggt ggcagtcagc atgtgaatg tgtacctgaa 180  
 gtgcaccac ggagagcacg agagaccgga gtcatcgcc taccacctc tccgcatcag 240  
 gaccaagccg tttccctggg gagatggtaa ccatactcta ttccataacc ctcatgtgaa 300  
 tccacttcca actggctacg aagatgaata aagagaatct ggaccactac cggggcacca 360  
 gggaccacag cactggtttg gaccgttact ctgcacatgg accagaaaaa gtatatggga 420  
 ccttaagctc accttcttta cttgtatcaa atgatgactg gtatactggt ctcccatccc 480  
 tttgcttggt gcaggagatg g 501

<210> 223  
 <211> 455  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(455)  
 <223> n = A,T,C or G

<400> 223  
 aatcttatgc aaaagggaca caggggttca aaaataaaaa tttctcttcc ccctcccaa 60  
 acctgtaccc cagctccccg accacaaccc ccttcctccc ccggggaaag caagaaggag 120  
 caggtgtggc atctgcagct gggaananag aggccgggga ggtgccgagc tcggtgctgg 180  
 tctctttcca aatataaata cgtgtgtcan aactggaaaa tcctccagca cccaccaccc 240  
 aagcactctc cgttttctgc cgggtgttgg agaggggcgg ggggcagggg cgccaggcac 300  
 cggctggctg cggctactg catccgctgg gtgtgcaccc cgcgagcctc ctgctgctca 360  
 ttgtagaaga gatgacactc ggggtccccc ccggtggng ggggtccct ggatcagctt 420  
 tccgnggnt ggggttcaca caccagcact tccca 455

<210> 224  
 <211> 507  
 <212> DNA  
 <213> Homo sapien

<220>  
 <221> misc\_feature  
 <222> (1)...(507)

71

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 224

ttaccacac	ccattgtagc	ccttgggtgn	gggatgtgcc	ctgtccctgc	agggccaaaa	60
gggtccatgt	ttccctcaaa	totcaaagca	gtcctggccc	aggetgcagg	caggagggaa	120
gtcgtgacct	cttggcaggc	tcagtctctgc	agctgcccc	agcagccana	ctgtccctgg	180
ggctcgtcca	ggcccgggcy	ctggctggga	ggggaggtgt	ctggcaggtc	ttggcatgga	240
ggaaaanagc	tgctgcaggg	cctntcgggg	gaggggttgg	ccaagtaggc	attcaccagc	300
tgcatgatct	cttccacctg	ggggctctgc	aggaggagct	gntctctcc	cacctcaag	360
gccagggtgn	gggggcccac	tagctggcag	gcggccacat	ggccatagct	gacactgnng	420
atgggctccg	tctcccctgg	ccggganagg	gacatggcct	tggtcccaa	gcccaggcac	480
agttnttggg	ggagcacccc	gaccagg				507

&lt;210&gt; 225

&lt;211&gt; 572

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(572)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 225

aaacctccct	taaagattct	ttgatgcttt	gtctatcac	tgatanacctg	gtctttttcc	60
cccagtttt	ttctttttta	cattctgggt	tgctattttc	anattaataa	tttgatgacc	120
ccatcacagt	accaaatac	ccccaaaat	gaagttcaaa	tttgatcaaa	acataaatca	180
gagngagnga	gtaaaattat	aaaggccagg	cagcaggaaa	agtcaccctc	aactaccatn	240
tgactggtca	ggtctcacc	atgccaagg	gggcaggaa	agganaaatc	tattatacat	300
gcaacactga	actggggaac	atggcttgg	gcctccagga	cagttcaggt	ccccaagcta	360
accccctact	tcccanacag	ctgctcgtac	agtttgggca	catagtcato	ccactcggcc	420
tggtaacacg	tgccagccac	cgggggccctg	agctcatact	ttttacggaa	ggacgccacc	480
ttgantttgc	gacgggggac	tccanaagg	ttgctgaaga	tggtctctc	acaattttgc	540
gggctgtcct	gctcgtaaac	canccaaaca	ta			572

&lt;210&gt; 226

&lt;211&gt; 401

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;400&gt; 226

gaagcgtctc	cgttgggtcc	ggccgctctg	cgggactctg	aggaaaagct	cgcaccaggt	60
ggacgcggat	ctgtcaacat	gggtaaagga	gacccaaca	agccgcgggg	caaaatgtcc	120
tcgtacgcct	tcttcgtgca	gacctgccgg	gaagagcaca	agaagaaca	cccggactct	180
tccgtcaatt	tcgcggaatt	ctccaagaag	tgttcggaga	gatggaagac	catgtctgca	240
aaggagaagt	cgaagtttga	agatatggca	aaaagtgaca	aagctcgcta	tgacaggag	300
atgaaaaatt	acgttcctcc	caaaggtgat	aagaagggga	agaaaaagga	ccccaatgct	360
cctaaaaggc	caccatctgc	cttcttctgt	tttgcctga	a		401

&lt;210&gt; 227

&lt;211&gt; 501

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(501)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 227

agcgcttcta	gaaatgctga	gccgattatc	aggattagca	aatgttggtt	tgcatgaatt	60
atcaggagat	gatgacactg	atcagaatat	gagggctccc	ctagaccctg	aattacacca	120
agaatctgac	atggaattta	ataatactac	acaagaagat	gttcaggagc	gcctggctta	180
tgcaagagca	ttggtggtgg	agctaaaaga	tattattaga	cagaaggatg	ttcaactgca	240
gcagaagat	gaagctctac	aggaagagag	aaaaagctgt	gatacaaaat	taaaaaacta	300
aacttctgcg	aaggccaatt	acttctttga	taatantaga	gaaatgaagc	acaggaggac	360
tggtgctcag	acctcagcag	agacacttcc	agctgcagag	tctcagagag	agtgggaatga	420
aagataacat	antcagagag	gagactatca	ncttgagcca	ntctcagcca	gagacacctg	480
acagaatggg	tgtgaaggag	c				501

&lt;210&gt; 228

&lt;211&gt; 501

&lt;212&gt; DNA

&lt;213&gt; Homo sapien

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(501)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 228

gcagggtccc	ttttatgggc	cagggtggtaa	ctggaacaca	gaacagtga	ggacagaacc	60
ttggaccaca	ggccattcct	caggatggca	gtataacaca	tcagatttct	aggcctaata	120
ctccaaattt	tggtccaggc	tttgtcaatg	attcacagcg	taagcagtat	gaagagtggc	180
tccaggagac	ccaacagctg	cttcaaatgc	agcagaagta	tcttgaagaa	caaattgggtg	240
ctcacagaaa	atctaaaga	gccctttcag	ctaaacaacg	tactgccaaag	aaagctgggc	300
gtgaatttcc	agaggaagat	gcagaacaac	tcaagcatgt	tactgaacag	caaagcatgg	360
ttcagaaaca	gctagaacag	attcgtaaac	aacagaaaaga	acatgctgaa	ttgattgaag	420
attatcggtg	caaacagcag	cancaatgng	caatggcccc	acctaccatg	atgccccagn	480
tccagcccca	nccccctaa	t				501

&lt;210&gt; 229

&lt;211&gt; 4099

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 229

cagctgccag	ccgaggaggc	gcggcgagga	ggggactgcg	gtcagctgcg	tccacttggg	60
gctgtgcggc	ggtcccgcg	ccggcgatgt	tccggggcac	tccctgagta	gcggcagctt	120
atcccccgcc	cgctagcccg	ccctggtccc	cggtctgctc	gctggctggc	gcggccccgg	180
ccccgctctg	cgctcgcccc	gccgcggtgg	aggcgcgcg	gggggacgcg	gccggggatg	240
agcggattgc	gggtgaactc	gccgccccgg	ggcccccgga	agccgtgagc	cgctgctttt	300
ctccgagtcg	ccgccttgcc	cttgatttgg	agatcatgtc	catccacatc	gtggcgtggg	360
ggaacgaggg	ggacacattc	caccaggaca	accggccgtc	ggggcttatc	cgcaacttacc	420
tggggagaag	ccctctggtc	tccggggacg	agagcagctt	ggtgtgaac	gcggccagca	480
cggtcgcgcg	tccggtgttc	accgagtatc	aggccagtgc	ggttggaat	gtcaagctgg	540
tggtccacga	ctgtcccgtc	tgggacatat	ttgacagtga	ttggtacact	tctcgaaatc	600
taattggggg	cgctgacatc	attgtgatca	aatacaacgt	taatgacaag	ttttcattcc	660
atgaagtaaa	ggataattat	attccagtga	taaaaagagc	attaaattca	gttccagtaa	720
ttattgctgc	tggttggtacc	agacaaaatg	aagagttacc	ttgtacatgc	ccactatgta	780
cctcagacag	agggagctgt	gttagtaca	ctgaagggat	ccaacttgca	aaagaactag	840
gagcaaccta	tcttgaactc	cacagccttg	atgacttcta	cataggaaag	tattttggag	900
gagtgttgga	gtattttatg	attcaagcct	taaatcagaa	gacaagtga	aaaatgaaga	960
aaagaaaaat	gagcaactcc	tttcatggaa	ttagaccacc	tcaacttgaa	caaccagaaa	1020
aaatgcctgt	cttaaggct	gaagcgtcac	attataactc	tgaacttaaat	aacttgcgtg	1080
tctgctgcca	gtgtgtggac	gtggtatgtt	ataaccccg	tttaagaaa	gttgtagagg	1140
cccacaagat	cgttctctgc	gctgtaagcc	atgttttcat	gctgcttttc	aatgtgaaga	1200

```

gtccactga cattcaggat tccagtatca tccgaactac ccaggatctt tttgtataa 1260
acagagatac tgcatttcca ggtgctagcc atgaatcttc aggcaacca ccattacgag 1320
tcattgttaa agacgccctc ttctgttctt gtttatcaga catccttcgc ttcatttatt 1380
caggtgcttt tcagtgggaa gaattggaag aagatatcag gaagaagtgt aaagattctg 1440
gggagtgttc aaatgtaatc gagaagtta aatgcatttt aaaaacacca ggaagatta 1500
attgcctaag gaattgcaaa acctatcaag ccagaaaacc tttgtggttt tataacactt 1560
ccctcaagtt ttctcttaat aagccgatgc ttgccgatgt tgtcttcgaa attcaaggta 1620
cgacagtgcc agcccacagg gccatcctgg tggcccgttg tgaagtgtg gcagccatgt 1680
ttaatggtaa ttacatggaa gcaaagagt tccgtattcc cgtttatggt gtttccaaag 1740
agactttctt gtcattttta gaatacctgt acacagactc ctgctgcca gctggcatat 1800
tccaggccat gtgtctcctg atctgtgccg agatgtacca agtgccaga ctgcagcaca 1860
tctgtgagct gttcatcatt acccagctgc agagcatgcc aagcagggaa ctggcatcca 1920
tgaaccttga tatagttgac ctgcttaaaa aggccaggtt tcaccactct gattgccttt 1980
caacctggct acttcatttc attgctacta actacctcat cttcagtcaa aagcctgaat 2040
ttcaggatct ttcagtggaa gaacgcagtt ttgttgaaaa gcacagatgg ccgtcgaata 2100
tgtacttgaa gcagcttgcg gaatacagga agtatattca ctcccggaaa tgcgttgct 2160
tagtaatgta acctggagct tttatacact acatttcttt tttattatta tgaagaatgg 2220
gatacctcca ggttccagta aaattcttct gaccgaaacc aatgtgggtg ttagaaaaat 2280
taccatatag cttaatatgt ttattagttc tctttgaaa aaaactacca ctgtggtctt 2340
aaaagggaac aaaatatacc ataggctaaa actaaggctt tcaactaga atgcaaaagt 2400
gttttgagc tggtttccct taaaagatgt ctgttgcttt agtgatattt agaccctct 2460
cagttaagaa atgcttagat taaaaaaaa aaattacgta ggattaatac agaaatttaa 2520
tcatgtctga ttaattgtct tattaaaaa aggggcattt aaagaccag cataaccatt 2580
tgtataatga gaaatctagg ggaaccacaa tcagtccaac atgagatttt aggaatagaa 2640
atttgcgggc catttgaaa gtgaaatgcc acttagttct caattgatga cagtgtttga 2700
atcatcataa aaaaaatacc tgcttttcat ctggacaacc caattgagcc actttatcto 2760
cttttgcaa tctgagtagg cggggaacct aggcagggtt ggctttctta gcgtgtaact 2820
tgtgtagcag cacagggtccc aacttagaa ggacccaca cttggttcaa ggctctgcta 2880
tagcggaat tcttaataat gttgaagaa gggccccatg atttcatttt gtgtgagcc 2940
ctcaaaatta tgtctgttct gtggtgggaa atatcctatg ttttcttgct caaacacctt 3000
tctctctgaa agcagaaaaa ggcaactgata taaagggaag agaaggaggc tcaccggagg 3060
gaagagaaca tagtgaagat tccgcctttt ggggaggtct ggaccacca gggcctccac 3120
tgagccttct gctggcagg gagaatgtg ttgtgtgtg ttgctttaa sacagtcaca 3180
gttcttgctc tatcatagat gaacaaatac tttcttgatc attctgtaag accaggaggt 3240
tggttaagagt gactaaccag cctaacttta atacacatgt ataaagatgt tcacagagaa 3300
agatgctctg tagagaattt gctaccgaag ttggctcaag aatttgtttt tagtgttatt 3360
taccaagatt aggacgtcag tggtttaaatt tctttgaatt cttttcaagg actgcaagat 3420
tatttgataa agagttagcat gaatcttgtg ctctaataat acacagtaag ttcaagaaa 3480
ggatgtatga caaagacttg ttacatagag ggaatatgga ctgggataga ggacagactg 3540
atagtttctt tctttcatat cacatgtata gagaaataat tatatcagaa actcacaac 3600
ctagacatgg aaaaacagat tactgtctat tgtcagcatc attttcatct gtaagtcact 3660
actggaatat atttttcttt taatttccag tgactttaga atacacacag tttttccgac 3720
ttttcaaaaa tttgattaaa tggttttata gtataatatt gggaccccat accgttagcc 3780
cttgatgta taccaacact gccaaagtaa aacattaggt caggcatggt ggctcaggcc 3840
tgtaatccca gcattttggg aggtgaggc aagtggataa cttgaggtca tgagttcgaa 3900
accagcctgg ccaaaacagt gaaacccgt ctctactaaa aatacaaaat tagccagatg 3960
tggtggcgca cacctgtaat ccagctact caggaagctg aggcaggaaa atcgcttgaa 4020
cctgggaggt ggaagtgtga gtgagccgag atcgaccac tgcactccag cctgggtgac 4080
aagagcgaaa ctccatctc 4099

```

&lt;210&gt; 230

&lt;211&gt; 2649

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 230

```

gagagagaga gagagagaga ggagcgagag agtgtgagcg agaaagaata aaaggaaaga 60
agattttctc tatgtatata aagatggcca cgttagcaaa cggacaggct gacaacgcaa 120
gcctcagtag caacgggctc ggcagcagcc cgggcagtgc cgggcacatg aacggattaa 180

```

```

gccacagccc ggggaacccg tcgaccatc ccatgaagga ccacgatgcc atcaagctgt 240
tcattgggca gatccccgc aacctggatg agaaggacct caagcccctc ttcgaggagt 300
ttggcaaaat ctacgagctt acggttctga aggacaggtt cacaggcatg cacaaggct 360
gcgccttctt cactactgc gagcgtgagt cagcgtgaa ggcccagagc gcgctgcacg 420
agcagaagac tctgcccggg atgaaccggc cgatccaggt gaagcctgcg gacagcgaga 480
gccgaggaga tagaaaactc ttcgtgggca tgctcaacaa gcaacagtcc gaggacgacg 540
tgccgcgcct tttcgaggcc tttgggaaca tcgaggagtg caccatcctg cgcgggcccg 600
acggcaacag caaggggtgc gcctttgtga agtactcctc ccacgccgag gcgcaggccg 660
ccatcaacgc gctacacggc agccagacca tgccgggagc ctctccagt ctggtggtca 720
agttcgccga caccgacaag gagcgcacga tgccggcgaat gcagcagatg gctggccaga 780
tgggcatggt caaccccatg gccatccctt tcggggccta cggcgctac gctcaggcac 840
tgatgcagca gcaagcgcc ctgatggcat cagtcgcgca gggcggtac ctgaacccca 900
tggtgcctt cgctgcgcgc cagatgcagc agatggcgcc cctcaacatg aatggcctgg 960
cgccgcgacc tatgacccca acctcaggtg gcagcaccct tccgggcctc actgcaccag 1020
ccgtgcctag catcccatcc ccatttgggg tgaatggctt caccggcctc ccccacagg 1080
ccaatgggca acctgctgcg gaagctgtgt tcgccaatgg catccaccct taccagcac 1140
agagccccac cgccgcgagc cccctgcagc aggcctacgc cggagtgcag cagtatgcag 1200
gtcctgccta cctgctgcc tatggtcaga taagccagc ctttccctcag ccgcctccaa 1260
tgatcccccga gacagagaga gaagggcccg agggctgtaa cctgttcctc taccatctgc 1320
cccaggagtt tggggacgct gagctgatgc agatgttctt cccttccggt aatgtcatct 1380
cctcgaaagt gtttgtggat cgggcgacta accaaagtaa atgctttggc ttcgtgagct 1440
tcgacaaccc ggccagcgcg cagaccgcca tccaggccat gaacggcttc cagatcgga 1500
tgaagaggct caaggtgcag ctgaagcggc ccaagacgc caatcgcccg tactgagcg 1560
cgccgggagc gtcccccggg ggagaccagg actcgacag ggcaggatgc tgaacgggt 1620
acattaaaaa acaaacctct ctctatatat atttataaat gagaactgtt ggatgacacc 1680
tttgacatat cagccaatat caatcaagct gaagactcca gacactgtct gtgtgactgt 1740
aacatttctt caaggaaagt atagcgtcta tggagttcag agggcacgtg tttgggggaa 1800
aatatatatg acatgaagaa gaagatgaag aaaaatgaga aaaaacaca caaaaggcaa 1860
ctttaaaaa aaatatcacg agcagacggg gaggtgaag ggctgggagc tgggaggaga 1920
cgctgcttac cgatcccggg gcttttccag cccacggcg cctgacgcag gctggggcaa 1980
gtggtgcgtg gggcctggtc cccaaggggc ggctgagagg ccgccactga gcatctctat 2040
ctgtcattcc tttagctatt tagggaccaa aggaccaaac tttttattgc agatgtgtag 2100
ctctatctca aatagcggg gcatggaga cccctctt gctggtggt gctgtgtgt 2160
gaaacagctt agagcgattc tatgaaaaaa tgtaataaaa aattaaaaaa aaaacaaaa 2220
acaaaaaaa caacaaaaaa aggaaaaata acgcttcaat gcttttaaaa cagcaagata 2280
atagttcttt gatactttga gaggcgcttt gatgaccctc atccaagtct atgacacttt 2340
cctatggttt tctgtattct atgtctggat ggagctgtta aaagatgaac aaattggtgg 2400
atatttgggg aaagcaacac aaatcttaaa actcaccctg gaagtgtgag aaaacaagga 2460
ggggaacaaa tgggacttac caagcaaggt cattgtgtg aaaaagtctg aaatgcttct 2520
aactcttccc cctcttaaaa tcataatagt tgtacagaat tttaaaaagg aaaagttaa 2580
aatacctata taatagaaga aaaattagag gaaagcaaaa aataaaaaaa aaaaaaaa 2640
aaactcgag 2649

```

&lt;210&gt; 231

&lt;211&gt; 3927

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 231

```

gcagcactct cttcgtcgct tcggccagtg tgtcgggctg ggccctgaca agccacctga 60
ggagaggctc ggagccgggc ccggaccocg gcgattgccg ccgcttctc tctagtctca 120
cgaggggttt ccgcctcgc acccccacct ctggacttgc ctttcttct cttctccgcg 180
tgtggaggga cccagcgctt aggcgggagc gagcctgggg gccgcccgcg gtgaagacat 240
cgccggggacc gattcaccat ggagggcgcc ggccggcgca acgacaagaa aaagataagt 300
tctgaacgtc gaaaagaaaa gtctcgagat gcagccagat ctggcggaag taaagaatct 360
gaagtttttt atgagcttgc tcatcagttg ccacttccac ataatgtgag ttcgcatctt 420
gataaggcct ctgtgatgag gcttaccatc agctatttgc gtgtgaggaa acttctggat 480
gctggtgatt tggatttga agatgacatg aaagcacaga tgaattgctt ttatttga 540
gccttgatg gttttgttat ggttctcaca gatgatggtg acatgattta catttctgat 600

```

```

aatgtgaaca aatacatggg attaactcag tttgaactaa ctggacacag tgtgtttgat 660
tttactcatc catgtgacca tgaggaaatg agagaaatgc ttacacacag aaatggcctt 720
gtgaaaaagg gtaaaagaaca aaacacacag cgaagctttt ttctcagaat gaagtgtacc 780
ctaactagcc gaggaagaac tatgaacata aagtctgcaa catggaagggt attgactgc 840
acaggccaca ttacagtata tgataccaac agtaaccaac ctcagtgtgg gtataagaaa 900
ccacctatga cctgcttggt gctgatttgt gaacccattc ctcacccatc aaatattgaa 960
attcctttag atagcaagac tttcctcagt cgacacagcc tggatatgaa attttcttat 1020
tgtgatgaaa gaattaccga attgatggga tatgagccag aagaactttt aggccgctca 1080
atttatgaat attatcatgc tttggactct gatcatctga ccaaaactca tcatgatatg 1140
tttactaaag gacaagtcac cacaggacag tacaggatgc ttgccaaaag aggtggatat 1200
gtctgggttg aaactcaagc aactgtcata tataacacca agaattctca accacagtgc 1260
attgtatgtg tgaattacgt tgtgagtggg attattcagc acgacttgat tttctccctt 1320
caacaaacag aatgtgtcct taaaccggtt gaatcttcag atatgaaaat gactcagcta 1380
ttcacaaaag ttgaatcaga agatacaagt agcctctttg acaaacttaa gaaggaaact 1440
gatgctttta ctttgctggc cccagccgct ggagacacaa tcatatcttt agattttggc 1500
agcaacgaca cagaaactga tgaccagcaa cttgagggaag taccattata taatgatgta 1560
atgctccctt caccacacga aaaattacag aatataaatt tggcaatgtc tccattaccc 1620
accgtgaaa cgccaaagcc acttcgaagt agtgctgacc ctgactcaa tcaagaagtt 1680
gcattaaaat tagaaccaaa tccagagtca ctggaacttt cttttaccat gcccagatt 1740
caggatcaga cactatgctc ttccgatgga agcactagac aaagttcacc tgagccta 1800
agtccagtg aatattgttt ttatgtggat agtgatatgg tcaatgaatt caagtggaa 1860
ttggtagaaa aactttttgc tgaagacaca gaagcaaaga acccattttc tactcaggac 1920
acagatttag acttgagat gttagctccc tatatcccaa tggatgatga cttccagtta 1980
cgttccttcg atcagttgtc accattagaa agcagttccg caagccctga aagcgcaagt 2040
cctcaagca cagttacagt attccagcag actcaaatat aagaacctac tgctaagtc 2100
accactacca ctgccaccac tgatgaatta aaaacagtga caaaagaccg tatggaagac 2160
attaaaatat tgattgcac tccatctcct accacatac ataaagaaac tactagtgc 2220
acatcatcac catatagaga tactcaaatg cggacagcct caccaaacag agcaggaaaa 2280
ggagtcagat aacagacaga aaaatctcat ccaagaagcc ctaacgtgtt atctgtcgt 2340
ttgagtcaaa gaactacagt tcttgaggaa gaactaaatc caaagatact agctttgcag 2400
aatgtcaga gaaagcgaaa aatggaacat gatggttcac tttttcaagc agtaggaatt 2460
ggaacattat tacagcagcc agacgatcat gcagctacta catcactttc ttggaaacgt 2520
cctctgatt tagcatgtag actgctgggg caatcaatgg atgaaagtgg attaccacag 2640
ctgaccagtt atgattgtga agtttaactg cctatacaag gcagcagaaa cctactgcag 2700
ggtgaagaat tactcagagc tttggatcaa gttaactgag ctttttctta atttcattcc 2760
tttttttgg cactgtggc tcaactaccta aagcagctca tttatatttt ctacatctaa 2820
ttttagaagc ctggctacaa tactgcacaa acttggttag ttcaattttt gatcccttt 2880
ctacttaatt tacattaatg ctctttttta gtatgttctt taatgctgga tcacagacag 2940
ctcattttct cagttttttg gtattttaac cattgcattg cagtagcatc attttaaaaa 3000
atgcaccttt ttattttatt atttttggct agggagttta tccctttttc gaattatttt 3060
taagaagatg ccaatataat ttttgaaga aggcagtaac ctttcatcat gatcataggg 3120
agttgaaaaa tttttacacc ttttttttca cattttacat aaataataat gctttgccag 3180
cagtcagtg tagccacaat tgcacaatat attttcttaa aaaataccag cagttactca 3240
tggaatatat tctgcgttta taaaactagt ttttaagaag aaattttttt tggcctatga 3300
aattgttaaa cctggaacat gacattgtta atcatataat aatgattctt aaatgctgta 3360
tggtttatta tttaaatggg taaagccatt tacataatat agaaagatat gcatatatct 3420
agaaggatg tggcatttat ttggataaaa ttctcaattc agagaaatca tctgatgttt 3480
ctatagtcac tttgccagct caaaagaaaa caatacccta tgtagtgtg gaagtttatg 3540
ctaattattg gtaactgata ttaaaccctaa atgttctgcc taccctgttg gtataaagat 3600
attttgagca gactgtaaac aagaaaaaaa aaatcatgca ttcttagcaa aattgcctag 3660
tatgttaatt tgctcaaaat acaatgtttg attttatgca ctttgcgct attaacatcc 3720
tttttttcat gtatgtttca ataattgagt aattttagaa gcattatttt aggaatatat 3780
agttgtcaca gtaaatatct gtgtttttct atgtacattg tacaattttt tcattccttt 3840
tgctctttgt ggttggtatc aacactaact gtattgtttt gttacatcaa ataaacatct 3900
tctgtggaag aaaaaaaaaa aaaaaaa 3927

```

&lt;210&gt; 232

&lt;211&gt; 6188

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 232

```
caacaacaac aactccaagc acaccggcca taagagtgcg tgtgtcccca acatgaccga 60
acgaagaagg gacgagctct ctgaagagat caacaactta agagagaagg tcatgaagca 120
gtcggaggag aacaacaacc tgcagagcca ggtgcagaag ctcacagagg agaaccaccac 180
ccttcgagag caagtggaaac ccaccctga ggatgaggat gatgacatcg agctccgcgg 240
tgctgcagca gctgtgcccc caccctctcc aatagaggaa gagtgccag aagacctccc 300
agagaagttc gatggcaacc cagacatgct ggctccttcc atggcccagt gccagatctt 360
catggaaaag agcaccaggg atttctcagt tgatcgtgtc cgtgtctgct tcgtgacaag 420
catgatgacc ggccgtgctg ccggttgggc ctcagcaaag ctggagcgct cccactacct 480
gatgcacaac taccagctt tcatgatgga aatgaagcat gtctttgaag accctcagag 540
gcgagagggt gccaaacgca agatcagacg cctgcgccaa ggcatggggg ctgtcatcga 600
ctaactcaat gctttccaga tgattgcccc ggacctggat tggaaacgagc ctgctgtgat 660
tgaccagtac cagcagggcc tcagcgacca cattcaggag gagctctccc acctcgagggt 720
cgccaagtgc ctgtctgctc tgattgggca gtgcattcac attgagagaa ggctggccag 780
ggctgtgcca gctcgcaagc cacgctcgcc accccgggcg ctggtgttgc ctcacattgc 840
aagccaccac caggtagatc caaccgagcc ggtgggagggt gcccgcatgc gcctgacgca 900
ggaagaaaaa gaaagacgca gaaagctgaa cctgtgcctc tactgtggaa caggagggtca 960
ctaagctgac aattgtcctg ccaaggcctc aaagtcttcg ccggcgggaa actccccggc 1020
cccgtgttag agggaccttc agcgaccggg ccagaaataa taaggctccc acaagatgat 1080
gcctcatctc cacacttgca agtgatgctc cagatttcatc ttccgggcag acacacctg 1140
ttcgtccgag ccatgatcga ttctggtgct tctggcaact tcattgatca cgaatatgtt 1200
gctcaaaatg gaattcctct aagaatcaag gactggccaa tacttgtgga agcaattgat 1260
ggcgcccca tagcatcggt ccagttgtc cagcaaaact acgacctgat agttgacctg 1320
ggagatcacc gagagggtgt gtcatttgat gtgactcagt ctccattctt ccctgtctgc 1380
ctaggggttc gctggtgtag cacacatgat cccaatatca catggagcac tcgatctatc 1440
gtctttgatt ctgaatactg ccgctaccac tgccggatgt attctccaat accaccatcg 1500
ctcccaccac cagcaccaca accgccactc tattatccag tagatggata cagagtttac 1560
caaccagtga ggtattacta tgtccagaat gtgtacactc cagtagatga gcacgtctac 1620
ccagatcacc gcctggttga ccctcacata gaaatgatac ctggagcaca cagtattccc 1680
agtggaacag tctattcact cctgggaact gaattggag actctcgaga ttttgggca 1740
agaaatgtaa aagatggggt aattactcca acgattgcac ctaatggagc ccaagttctc 1800
caggtgaaga gggggtggaa actgcaagtt tcttatgatt gccgagctcc aaacaatttt 1860
actatccaga atcagtatcc tcgcctatct attccaaatt tagaagacca agcacacctg 1920
gcaacgtaca ctgaattcgt acctcaataa cctggatacc aaacataccc cacatatgcc 1980
gcgtacccca cctaccagt aggtatcgcc tggtagccag tgggacgaga cggacaagga 2040
gatcactcat atgtacctgt gatgatcact tggaaatccac actggtacgg ccagcctccg 2100
gtaccacagt acccgccgac acagccgccc cctccaccac caccaccgcc gccgcctcca 2160
tcttacagta ccctgtaaat acctgtcatg tcttcagga tctctgccct caaaatttat 2220
tctgttcag cttctcaatc agtgactgtg tgctaaattt taggctactg tatcttcagg 2280
ccacctgagg cacatcctct ctgaaacggc tatggaaggt tagggccact ctggactggc 2340
acacatccta aagcaccaaa agaccttcaa cattttctga gagcaacaga gtatttgcca 2400
ataaatgata tctcattttt ccaccttgac tgccaatcta actaaaataa ttaataagtt 2460
tactttccag ccagtcctgg aagtctgggt tttacctgcc aaaacctcca tcaccatcta 2520
aattatagga tgccaaattt gctgtttaac atttacagag aagctgatac aaacgcagga 2580
aatgctgatt tctttatgga gggggagacg agggaggaga ggacatgact tttcttgagg 2640
tttcggtacc ctctttttaa atcactggag gactgaggcc ttattaagga agccaaaatt 2700
atcgggtcag tgtggaaagg cttccgtgat cctctcgtcg cacccttaga aacttcaccg 2760
tcttcaaaact ccatttccat ggttctgtta attctcaagg agcagcaact cgactggttc 2820
tcccaggagc aggaaaaacc cttgtgacat gaaacatctc aggcctgaaa agaaagtgtc 2880
ctctcagatg gactcttgca tgtaagact atgtcttca atcatggtgc aaatcacatg 2940
tacccaatga ctccggcttt gacacaacac cttaccatca tcatgccatg atggcttcca 3000
caaagcatta aacctggtaa ccagagatta ctgggtgctc cagcgttgtt agatgttcat 3060
gaaatgtgac cacctctcaa tcaccttga gggctaaaga gtagcacatc aaaaggactc 3120
caaaatccca tacccaactc ttaagagatt tgcctcggtg cttcagaaag aattttcatg 3180
agtgttctta attggctgga aaagcaccag ctgacgtttt ggaagaatct atccatgtgt 3240
ctgcctccat atgcatctgg gcatttcac ttcagtcccc tcattagact gtagcattag 3300
```

77

```

gatgtgtgga gagaggagaa atgatttagc acccagattc acactcctat gcctggaagg 3360
gggacatctt tgaagaagag gaattagggc tgtggacact gtcttgagga tgtggacttc 3420
cttagtgagc tccacattac ttgatggtaa ccacttcaaa aggatcagaa tccacgtaat 3480
gaaaaaggtc cctctagagg atggagctga tgtgaagctg ccaatggatg aaaagcctca 3540
gaaagcaact caaaggactc aaagcaacgg acaacacaag agttgtcttc agcccagtga 3600
cacctctgat gtcccttgga agctttgtgc taacctggga ctgcctgact tcctttagcc 3660
ttcttgcatg tttaaacact taaaattttt agtataattt ttagtgtgtt ttgaagtgg 3720
tgctactgcc attgacctg ctgcaggatt tgtgtcattt tcctgcctgg ttgctgagac 3780
tccattttgc tgccacacac agagatgtaa gaggcaggct ttaattgcc aagcacagtt 3840
tgagcagtag aaaaacaacat ggtgtatata tcaaattgcc tgacatgaag aggagtctaa 3900
cgggtgaagt tcaacttttca tcagcatcat ctttcacatg ttcattatca tccgctctta 3960
ttcttgcatg tttaaacact taaaattttt agtataattt ttagtgtgtt ttgaagtgg 4020
gactaggctt tcaaaaactt ccattgaatt acaaagcact atccagttct tattgttaaa 4080
ctaagtaaaa atgataagta acatagtgtg aaatattcct ttagtgtgaa cttcttcaaa 4140
tgctgtgaat gagaggctcc tcagaactgg agcatttgta taataattca tcctgttcat 4200
cttcaatttt aacatcatat ataatttcaa ttctatcaat tgggccttta aaaatcatat 4260
aaaaggatat aaaatttgaa aagagaaccc taattggcta tttaatccaa aacaactttt 4320
ttttttcctt caatggaatc agaaagcttg tcaatcactc atgtgtttta gagtaattac 4380
ttttaaaatg gtgcatttgt gcttctgaac tattttgaag agtcacttct gtttacctca 4440
agtatcaatt catcctccat acatttgaat tcaagttgtt ttttgtcaaa tttacagttg 4500
tcaattgatc ttcaagctgc aggggtgccta gaaatgggcc gttgtctgta gccctggcat 4560
gtgcacacgg caactttgcca ccactgcaag caaaagtctg gagaagttca ccaacgacaa 4620
gaacgattag ggaataatg ctgctgtggg ttaacaactc agaaagtcct tgatccacat 4680
ttggctgttt actaaagctt gtgattaact ttttgccagt gtgtactatg ctctattgct 4740
atatatgcta tctataaatg tagatgttaa ggataagtaa ttctaaattt attattctat 4800
agttttgaag tttggttaag tttcctttca ctcaattgat ttattttgtt gttaatcaaa 4860
tttatgttaa ttggtacctt taaatttttt ttggcatttt ccaacaaaaa tggctttatt 4920
cataagaaag gaaaaaaatc aatggaattt gatattctaa gaagttagaa agggagcaaa 4980
ataaaaaaca taaaggagat agatgaatta gtaagcaaat cagtagtcga gtttttcaaa 5040
ctggcaaaat taattaattg acttttagcc caaatttaca ttgttaatta aatcaagaag 5100
gaagaagatc taagagctcc cattgatagg caagcctaga gagaactagc taaatttatc 5160
atgctaggat attgaaacac agaaagttaa catacattta tgaagggtca atttagttt 5220
gaaagtggg tatttgttct cgttgcaaaa agggagctta gtctgctatc atagtgaag 5280
aatacagtg aactgcaggt gcacaaaata agagggccac atctatatgg tgcagtctgg 5340
aattctgttt aagttttag gtacctcttg gacttctgaa ttgatccagt tgtcatccac 5400
cacagacatc tcacatcaga tacagacagt tccaagattg acaacagaga acaacctgct 5460
ggaaagacct gggcagaaat ggagagccct gcgggaacca tgctacattt tcatctaaag 5520
agagaatgca catctgatga gactgaaagt tctttgttgt ttagatttgt agaatgggat 5580
tgaattggtc tgtgaaaaat tgcattgctt ttatttcttt gtgtaatcaa gtttaagtaa 5640
taggggatat ataatcataa gcatttttag gtgggaggga ctattaagta attttaagtg 5700
ggtgggggta tttagaatgt tagaataata ttatgtatta gatatcgcta taagtggaca 5760
tgctacttta cttgtaaccc tttaccctat aattgctatc cttaaagatt tcaaataaac 5820
tcggagggaa ctgcaggag accaacttat ttagagcgaa ttggacatgg ataaaaaccc 5880
cagtgggaga aagttaaag gtgattagat taataattta atagaggatg agtgacctct 5940
gataaattac tgctagaatg aacttgtcaa tgatggatg taaattttca tggaagttat 6000
aaaagtgata aataaaaaacc cttgctttta cccctgtcag tagccctcct cctaccactg 6060
aaccocattg cccctacccc tcttctaac tttattgctg tattctcttc actctatatt 6120
tctctctatt tgctaataatt gcattgctgt tacaataaaa attcaataaa gatttagtgg 6180
ttaagtgc 6188

```

&lt;210&gt; 233

&lt;211&gt; 611

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 233

```

Met Ser Ile His Ile Val Ala Leu Gly Asn Glu Gly Asp Thr Phe His
      5              10              15
Gln Asp Asn Arg Pro Ser Gly Leu Ile Arg Thr Tyr Leu Gly Arg Ser

```





79

Cys Ala Glu Met Tyr Gln Val Ser Arg Leu Gln His Ile Cys Glu Leu  
 500 505 510  
 Phe Ile Ile Thr Gln Leu Gln Ser Met Pro Ser Arg Glu Leu Ala Ser  
 515 520 525  
 Met Asn Leu Asp Ile Val Asp Leu Leu Lys Lys Ala Lys Phe His His  
 530 535 540  
 Ser Asp Cys Leu Ser Thr Trp Leu Leu His Phe Ile Ala Thr Asn Tyr  
 545 550 555 560  
 Leu Ile Phe Ser Gln Lys Pro Glu Phe Gln Asp Leu Ser Val Glu Glu  
 565 570 575  
 Arg Ser Phe Val Glu Lys His Arg Trp Pro Ser Asn Met Tyr Leu Lys  
 580 585 590  
 Gln Leu Ala Glu Tyr Arg Lys Tyr Ile His Ser Arg Lys Cys Arg Cys  
 595 600 605  
 Leu Val Met  
 610

&lt;210&gt; 234

&lt;211&gt; 494

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 234

Met Tyr Ile Lys Met Ala Thr Leu Ala Asn Gly Gln Ala Asp Asn Ala  
 5 10 15  
 Ser Leu Ser Thr Asn Gly Leu Gly Ser Ser Pro Gly Ser Ala Gly His  
 20 25 30  
 Met Asn Gly Leu Ser His Ser Pro Gly Asn Pro Ser Thr Ile Pro Met  
 35 40 45  
 Lys Asp His Asp Ala Ile Lys Leu Phe Ile Gly Gln Ile Pro Arg Asn  
 50 55 60  
 Leu Asp Gln Lys Asp Leu Tyr Pro Leu Phe Gln Gln Phe Gly Lys Ile  
 65 70 75 80  
 Tyr Glu Leu Thr Val Leu Lys Asp Arg Phe Thr Gly Met His Lys Gly  
 85 90 95  
 Cys Ala Phe Leu Thr Tyr Cys Glu Arg Glu Ser Ala Leu Lys Ala Gln  
 100 105 110  
 Ser Ala Leu His Glu Gln Lys Thr Leu Pro Gly Met Asn Arg Pro Ile  
 115 120 125  
 Gln Val Lys Pro Ala Asp Ser Glu Ser Arg Gly Asp Arg Lys Leu Phe  
 130 135 140  
 Val Gly Met Leu Asn Lys Gln Gln Ser Glu Asp Asp Val Arg Arg Leu  
 145 150 155 160  
 Phe Glu Ala Phe Gly Asn Ile Glu Glu Cys Thr Ile Leu Arg Gly Pro  
 165 170 175  
 Asp Gly Asn Ser Lys Gly Cys Ala Phe Val Lys Tyr Ser Ser His Ala  
 180 185 190  
 Glu Ala Gln Ala Ala Ile Asn Ala Leu His Gly Ser Gln Thr Met Pro  
 195 200 205  
 Gly Ala Ser Ser Ser Leu Val Val Lys Phe Ala Asp Thr Asp Lys Glu  
 210 215 220  
 Arg Thr Met Arg Arg Met Gln Gln Met Ala Gly Gln Met Gly Met Phe  
 225 230 235 240  
 Asn Pro Met Ala Ile Pro Phe Gly Ala Tyr Gly Ala Tyr Ala Gln Ala  
 245 250 255  
 Leu Met Gln Gln Gln Ala Ala Leu Met Ala Ser Val Ala Gln Gly Gly  
 260 265 270  
 Tyr Leu Asn Pro Met Ala Ala Phe Ala Ala Ala Gln Met Gln Gln Met

80

275	280	285
Ala Ala Leu Asn Met Asn Gly Leu Ala Ala Ala Pro Met Thr Pro Thr		
290	295	300
Ser Gly Gly Ser Thr Pro Pro Gly Ile Thr Ala Pro Ala Val Pro Ser		
305	310	315
Ile Pro Ser Pro Ile Gly Val Asn Gly Phe Thr Gly Leu Pro Pro Gln		
	325	330
Ala Asn Gly Gln Pro Ala Ala Glu Ala Val Phe Ala Asn Gly Ile His		
	340	345
Pro Tyr Pro Ala Gln Ser Pro Thr Ala Ala Asp Pro Leu Gln Gln Ala		
	355	360
Tyr Ala Gly Val Gln Gln Tyr Ala Gly Pro Ala Tyr Pro Ala Ala Tyr		
	370	375
Gly Gln Ile Ser Gln Ala Phe Pro Gln Pro Pro Pro Met Ile Pro Gln		
385	390	395
Gln Gln Arg Glu Gly Pro Glu Gly Cys Asn Leu Phe Ile Tyr His Leu		
	405	410
Pro Gln Glu Phe Gly Asp Ala Glu Leu Met Gln Met Phe Leu Pro Phe		
	420	425
Gly Asn Val Ile Ser Ser Lys Val Phe Val Asp Arg Ala Thr Asn Gln		
	435	440
Ser Lys Cys Phe Gly Phe Val Ser Phe Asp Asn Pro Ala Ser Ala Gln		
	450	455
Thr Ala Ile Gln Ala Met Asn Gly Phe Gln Ile Gly Met Lys Arg Leu		
465	470	475
Lys Val Gln Leu Lys Arg Pro Lys Asp Ala Asn Arg Pro Tyr		
	485	490

&lt;210&gt; 235

&lt;211&gt; 826

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 235

Met Glu Gly Ala Gly Gly Ala Asn Asp Lys Lys Lys Ile Ser Ser Glu	
	5 10 15
Arg Arg Lys Glu Lys Ser Arg Asp Ala Ala Arg Ser Arg Arg Ser Lys	
	20 25 30
Glu Ser Glu Val Phe Tyr Glu Leu Ala His Gln Leu Pro Leu Pro His	
	35 40 45
Asn Val Ser Ser His Leu Asp Lys Ala Ser Val Met Arg Leu Thr Ile	
	50 55 60
Ser Tyr Leu Arg Val Arg Lys Leu Leu Asp Ala Gly Asp Leu Asp Ile	
	65 70 75 80
Glu Asp Asp Met Lys Ala Gln Met Asn Cys Phe Tyr Leu Lys Ala Leu	
	85 90 95
Asp Gly Phe Val Met Val Leu Thr Asp Asp Gly Asp Met Ile Tyr Ile	
	100 105 110
Ser Asp Asn Val Asn Lys Tyr Met Gly Leu Thr Gln Phe Glu Leu Thr	
	115 120 125
Gly His Ser Val Phe Asp Phe Thr His Pro Cys Asp His Glu Glu Met	
	130 135 140
Arg Glu Met Leu Thr His Arg Asn Gly Leu Val Lys Lys Gly Lys Glu	
	145 150 155 160
Gln Asn Thr Gln Arg Ser Phe Phe Leu Arg Met Lys Cys Thr Leu Thr	
	165 170 175
Ser Arg Gly Arg Thr Met Asn Ile Lys Ser Ala Thr Trp Lys Val Leu	
	180 185 190

81

His	Cys	Thr	Gly	His	Ile	His	Val	Tyr	Asp	Thr	Asn	Ser	Asn	Gln	Pro
	195						200					205			
Gln	Cys	Gly	Tyr	Lys	Lys	Pro	Pro	Met	Thr	Cys	Leu	Val	Leu	Ile	Cys
	210					215					220				
Glu	Pro	Ile	Pro	His	Pro	Ser	Asn	Ile	Glu	Ile	Pro	Leu	Asp	Ser	Lys
	225					230				235					240
Thr	Phe	Leu	Ser	Arg	His	Ser	Leu	Asp	Met	Lys	Phe	Ser	Tyr	Cys	Asp
				245					250					255	
Glu	Arg	Ile	Thr	Glu	Leu	Met	Gly	Tyr	Glu	Pro	Glu	Glu	Leu	Leu	Gly
			260					265						270	
Arg	Ser	Ile	Tyr	Glu	Tyr	Tyr	His	Ala	Leu	Asp	Ser	Asp	His	Leu	Thr
		275					280					285			
Lys	Thr	His	His	Asp	Met	Phe	Thr	Lys	Gly	Gln	Val	Thr	Thr	Gly	Gln
	290					295					300				
Tyr	Arg	Met	Leu	Ala	Lys	Arg	Gly	Gly	Tyr	Val	Trp	Val	Glu	Thr	Gln
	305				310					315					320
Ala	Thr	Val	Ile	Tyr	Asn	Thr	Lys	Asn	Ser	Gln	Pro	Gln	Cys	Ile	Val
				325					330					335	
Cys	Val	Asn	Tyr	Val	Val	Ser	Gly	Ile	Gln	His	Asp	Leu	Ile	Phe	
			340					345					350		
Ser	Leu	Gln	Gln	Thr	Glu	Cys	Val	Leu	Lys	Pro	Val	Glu	Ser	Ser	Asp
		355					360					365			
Met	Lys	Met	Thr	Gln	Leu	Phe	Thr	Lys	Val	Glu	Ser	Glu	Asp	Thr	Ser
	370					375					380				
Ser	Leu	Phe	Asp	Lys	Leu	Lys	Lys	Glu	Pro	Asp	Ala	Leu	Thr	Leu	Leu
	385				390					395					400
Ala	Pro	Ala	Ala	Gly	Asp	Thr	Ile	Ile	Ser	Leu	Asp	Phe	Gly	Ser	Asn
				405					410					415	
Asp	Thr	Glu	Thr	Asp	Asp	Gln	Gln	Leu	Glu	Glu	Val	Pro	Leu	Tyr	Asn
		420						425					430		
Asp	Val	Met	Leu	Pro	Ser	Pro	Asn	Glu	Lys	Leu	Gln	Asn	Ile	Asn	Leu
		435					440					445			
Ala	Met	Ser	Pro	Leu	Pro	Thr	Ala	Gln	Thr	Pro	Lys	Pro	Leu	Arg	Ser
	450					455					460				
Ser	Ala	Asp	Pro	Ala	Leu	Asn	Gln	Glu	Val	Ala	Leu	Lys	Leu	Glu	Pro
	465				470					475					480
Asn	Pro	Glu	Ser	Leu	Glu	Leu	Ser	Phe	Thr	Met	Pro	Gln	Ile	Gln	Asp
				485					490					495	
Gln	Thr	Pro	Ser	Pro	Ser	Asp	Gly	Ser	Thr	Arg	Gln	Ser	Ser	Pro	Glu
		500						505						510	
Pro	Asn	Ser	Pro	Ser	Glu	Tyr	Cys	Phe	Tyr	Val	Asp	Ser	Asp	Met	Val
		515					520					525			
Asn	Glu	Phe	Lys	Leu	Glu	Leu	Val	Glu	Lys	Leu	Phe	Ala	Glu	Asp	Thr
	530					535					540				
Glu	Ala	Lys	Asn	Pro	Phe	Ser	Thr	Gln	Asp	Thr	Asp	Leu	Asp	Leu	Glu
	545				550					555					560
Met	Leu	Ala	Pro	Tyr	Ile	Pro	Met	Asp	Asp	Asp	Phe	Gln	Leu	Arg	Ser
				565					570					575	
Phe	Asp	Gln	Leu	Ser	Pro	Leu	Glu	Ser	Ser	Ser	Ala	Ser	Pro	Glu	Ser
			580					585					590		
Ala	Ser	Pro	Gln	Ser	Thr	Val	Thr	Val	Phe	Gln	Gln	Thr	Gln	Ile	Gln
		595					600					605			
Glu	Pro	Thr	Ala	Asn	Ala	Thr	Thr	Thr	Thr	Ala	Thr	Thr	Asp	Glu	Leu
	610					615						620			
Lys	Thr	Val	Thr	Lys	Asp	Arg	Met	Glu	Asp	Ile	Lys	Ile	Leu	Ile	Ala
	625				630					635					640
Ser	Pro	Ser	Pro	Thr	His	Ile	His	Lys	Glu	Thr	Thr	Ser	Ala	Thr	Ser
				645					650					655	
Ser	Pro	Tyr	Arg	Asp	Thr	Gln	Ser	Arg	Thr	Ala	Ser	Pro	Asn	Arg	Ala

660					665					670					
Gly	Lys	Gly	Val	Ile	Glu	Gln	Thr	Glu	Lys	Ser	His	Pro	Arg	Ser	Pro
675					680					685					
Asn	Val	Leu	Ser	Val	Ala	Leu	Ser	Gln	Arg	Thr	Thr	Val	Pro	Glu	Glu
690					695					700					
Glu	Leu	Asn	Pro	Lys	Ile	Leu	Ala	Leu	Gln	Asn	Ala	Gln	Arg	Lys	Arg
705					710					715					
Lys	Met	Glu	His	Asp	Gly	Ser	Leu	Phe	Gln	Ala	Val	Gly	Ile	Gly	Thr
725					730					735					
Leu	Leu	Gln	Gln	Pro	Asp	Asp	His	Ala	Ala	Thr	Thr	Ser	Leu	Ser	Trp
740					745					750					
Lys	Arg	Val	Lys	Gly	Cys	Lys	Ser	Ser	Glu	Gln	Asn	Gly	Met	Glu	Gln
755					760					765					
Lys	Thr	Ile	Ile	Leu	Ile	Pro	Ser	Asp	Leu	Ala	Cys	Arg	Leu	Leu	Gly
770					775					780					
Gln	Ser	Met	Asp	Glu	Ser	Gly	Leu	Pro	Gln	Leu	Thr	Ser	Tyr	Asp	Cys
785					790					795					
Glu	Val	Asn	Ala	Pro	Ile	Gln	Gly	Ser	Arg	Asn	Leu	Leu	Gln	Gly	Glu
805					810					815					
Glu	Leu	Leu	Arg	Ala	Leu	Asp	Gln	Val	Asn						
820					825										

```
<210> 236
<211> 342
<212> PRT
<213> Homo sapiens
```

<400> 236																
Asn	Asn	Asn	Asn	Ser	Lys	His	Thr	Gly	His	Lys	Ser	Ala	Cys	Val	Pro	
				5					10					15		
Asn	Met	Thr	Glu	Arg	Arg	Arg	Asp	Glu	Leu	Ser	Glu	Glu	Ile	Asn	Asn	
			20					25					30			
Leu	Arg	Glu	Lys	Val	Met	Lys	Gln	Ser	Glu	Glu	Asn	Asn	Asn	Leu	Gln	
		35					40					45				
Ser	Gln	Val	Gln	Lys	Leu	Thr	Glu	Glu	Asn	Thr	Thr	Leu	Arg	Glu	Gln	
	50					55					60					
Val	Glu	Pro	Thr	Pro	Glu	Asp	Glu	Asp	Asp	Asp	Ile	Glu	Leu	Arg	Gly	
	65				70					75					80	
Ala	Ala	Ala	Ala	Ala	Ala	Pro	Pro	Pro	Pro	Ile	Glu	Glu	Glu	Cys	Pro	
				85					90					95		
Glu	Asp	Leu	Pro	Glu	Lys	Phe	Asp	Gly	Asn	Pro	Asp	Met	Leu	Ala	Pro	
			100					105					110			
Phe	Met	Ala	Gln	Cys	Gln	Ile	Phe	Met	Glu	Lys	Ser	Thr	Arg	Asp	Phe	
	115						120					125				
Ser	Val	Asp	Arg	Val	Arg	Val	Cys	Phe	Val	Thr	Ser	Met	Met	Thr	Gly	
	130					135					140					
Arg	Ala	Ala	Arg	Trp	Ala	Ser	Ala	Lys	Leu	Glu	Arg	Ser	His	Tyr	Leu	
145					150					155				160		
Met	His	Asn	Tyr	Pro	Ala	Phe	Met	Met	Glu	Met	Lys	His	Val	Phe	Glu	
			165						170					175		
Asp	Pro	Gln	Arg	Arg	Glu	Val	Ala	Lys	Arg	Lys	Ile	Arg	Arg	Leu	Arg	
			180					185					190			
Gln	Gly	Met	Gly	Ser	Val	Ile	Asp	Tyr	Ser	Asn	Ala	Phe	Gln	Met	Ile	
	195						200					205				
Ala	Gln	Asp	Leu	Asp	Trp	Asn	Glu	Pro	Ala	Leu	Ile	Asp	Gln	Tyr	His	
	210					215					220					
Glu	Gly	Leu	Ser	Asp	His	Ile	Gln	Glu	Glu	Leu	Ser	His	Leu	Glu	Val	
225					230					235					240	

[illegible]

```
<210> 237
<211> 403
<212> DNA
<213> Homo sapiens
```

<400> 237							
ccagtggtggt	ggaattccag	cctcgtgccg	ggagtcgccg	cattctggtc	cgcttctctg	60	
cactatgtgc	ggtggcctcc	tgaaggcgct	gcgcagcgac	tctctacgtg	agctgagcca	120	
gtaccgggac	cagcacttcc	ggggtgacaa	tgaagaacaa	gaaaaattac	tgaagaaaag	180	
ctgtacgtta	tatgttgtaa	atctttcttt	ttacacaact	gaagaacaaa	tctatgaact	240	
cttcagcaaa	agtggtgaca	taaagaaaaa	cattatgggt	ctggataaaa	tgaagaaaac	300	
agcattgtga	tgtctgtttg	tggaatatata	ctcacgcgca	gatgcggaaa	acgccatgat	360	
gtacataaatt	ggcgcgctgc	ttgatgaccg	aatcattcgc	aca		403	

<210> 238  
<211> 183  
<212> DNA  
<213> Homo sapiens

```
<400> 238
tattaatagt aatcaattac ggggtcatta gttcatagcc catatatgga gttccgcggt 60
cataaactta cggtaaatgg cccgcctggc tgaccgccca acgacccccg cccattgacg 120
tcaataatga cgtatgttcc catagtaacg ccaataggga ctttccattg acgtcaatgg 180
gtg                                     183
```

```
<210> 239
<211> 403
<212> DNA
<213> Homo sapiens
```

```

<400> 239
ttttgatgct ttctttcatg ggaatagtc cttttttatt tagtaaatcg cattgctgga 60
accaccaagg agtgctggaat gctcttgagt gtattatttta tgcaagtcac agtcacgttg 120
cccatcatggc agctatgtga aacactaata aatgtgtttt tactttttat tcccgctaaa 180
actgatgtaa aacaggataa aggcttgtaa tagtcactta taagtatctg ggtctaagta 240
atttccttag atgtttctaa agaaacattt tcagctttgc tccgattatg attccaataa 300
ggaacgcttt cctagtgcaa ttttaggagt aaagtttgaa gagataaaaa tagccaaaga 360
taggagacgt ctgaattttg aatgataaac agtgatgttt taa 403

```

```
<210> 240
<211> 3148
<212> DNA
<213> Homo sapiens
```

&lt;400&gt; 240

aacttctcgg gaagatgagg cagtttgcca tctgtggccg agttgctgtt gccgggtgat 60  
agttggagcg gagacttagc ataattggcag aacctgtttc tccactgaag cactttgtgc 120  
tggctaagaa ggcgattact gcagtctttg accagttact ggagtttgtt actgaaggat 180  
cacattttgt tgaagcaaca tataagaatc cggaacttga tcgaatagcc actgaagatg 240  
atctggtaga aatgcaagga tataaagaca agctttccat cattggtgag gtgctatctc 300  
ggagacacat gaaggtggca ttttttggca ggacaagcag tgggaagagc tctgttatca 360  
atgcaatgtt gtgggataaa gttctcccta gtgggattgg ccatataacc aattgcttcc 420  
taagtgttga aggaactgat ggagataaag cctatcttat gacagaagga tcagatgaaa 480  
aaaagagtgt gaagacagt aatcaactgg cccatgccct tcacatggac aaagatttga 540  
aagctggctg tcttgtacgt gtgttttggc caaaagcaaa atgtgccctc ttgagagatg 600  
acctggtgtt agtagacagt ccaggcacag atgtcactac agagctggat agctggattg 660  
ataagttttg cctagatgct gatgtctttg ttttggctgc aaactctgaa tcaacactaa 720  
tgaatcagga aaaacacttt tttcacaagg tgaatgagcg gctttccaag cctaataatt 780  
tcattctcaa taatcgttgg gatgcctctg catcagagcc agaataatag gaagacgtac 840  
gcagacagca catggaaaga tgcctgcatt tcttgggtga ggagctcaaa gttgtaaatg 900  
ctttagaagc acagaatcgt atcttctttg tttcagcaaa ggaagtctt agtgctagaa 960  
agcaaaaagc acaggggatg ccagaaagtg gtgtggcact tgctgaagga tttcatgcaa 1020  
gattacagga atttcagaat tttgaacaaa tctttgagga gtgtatctcg cagtcagcag 1080  
tgaaaacaaa gttcgaacag cacactatca gagctaaaca gatactagct actgtgaaaa 1140  
acataatgga ttcagtaaac ctggcagctg aagataaaag gtttcatgtg caatgacaga 1200  
tgaaatttgt cgactgtctg ttttgggtga tgaatttgt tcagagtttc atcctaatacc 1260  
agatgtatta aaaatatata aaagtgaatt aaataagcac atagaggatg gtatgggaag 1320  
aaatttggct gatctgagca ccgatgaagt aaacgcctta gtgcttcaga cccagcaaga 1380  
aattattgaa aatttgaagc cattacttcc agctggtata caggataaac tacatacact 1440  
gatcccttgc aagaaatttg atctcagtta taatctaaat taccacaagt tatgttcaga 1500  
ttttcaagag gatattgtat ttctgttttc cctgggctgg tcttcccttg tacatcgatt 1560  
tttgggccct agaaatgctc aaagggtgct cctaggatta tcagagccta tctttcagct 1620  
ccctagatct tttagcttcta ctcccactgc tctaccact ccagcaacgc cagataatgc 1680  
atcacaggaa gaactcatga ttacattagt aacaggattg gcgtccgcta catctagaac 1740  
ttctatgggc atcattattg ttggaggagt gatttggaaa actataggct ggaaactcct 1800  
atctgttttc ttaactatgt atggagcttt gtatcttttc gaaagactga gctggaccac 1860  
ccatggcaag gagcagcct ttaaacagca gtttgaatac tatgcaactg aaaaactgag 1920  
gatgtattgt agctccacga gtgcaactg cagtcaccaa gtaaaacaac aaatagctac 1980  
cacttttgcct cgctgtgcc aacaagttga tattactcaa aaacagctgg aagaagaaat 2040  
tgctagatta cccaaagaaa tagatcagtt ggagaaaata caaaacaatt caaagctctt 2100  
aagaaataaa gctgttcaac ttgaaaatga gctggagaat tttactaagc agtttctacc 2160  
ttcaagcaat gaagaatcct aacaatagag attgctttgg tgaccatgat aggaggaaac 2220  
gaaacttgta agatttgaac agttgttatt tttatgaaat tactttaaat atgaattgta 2280  
ctaactgtac ctaaatagca aagccctgtg tagattctgg taatgatctg tctcagggtg 2340  
tgtgtatttt tgaagagtgt tatgtcctta gttttaaatt tgagtaaaga aaaggctaaa 2400  
atcatgaatt agttacaagc aacagtacca acttatgtga cccctgaggg gtggggctgt 2460  
gagctcttaa tttgtttttg attctgaaaa actctgcttc ctggcatcca ggagttagag 2520  
attgagcctt tcatcttctt tctcaaaact agtttttgat gctttctttc atgggaatag 2580  
tcactttttt atttagtaaa tcgcattgct ggaaccacca aggagtgtgg aatgtccttg 2640  
agtgtattat ttatgcaagt cacagtcacg ttgccatcat ggcagctatg tgaaacacta 2700  
ataaatgtgt ttttactttt tattcccggt aaaaactgat taaaacagga taaaggcttg 2760  
ttatagtcac ttataagtat ctgggtctaa gtaatttctt tagatgtttc taaagaaaca 2820  
ttttcagctt tgctccatt atgattccaa taaggaaacgc tttcctagtg caattttagg 2880  
agtaaagttt gaagagataa aaatagccaa agataggaga cgtctgaatt ttgaatgata 2940  
aacagtgatg ttttaaaaaa gctgttgttc ttcaggagcg atttgcctag gatattgctg 3000  
gattataccc cattggaggc ttttaatttt atttgtatga atttccagg atttcattaa 3060  
aaattattat tgtatttttt accttaatga aagatttttg gttcaaatat ctttctatat 3120  
taaaagctga ttgagtctgt acatatgt 3148

&lt;210&gt; 241

&lt;211&gt; 283

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 241

```

ttatTTTTcc cctcaaattc atgattttta cgtctgttac aaaggggaatt ttgctgatag 60
ctcttttgggt cccactgttc catttttatgc taatagattc cattctaggg cccagccgtc 120
tcttgactga tgggtgttccc ttttaaccott ggcatgtata atagaatttt ggtgaatgaa 180
agaacccaaa taggccagat agtcccccca ggccctgata tccataaaaag gcttggaat 240
gcattatgta attgtcctta gtctttttgt tgttttagaa aaa 283

```

&lt;210&gt; 242

&lt;211&gt; 5526

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 242

```

cgggccctgg ggctcgggag tggggggcgg tgggacagtg cggctactct tgatcctctc 60
cggctgcttg gtctacggca cagctgaaac tgatgtaaatt gtggctcatgc ttcaggaatc 120
ccaagtttgt gaaaagcgtg ccagccaaca attctgttac acaaatgtgc ttatcccaaa 180
atggcatgat atatggacac ggatacagat ccgagtaaatt agttccagat tggttcagat 240
caccacagtg gagaatgagg agaaactgaa ggagctagag cagtttagta tctggaactt 300
tttttctccc tttttaaaag agaaattgaa tgacacctat gttaacgtgg gtctatacag 360
cacaaaaacc tgcctcaaaag ttgagattat agagaaggac accaagtaca gtgtcattgt 420
gatccggaga tttgatccca aactctttct tgttttccct ctggactta tgctattttt 480
ttgtggagac ttgctgagca gaagtcaaat tttctactac tctactggga tgactgtggg 540
aattgtggcc tctctgctaa tcatcatttt tatactatct aagtttatgc ctaagaaaag 600
tcccatttac gtcatcctgg tgggaggctg gtctttttct ctgtacctca ttcaactagt 660
ttttaaaaat ttacaagaga tctggagggtg ttactggcag tatcttttaa gttatgtcct 720
cacagttgga ttcattgagt ttgcagtatg ttacaagtat gggcccttgg agaatgaacg 780
aagtatcaac ctgctgacct ggaccttgca gctgatgggc ctgtgtttca tgtattctgg 840
catccagata ccacatattg ccttgccat tatcatcatt gctctttgta ctaagaacct 900
ggaacaccct attcagtggc tgtacatcac ctgcagaaag gtgtgtaagg gagcagaaaa 960
gctgttccc cctcgtctcc tgacagaaga agaatatcgg atacaaggag aggtagaaac 1020
caggaagggt tttagaggag tccagagaatt ttgtaacngt ccagactgot ctgcttggag 1080
gactgtttct cgaatccagt ctccaaaaag atttgcctgac tttgtggaag gctcttccca 1140
cctcacgcca aatgaagttt ctgtccatga gcaggagtat ggattaggga gcattattgc 1200
ccaggatgaa atctatgagg aagcatcctc tgaggaggag gactcatatt ctcggtgtcc 1260
tgctatcaca cagaacaact ttctaacctt ggtagtggtc agttatcttt acgtggactg 1320
gcttggtgcc ttggtccatg ttgcattgtt tgtgcaattg ctttcaaccc tttgaaacag 1380
agtgaatag atagggtaga aattctccta ctgaaataag aggcctaaaa aggcctccct 1440
ttggaatagg gaggtctcta tgggatccct gaggaaggag agtggataaa gtagtgaatg 1500
ctgggtagtt cacttcccat tggttaagct aacagccac ttttatgttt ccagagaaat 1560
tggatggcca cagctagcat ggcattctag ctcttctctg aaagtgtatt caatcatggc 1620
atttctgtca ctggctggct ctccaaagta agaactgttg ttaagtgcag gaatgctttt 1680
agactatagg ctgcaacttc cagagagaaa tccacaaatc tgagcctcct tcaactccagc 1740
ttttatttca gtgactttag aataattatt gatttaactg ttttgggagg aaaatagatt 1800
tttattgttt tgttttttaa atgaatgtct tttaaaaaac ataacaact catgttccag 1860
aaccagcaag tgctccagag tgacacaccc cctaggcccc tacatatatta ttaatatgga 1920
ttatccatta aagccccagg agctgttggt ttaagctttg atttagttct catacatatg 1980
atagaaagtc ctatttgctt tttaggaacat gctgtaggc tcttctgcag gtgagatgta 2040
ctgggctttt tatttatatt aactttcaat tccatcttaa aaaacatttg tattcttctc 2100
tccccattct tccctaccct gcctttgccc tttcaggaag ggtcagttcc cttacctgtg 2160
aactatgtat gttcagagta gcattattcc tgcctagctag gagaagtcac cttgttttagg 2220
ggatttggat gctttttata cgttctccat tttcctgtca ttgggtcatg ttatctttga 2280
gttgctatga aatcaggaaa ctgtctcctt ttcctttccc ttcctttgtc tacatgctct 2340
gtccattcct ttcagccttt tctcaccacc catactcccc caaatctggg taatttttaa 2400
gccttgaaac tatgtagttt cttgatcac aattttagt tatgcagcag ccacaatttg 2460
cattgccagg aaataggctc caggttatct tcatgctct gggtgctcat tcagctgtca 2520
agtttccatg aacttacact tatttatgat tgcgtttctg acctgagatg tatgctgcct 2580
gttattgcag tagcattagt ttcagattct tttgccattg caaagtaccc cttataaacc 2640

```



```

agcaatgtca tctgtgagga agcaaatctt caagtgtctg tcatttactt ggttcttttt 2700
ctttgtggtc ttcacctta taccctggaa aagtctgtaa ttaccttagc caggaagata 2760
gatggtcatg gcaagcgac agcaccagac ttactggctc accaagatga tggaaaaagg 2820
cagatgattt tttaaaaagc cgtaatgact ccttttagacc agccatttag cgtggtaatt 2880
ttgaaaggcc tagctccatt gcagacttcc aaagggtcag ctctgagact gccctccagg 2940
tgggcagttg attattttcca ccagtgtttt ccagagcctt aaactgtcct aagtgaacaac 3000
tacctcagtt ggcaaggaa agacatatag tagaaagtga aaaatgagca gtatttgggc 3060
agatgctatg ggttacagtt gaagggtaaa aggaacttta cattgggaaa cttttatacc 3120
cttgtgaatt atgtacatgg taaaatgttc tctctctaca aagaactatt aaaacttctg 3180
aaatatacta ttttttacct tatttataga aattgagacc tagcatattt aagcataagt 3240
ttatttttaa aaataattca actcgtgcaa gtggtctcag gattctctgg agatttttgg 3300
gcctcccta cttagggagg tgatagcttg cctataaggg tgacttttcc tgatcatgtc 3360
tttatttcaa tgagaaagca ctgtgaaatt gtgaaagatt ctctcttttc tctgtttaat 3420
aaaccccat gaaatatagt ttccatctct agaccagttt tttttccacc gtgttttagac 3480
ttgaggtgaa taaaatcaaa ctgtttttta ctccctatct ggtagtgtga gacctgagct 3540
gtaggcagtg gagatggcaa ttggttctgc agcctgagag ttgctctcac acagtgaagg 3600
acgggtctgc tctggtgtgc tgtgtgtcct tgccctgcct gcctgtggct ctgccagat 3660
gcttcagatc ctctgtgttc cggagattgc ttgacttcaa ccttctttag gagctgctct 3720
tgtctccctc ttggccactt agtttgtctg ctccagtcact acttgaagac cccatttaat 3780
ttttctctgg cagttatagc tcttgtgatt tcagtacagt ctcatctctc agaccaatct 3840
catcaagaag gattgaaggg ataactatga ggtaagctgg acattggagc cgtgtttgct 3900
gccacgtcag cgtcttctg ggtgaatgtc aagccataaa tgggctccag ggctctggat 3960
ctcatcagca ttggaaatct attgcctctc atcagctctga ccaaattatg tagagcatta 4020
atgtagagac tccattaat gggaatacaa gaggcagctg gcataaaaca tttctttcac 4080
tttcttttcc cactcagatt gcttcaagag accaacagaa cacagggac aaaaacaagg 4140
aaaatttagc aacttcatta ccttctaata agtaattcct gttagccact gcattcccac 4200
aaaactagtt tatttttccc ctcaaattca tgatttttac gtctgttaca aagggaattt 4260
tgctgatagc tctttgggtc ccaactgttc attttatgct aatagattcc attctagggc 4320
ccagccgtct cttgactgat ggtgttccct ttaacccttg gcatgtataa tagaattttg 4380
gtgaatgaaa gaacccaaat aggccagata gtcccccag gccctgatat ccataaaaag 4440
cttggaatg cattatgtaa ttgtccttag tctttttggt gttttagaaa aaaaaaaca 4500
gatgggtcga gatggatgcc tacgtaaaaa tggttcctag ctgtgtactc ataacttttc 4560
tttggatgca gatggatgag gahggaggag gaaggagat taaatgtcct tctagttatc 4620
tctggactca agtcgacat atgagataat aacctatatt gaaatgccaa gaattgtatc 4680
tgaacaaga gaacagtttg acacatttat catgccttca tattacatat taactgaac 4740
caattaataa acatatgaaa tatccattgc acaaggcaaa ggcacctaaa ccttttgttt 4800
ctttttctac atagcagaaa ttgatttttt ttttattttt ttaggggaac ctatataatt 4860
atgacccagt gatgtctttt ggtgacttaa gcttatgaat tcaggttaca attgagtga 4920
ttctagatgg ttactacctt gaaaaggatg ttggtgcctt atgtgacacg agccagagcc 4980
tgctgggaat aaacaaagca gattcatgcc aacaccaact cgtagcttta gtggcagatg 5040
ggagtgttca cagactccca aaatgtggg ctttggattt ccacaccatc ccacgtgtgt 5100
gtcatcttcc tctttcacac tcttgatgat aatttgaaaa tgatgaaatc acctctgaat 5160
ttgcctatag catgagcaca ttcttatgac aacataacaa atagttcata atgtgaatat 5220
tagaaactgt tacagcctgc agttaccata attttccatg tttgtggaat tgatattgaa 5280
atagcagggc taaggaaatta ctggcaagtt ttagcctgtg ggttaatacct tagggttatt 5340
taaatatttg taattttatt taaatgttca tgaatgtttg aaaggaacaa aattatcagg 5400
gatggctctt tgccatgggt cttattttca cctcttttcc tgtaagaaaa aagaacaatg 5460
tcttaatgta tttttaagtt ttttggatata gtttctaatt ccaattttta taaaagtttt 5520
atagat 5526

```

&lt;210&gt; 243

&lt;211&gt; 303

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 243

```

cataaagggt gtgcgctctc tcgacgtggc ggtcttggcg ccaactgctgc gagaccgggc 60
cctggacctc aaggtcatcc acttgggtgc tgatccccgc gcggtggcga gttcacggat 120
ccgctcgcgc cacggcctca tccgtgagag cctacaggtg gtgcgcagcc gagaccggcg 180

```

87

agctcaccgc atgcccttct tggaggccgc gggccacaag cttggcgcca agaaggagg 240  
cgtgggcggc cccgcagact accacgctct gggcgctatg gaggtcatct gcaatagtat 300  
ggc 303

&lt;210&gt; 244

&lt;211&gt; 2393

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 244

cgaggaacga gtgacagccg gacagtccgc cggggcgtga tccggggccg ctcccggcg 60  
cgccctcggc tccaggtcct acccgagacc gctgccatgg gagagccagc cttgggcgct 120  
ggggaccagc cgcgcgcccc gcctcggagt cgcggcccca gtcccggcgc cagcagccag 180  
cccgtgcgt ccccttcccg ggctgcaggg ctgcctccgc cgcgcgcgcg gcccgattg 240  
tgctgtgat gagccgcagc ccgcagcgag ctctgcccc gggcgcgctc cctcggctgc 300  
tccaggctgc gcctgcagcg cagccgcgtg ccctgctccc gcagtggccc cggcgcccag 360  
gacgcgcgtg gcccgcgctc cctctcgga tgaagggtgt ccgtaggaag gcgctgggtg 420  
tgtgcgctgc ctatgcactg ctgctgggtg tcaactatgt caacctctg gactacaagt 480  
ggcacaagga gccgctgcag cagtgcaccc ccgatgggccc gctgggtgcc gcagcggggg 540  
cagccggagg caagctgggg gcgcccaggg ccgctcccg cggggccgc cctgctcat 600  
gcccgcttgg acctccgcac tccttaccgc cctcccgctg ccgccgctcg ggcgatactc 660  
tgcaagccgc gcagggtgg gcgggggtgc gggccctcca ggcaatggca ctccgggcac 720  
cggagggcgt cggggacaag cggcactgga tgtacgtgt caccacgtgg cgtctgtgt 780  
cgtcgttctt cggcgagcta ttcaaccaga atcccgaggt gttctttctc tacgagccag 840  
tgtggcatgt atggcaaaaa ctgtatccgg gggacgcgt ttccctgcag ggggcagcgc 900  
gggacatgct gagcgctctt tacgctgcg acctctctgt cttccagtgt tatagcccg 960  
cgggcagcgc ggggcgcaac ctaccacgc tggcatctt cggcgcagcc accaacaagg 1020  
tgggtgtctc gtcaccactc tgccccgct accgcaagga ggtcgtggg ttggtggag 1080  
accgctgtg caagaagtgc ccgccacagc gcctggcgcg ttccgaggag gactgcccga 1140  
agtaccgcac actagtcata aagggtgtgc gcgtcttca cgtggcggtc ttggcgccac 1200  
tgtgcgaga cccggccctg gacctcaagg tcctccactt ggtgcgtgat ccccgcgcg 1260  
tggcgagttc acggatccgc tcgcgccacg gctcatccg tgagagccta cagggtgtgc 1320  
gagcagcgc cccgagcgt cccg. ctgc cctctctg. cgttcgggc cccagcttg. 1380  
gcccgaagaa ggagggcggt ggccggcccc cagactacca cgctctgggc gctatggagg 1440  
tcctctgcaa tagtatggct aagacgctgc agacagccct gcagccccct gactggctgc 1500  
agggccacta cctggtgggt cggtagcagg acctggtggg agaccccgtc aagacactac 1560  
ggagagtgtc cgattttgtg ggactgttgg tgagccccga aatggagcag ttgcccctga 1620  
acatgaccag tggctcgggc tcctcctcca agcctttcgt ggtatctgca cgcaatgcca 1680  
cgcaggccgc caatgcctgg cggaccgccc tcacctcca gcagatcaaa cagggtggag 1740  
agttttgcta ccagcccatg gccgtcctgg gctatgagcg ggtcaacagc cctgaggagg 1800  
tcaaagacct cagcaagacc ctgcttcgga agccccgtct ctaaaagggg ttcccaggag 1860  
acctgattcc ctgtgggtgat acctataaa aggatcgtag tgtgtttaa taaacacagt 1920  
ccagactcaa acggagggaag cccacatatt ctattataga tatataaata atcacacaca 1980  
cacttgctgt caatgttttg agtcagtgc tttcaaggaa cagccacaaa atacacaccc 2040  
ctaagaaaag gcaagacttg aacgttctga ccagggtgcc ctcttcttct ttgccttctc 2100  
ttgtcctctt tctcctattt cttaccctgt cctccacctg ccttccattt tgaagtggga 2160  
tgttaaatgaa atcaagttcc agtaacccaa atcttgttta caaaatattc gtggtatctg 2220  
tgaacatggt aagagtaatt tggatgtggg ggtgggggtg gagaaaaggg aagtgtcca 2280  
gaaacaaaaa gccccattgg gcatgataag ccgaggaggc attcttcccta aaagtagact 2340  
tttgtgtaaa aagcaaaagg tacatgtgag tattaataaa gaagataata aat 2393

&lt;210&gt; 245

&lt;211&gt; 473

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 245

ccaacacagt cagaaacatt gttttgaatc ctctgtaaac caaggcatta atottaataa 60  
accaggatcc atttaggtac cacttgatat aaaaaggata tccataatga atattttata 120

88

ctgcatcctt tacattagcc actaaatagc ttattgcttg atgaagacct ttcacagaat 180  
 cctatggatt gcagcatttc acttggctac ttcataccca tgccttaaag aggggcagtt 240  
 tctcaaaagc agaaacatgc cgccagttct caagttttcc tccctaactcc atttgaatgt 300  
 aagggcagct ggcccccaat gtggggaggt ccgaacattt tctgaattcc cattttcttg 360  
 ttccgggcta aatgacagtt tctgtcatta cttagattcc gatctttccc aaaggtgttg 420  
 atttacaag aggccagcta atagcagaaa tcatgaccct gaaagagaga tga 473

&lt;210&gt; 246

&lt;211&gt; 513

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 246

ggcattaact tttagaattt gggctggtga gattaatttt ttttaatatc ccagctagag 60  
 atatggcctt taactgacct aaagaggtgt gttgtgattt aattttttcc cgttcctttt 120  
 tcttcagtaa acccaacaat agtctaacct taaaaattga gttgatgtcc ttataggtca 180  
 ctacccttaa ataaacctga agcaggtgtt ttctcttgga cataactaaa aatacctaaa 240  
 aggaagctta gatggtctgt gacacaaaaa attcaattac tgtcatctaa tgccagctgt 300  
 taaaagtgtg gccactgagc atttgatttt ataggaaaa atagtatttt tgagaataac 360  
 atagctgtgc tattgcacat ctgttgaggg acatcccaga tttgcttata ctcaagtgcct 420  
 gtgatattga gtttaaggat ttgaggcagg ggtaattatt aaacatattg cttctattct 480  
 tggaaaaata gaagtgtaaa atgttaataa tac 513

&lt;210&gt; 247

&lt;211&gt; 533

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 247

ccagtggtgt ggaattcgcg gtaggctggg accataacac aagcatgact atatgaagga 60  
 agaggaaggt tttcctgaag atgaggcgac tgaatcggaa aaaaacttta agtttggtta 120  
 aagagttgga tgcctttccg aaggttcctg agagctatgt agagacttca gccagtgag 180  
 tatatcaaga tacatggatg aagtatgaat acgaagtaga caaggatttt tctagcaaat 240  
 taagaattaa tatagatatt actgttgcca tgaagtgtca atatgttgga gcggatgtat 300  
 tggatttagc agaaacaatg gttgcatctg cagatgggtt agtttatgaa ccaacagtat 360  
 ttgatctttc accacagcag aaagagtggc agaggatgct gcagctgatt cagagtaggc 420  
 tacaagaaga gcattcactt caagatgtga tatttaaaag tgcttttaaa agt 533

&lt;210&gt; 248

&lt;211&gt; 1362

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 248

gggacccggg cttctgtgaa acatggcggg aggctgggac cataacacaa gcatgactat 60  
 atgaaggaag aggaagggtt tctgaagat gaggcgactg aatcggaaaa aaactttaag 120  
 tttggtaaaa gagttggatg cctttccgaa ggttcctgag agctatgtag agacttcagc 180  
 cagtggaggt acagtttctc taatagcatt tacaactatg gctttattaa ccataatgga 240  
 attctcagta tatcaagata catggatgaa gtatgaatac gaagtagaca aggatttttc 300  
 tagcaaatga agaattaata tagatattac tgttgccatg aagtgtcaat atgttgagc 360  
 ggtgtattg gatttagcag aaacaatggt tgcactgca gatggtttag tttatgaacc 420  
 aacagtattt gatctttcac cacagcagaa agagtggcag aggatgctgc agctgattca 480  
 gagtaggcta caagaagagc attcacttca agatgtgata tttaaaagtg cttttaaaag 540  
 tacatcaaca gctcttcac caagagaaga tgattcatca cagtctccaa atgcatgcag 600  
 aattcatggc catctatag tcaataaagt agcagggaa tttcacataa cagtgggcaa 660  
 ggcaattcca catctcgtg gtcatgcaca ttgggcagc acttgtcaac catggaatct 720  
 tacaattttt tctcatagaa tagatcattt gtcttttgga gagcttggtc cagcaattat 780  
 taatccttta gatggaactg aaaaaattgc tatagatcac aaccagatgt tccaatattt 840

89

```

tattacagtt gtgccaacaa aactacatac atataaaata tcagcagaca cccatcagtt 900
ttctgtgaca gaaaggggaa gtatcattaa ccatgctgca ggcagccatg gagtctctgg 960
gatatttatg aaatatgac tcagttctct tatggtgaca gttactgagg agcacatgcc 1020
attctggcag ttttttgtaa gactctgtgg tattgttgga ggaatctttt caacaacagg 1080
catgttacat ggaattggaa aatttatagt tgaaataatt tgctgtcgtt tcagacttgg 1140
atcctataaa cctgtcaatt ctgttccttt tgaggatggc cacacagaca accacttacc 1200
tcttttagaa aataatacac attaacacct cccgattgaa ggagaaaaac tttttgcctg 1260
agacataaaa ccttttttta ataataaat attgtgcaat atattcaaag aaaagaaaaa 1320
acaaataagc agaaaacata cttattttta aaaaaaaaaa aa 1362

```

&lt;210&gt; 249

&lt;211&gt; 513

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(513)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 249

```

ccagngnggt ggaattcctt agacatattc tgagcctaca gcagaggaac ctccagtctc 60
agcaccatga atcaaaactgc cattctgatt tgctgcctta tctttctgac tctaagtggc 120
attcaaggag tacctctctc tagaactgta cgctgtacct gcatcagcat tagtaatcaa 180
cctgttaatc caaggtcttt agaaaaactt gaaattattc ctgcaagcca attttgtcca 240
cgtgttgaga tcattgctac aatgaaaaag aagggtgaga agagatgtct gaatccagaa 300
tcgaaggcca tcaagaattt actgaaagca gttagcaagg aaaggtctaa aagatctcct 360
taaaaccaga ggggagcaaa atcgatgcag tgcttccaag gatggaccac acagaggctg 420
cctctcccat cacttcctta catggagtat atgtcaagcc ataattgttc ttagtttgca 480
gttacactaa aaggtgacca atcatgtgca cca 513

```

&lt;210&gt; 250

&lt;211&gt; 1172

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 250

```

gagacattcc tcaattgctt agacatattc tgagcctaca gcagaggaac ctccagtctc 60
agcaccatga atcaaaactgc gattctgatt tgctgcctta tctttctgac tctaagtggc 120
attcaaggag tacctctctc tagaaccgta cgctgtacct gcatcagcat tagtaatcaa 180
cctgttaatc caaggtcttt agaaaaactt gaaattattc ctgcaagcca attttgtcca 240
cgtgttgaga tcattgctac aatgaaaaag aagggtgaga agagatgtct gaatccagaa 300
tcgaaggcca tcaagaattt actgaaagca gttagcaagg aaatgtctaa aagatctcct 360
taaaaccaga ggggagcaaa atcgatgcag tgcttccaag gatggaccac acagaggctg 420
cctctcccat cacttcctta catggagtat atgtcaagcc ataattgttc ttagtttgca 480
gttacactaa aaggtgacca atgatgtgca ccaaatcagc tgctactact cctgtaggaa 540
ggtaaatgtt catcatccta agctattcag taataactct accctggcac tataatgtaa 600
gtctactga ggtgctatgt tcttagtgga tgctctgacc ctgcttcaaa tatttccttc 660
acctttccca tcttccaagg gtactaagga atctttctgc tttgggggtt atcagaattc 720
tcagaatctc aaataactaa aaggatgca atcaaatctg ctttttaaaag aatgctcttt 780
acttcagga cttccactgc catcctccca aggggcccaa attctttcag tggctaccta 840
catacaattc caaacacata caggaaggta gaaatatctg aaaatgtatg tgtaagtatt 900
cttatttaat gaaagactgt acaaagtata agtcttagat gtatatattt cctatattgt 960
tttcagtgtg catggaataa catgtaatta agtactatgt atcaatgagt aacaggaaaa 1020
ttttaaaat acagatagat atatgctctg catgttacat aagataaatg tgctgaatgg 1080
ttttcaaata aaaatgaggt actctcctgg aaatattaag aaagactatc taaatgttga 1140
aagatcaaaa ggttaataaa gtaattataa ct 1172

```

&lt;210&gt; 251

90

<211> 483  
 <212> DNA  
 <213> Homo sapiens

<400> 251  
 atataccatt taatacattt acactttctt atttaagaag atattgaatg caaaataatt 60  
 gacatataga actttacaaa catatgtcca aggactctaa attgagactc ttccacatgt 120  
 acaatctcat catcctgaag cctataatga agaaaaagat ctagaactg agttgtggag 180  
 ctgactctaa tcaaatgtga tgattggaat tagaccattt ggcctttgaa ctttcatagg 240  
 aaaaatgacc caacatttct tagcatgagc tacctcatct ctagaagctg ggatggactt 300  
 actattcttg tttatatattt agatactgaa aggtgctatg cttctgttat tattccaaga 360  
 ctggagatag gcagggctaa aaaggtatta ttatttttcc tttaatgatg gtgctaaaat 420  
 tcttcctata aaattcctta aaaataaaga tggtttaatc actaccattg tgaaaacata 480  
 act 483

<210> 252  
 <211> 156  
 <212> PRT  
 <213> Homo sapiens

<400> 252  
 Met Ser Gly Gly Leu Leu Lys Ala Leu Arg Ser Asp Ser Tyr Val Glu  
 5 10 15  
 Leu Ser Gln Tyr Arg Asp Gln His Phe Arg Gly Asp Asn Glu Glu Gln  
 20 25 30  
 Glu Lys Leu Leu Lys Lys Ser Cys Thr Leu Tyr Val Gly Asn Leu Ser  
 35 40 45  
 Phe Tyr Thr Thr Glu Glu Gln Ile Tyr Glu Leu Phe Ser Lys Ser Gly  
 50 55 60  
 Asp Ile Lys Lys Ile Ile Met Gly Leu Asp Lys Met Lys Lys Thr Ala  
 65 70 75 80  
 Cys Gly Phe Cys Phe Val Glu Tyr Tyr Ser Arg Ala Asp Ala Glu Asn  
 85 90 95  
 Ala Met Arg Tyr Ile Asn Gly Thr Arg Leu Asp Asp Arg Ile Ile Arg  
 100 105 110  
 Thr Asp Trp Asp Ala Gly Phe Lys Glu Gly Arg Gln Tyr Gly Arg Gly  
 115 120 125  
 Arg Ser Gly Gly Gln Val Arg Asp Glu Tyr Arg Gln Asp Tyr Asp Ala  
 130 135 140  
 Gly Arg Gly Gly Tyr Gly Lys Leu Ala Gln Asn Gln  
 145 150 155

<210> 253  
 <211> 370  
 <212> PRT  
 <213> Homo sapiens

<400> 253  
 Met Ala Glu Pro Val Ser Pro Leu Lys His Phe Val Leu Ala Lys Lys  
 5 10 15  
 Ala Ile Thr Ala Val Phe Asp Gln Leu Leu Glu Phe Val Thr Glu Gly  
 20 25 30  
 Ser His Phe Val Glu Ala Thr Tyr Lys Asn Pro Glu Leu Asp Arg Ile  
 35 40 45  
 Ala Thr Glu Asp Asp Leu Val Glu Met Gln Gly Tyr Lys Asp Lys Leu  
 50 55 60  
 Ser Ile Ile Gly Glu Val Leu Ser Arg Arg His Met Lys Val Ala Phe  
 65 70 75 80

[illegible]

```
<210> 254
<211> 429
<212> PRT
<213> Homo sapiens
```

<400> 254																
Gly	Pro	Trp	Gly	Ser	Gly	Val	Gly	Gly	Gly	Gly	Thr	Val	Arg	Leu	Leu	
				5				10						15		
Leu	Ile	Leu	Ser	Gly	Cys	Leu	Val	Tyr	Gly	Thr	Ala	Glu	Thr	Asp	Val	
			20					25					30			
Asn	Val	Val	Met	Leu	Gln	Glu	Ser	Gln	Val	Cys	Glu	Lys	Arg	Ala	Ser	
		35					40					45				
Gln	Gln	Phe	Cys	Tyr	Thr	Asn	Val	Leu	Ile	Pro	Lys	Trp	His	Asp	Ile	
	50					55					60					
Trp	Thr	Arg	Ile	Gln	Ile	Arg	Val	Asn	Ser	Ser	Arg	Leu	Val	Arg	Val	
	65				70					75					80	
Thr	Gln	Val	Glu	Asn	Glu	Glu	Lys	Leu	Lys	Glu	Leu	Glu	Gln	Phe	Ser	
				85					90					95		
Ile	Trp	Asn	Phe	Phe	Ser	Ser	Phe	Leu	Lys	Glu	Lys	Leu	Asn	Asp	Thr	

```
<210> 255
<211> 531
<212> PRT
<213> Homo sapiens
```

```

<400> 255
Met Ser Arg Ser Pro Gln Arg Ala Leu Pro Pro Gly Ala Leu Pro Arg
              5              10              15
Leu Leu Gln Ala Ala Pro Ala Ala Gln Pro Arg Ala Leu Leu Pro Gln
              20              25              30
Trp Pro Arg Arg Pro Gly Arg Arg Trp Pro Ala Ser Pro Leu Gly Met
              35              40              45
Lys Val Phe Arg Arg Lys Ala Leu Val Leu Cys Ala Gly Tyr Ala Leu
              50              55              60
Leu Leu Val Leu Thr Met Leu Asn Leu Leu Asp Tyr Lys Trp His Lys
              65              70              75              80

```





<210> 256  
 <211> 378  
 <212> PRT  
 <213> Homo sapiens

<400> 256

```

Met Arg Arg Leu Asn Arg Lys Lys Thr Leu Ser Leu Val Lys Glu Leu
      5              10              15
Asp Ala Phe Pro Lys Val Pro Glu Ser Tyr Val Glu Thr Ser Ala Ser
      20              25              30
Gly Gly Thr Val Ser Leu Ile Ala Phe Thr Thr Met Ala Leu Leu Thr
      35              40              45
Ile Met Glu Phe Ser Val Tyr Gln Asp Thr Trp Met Lys Tyr Glu Tyr
      50              55              60
Glu Val Asp Lys Asp Phe Ser Ser Lys Leu Arg Ile Asn Ile Asp Ile
      65              70              75              80
Thr Val Ala Met Lys Cys Gln Tyr Val Gly Ala Asp Val Leu Asp Leu
      85              90              95
Ala Glu Thr Met Val Ala Ser Ala Asp Gly Leu Val Tyr Glu Pro Thr
      100             105             110
Val Phe Asp Leu Ser Pro Gln Gln Lys Glu Trp Gln Arg Met Leu Gln
      115             120             125
Leu Ile Gln Ser Arg Leu Gln Glu Glu His Ser Leu Gln Asp Val Ile
      130             135             140
Phe Lys Ser Ala Phe Lys Ser Thr Ser Thr Ala Leu Pro Pro Arg Glu
      145             150             155             160
Asp Asp Ser Ser Gln Ser Pro Asn Ala Cys Arg Ile His Gly His Leu
      165             170             175
Tyr Val Asn Lys Val Ala Gly Asn Phe His Ile Thr Val Gly Lys Ala
      180             185             190
Ile Pro His Pro Arg Gly His Ala His Leu Gly Ser Thr Cys Gln Pro
      195             200             205
Trp Asn Leu Thr Ile Phe Ser His Arg Ile Asp His Leu Ser Phe Gly
      210             215             220
Glu Leu Val Pro Ala Ile Ile Asn Pro Leu Asp Gly Thr Glu Lys Ile
      225             230             235             240
Ala Ile Asp His Asn Gln Met Phe Gln Tyr Phe Ile Thr Val Val Pro
      245             250             255
Thr Lys Leu His Thr Tyr Lys Ile Ser Ala Asp Thr His Gln Phe Ser
      260             265             270
Val Thr Glu Arg Glu Arg Ile Ile Asn His Ala Ala Gly Ser His Gly
      275             280             285
Val Ser Gly Ile Phe Met Lys Tyr Asp Leu Ser Ser Leu Met Val Thr
      290             295             300
Val Thr Glu Glu His Met Pro Phe Trp Gln Phe Phe Val Arg Leu Cys
      305             310             315             320
Gly Ile Val Gly Gly Ile Phe Ser Thr Thr Gly Met Leu His Gly Ile
      325             330             335
Gly Lys Phe Ile Val Glu Ile Ile Cys Cys Arg Phe Arg Leu Gly Ser
      340             345             350
Tyr Lys Pro Val Asn Ser Val Pro Phe Glu Asp Gly His Thr Asp Asn
      355             360             365
His Leu Pro Leu Leu Glu Asn Asn Thr His
      370             375

```

<210> 257  
 <211> 98

95

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 257

```

Met Asn Gln Thr Ala Ile Leu Ile Cys Cys Leu Ile Phe Leu Thr Leu
      5      10      15
Ser Gly Ile Gln Gly Val Pro Leu Ser Arg Thr Val Arg Cys Thr Cys
      20      25      30
Ile Ser Ile Ser Asn Gln Pro Val Asn Pro Arg Ser Leu Glu Lys Leu
      35      40      45
Glu Ile Ile Pro Ala Ser Gln Phe Cys Pro Arg Val Glu Ile Ile Ala
      50      55      60
Thr Met Lys Lys Lys Gly Glu Lys Arg Cys Leu Asn Pro Glu Ser Lys
      65      70      75      80
Ala Ile Lys Asn Leu Lys Lys Ala Val Ser Lys Glu Met Ser Lys Arg
      85      90      95
Ser Pro

```

&lt;210&gt; 258

&lt;211&gt; 530

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 258

```

gaattcggca cgagggctgg aggctgagat gcaggagctc gccatccagc tgcacaagcg 60
ctgcgaggag gtagaggcca cgcggggcca ggtgtgtcag gaggaggagc tgcgcgcctt 120
ggtggagagc tgctgctgga gcaggaccgc gcccgcgagg acctccaggc ccggtctgcg 180
gagacgtggg ccctggcccg gcatgctgcc ctctctcttg accagctgcg agcctgtcaa 240
gctgagctgt catctcgagt gaggcaggac cagccccttg gtacagccac tctgggccta 300
gccgtcccc cagctgactc caagggctgg caagcgtccc tgcaggccat gagcctcccc 360
gagctctcgg gagccctgga ggaccgtgtc cgtgagatgg ggcaagcact gtgcttagtg 420
gagcagcagc gacagcagc gacagcagc gacagcagc gacagcagc gacagcagc 480
gcggggccgaa tctgacgttg ggtgattggt ccaccctgaa gctgtgtgcc 530

```

&lt;210&gt; 259

&lt;211&gt; 349

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 259

```

gaattcggca cgaggccagt tcagtctgca agcgccagct cctctcatgg ccggcttacc 60
caccgccttg ccaatgccca ggggcaaacc tcataccacc acttccagaa cactgatcat 120
gacacccaac aatcaggtac gtggtcctct ggcacccttc ccgctggtgg tccctgggaa 180
cagcatccga gctgtgatat gcactagagg agattgatgg tcctttgaat tagaagagta 240
actttttgag tatttgcca ttggtgtgtt gttctaggaa atcctctctt ttttgtggtg 300
ttgaggtccc ccatgtatag tttcagcagc gaggacactg tggttcttg 349

```

&lt;210&gt; 260

&lt;211&gt; 509

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 260

```

gaattcggca cgaggcaatc atggcgccac ctgtgagata ctgcatcccc ggccaacgtc 60
tgtgtaactt ggaggagggc agcccgggca gcggcaccta caccgcccac ggctacatct 120
tttcgtcgtc tgccggtcgt ctgatgaaga gcagcgagaa tggcgcgctt ccagtgggtg 180
ctgtagttag agaaacagag tcccagttac tgccagatgt gggagctatt gtaacctgta 240
aggtctctag catcaattca cgctttgcca aagtacacat cctgtatgtg ggggtccatgc 300

```

96

ctcttaagaa ctcttttcga ggaactatcc gcaaggaaga tgtccgagca actgaaaaag 360  
 acaaggttga aatttataag agtttccgcc caggtgacat tgtcttgccc aaagtgatct 420  
 ccttaggtga tgcacagtcc aactacctgc taaccaccgc cgagaacgag ctgggagtgg 480  
 tggtagccca cagttagtca ggtatccag 509

<210> 261  
 <211> 510  
 <212> DNA  
 <213> Homo sapiens

<400> 261  
 gaattcggca cgaggtgcat gttgtgtgag gatccccggg cgcgcgcgtc gctcgggccc 60  
 cgccatggcc gtcacccatca cgctcaaac gctgcagcag cagaccttca agatccgcat 120  
 ggagcctgac gagacggtga aggtgctaaa ggagaagata gaagctgaga agggctcgtga 180  
 tgccttcccc gtggctggac agaaactcat ctatgccggc aagatcttga gtgacgatgt 240  
 ccctatcagg gactatcgca tcgatgagaa gaactttgtg gtcgtcatgg tgaccaagac 300  
 caaagccggc cagggtagct cagcaccccc agaggcctca cccacagctg cccagagctc 360  
 ctctacatcc ttccccctg cccccacctc aggcattgtc catccccac ctgccgccag 420  
 agaggacaag agcccatcag aggaatccgc cccacagcag tccccagagt ctgtgtcagg 480  
 ctcttggtcc ctcttcagggt aacaaccggg 510

<210> 262  
 <211> 432  
 <212> DNA  
 <213> Homo sapiens

<400> 262  
 gacatgtaat tcttatttat ttttcacct caacaaggaa gaaaggtctc tccctcaatt 60  
 ctgctcttcc aataacttgag gataggcacc cctaaccctc ctccctccag ggaggcctca 120  
 gcatcagtg ctgtggacgt agtctctgaa gagtgttca gctgatggg aaggagaaac 180  
 tcaagacaga gatcctccta gggatggcgt cactttctct ccaactttct cgttgctct 240  
 ccttgaaagc agaagaagt ccagccctca gcttccgtca gatcttgggc tccataggcc 300  
 ttttaaacg ccatggcctc tgggttcag tccaggacgg ccaggcgga tggggcag 360  
 cccttateca aggccacctc agccacctt ttgattatt tggaaacca ccttgagcc 420  
 cgatattccg gc 432

<210> 263  
 <211> 614  
 <212> DNA  
 <213> Homo sapiens

<400> 263  
 gaattcggca cgaggcgag agttgtcgt actggagaag tccctgggac tgagtaagg 60  
 gaataaatac agtgctcagg gcgagcgaca gattccagtt ctccagacaa acaatggtcc 120  
 aagtctaaca ggattgacta ctatagcagc tcatctagtc aagcaagcca acaaagaata 180  
 tttgtcggg agtactgcag aagaaaaagc aatcgttcag cagtgggttag aatacaggt 240  
 cactcaagta gatgggcact ccagtaaaaa tgacatccac aactgttga aggatcttaa 300  
 ttcatacttt gaagataaag tctaccttac agggataaac ttacattag cagatatact 360  
 attgtactat ggacttcac gctttatagt tgacctgaca gttcaagaaa aggagaaata 420  
 tcttaagtga tctcgttgt tttgtcacat tcagcattat ccaggcatca ggcaacatct 480  
 gtctagtgtt ggtcttcac aagaacagac tatatactaa ttcccctaga aagctgtcca 540  
 tgccatacag aagatctatt aaaaaatgtt ttaaaatgga aaatgtactc ttagaaccac 600  
 aggacttaat ggta 614

<210> 264  
 <211> 336  
 <212> DNA  
 <213> Homo sapiens

97

&lt;400&gt; 264

```

gaattcggca cgagggggcac aacagagcgc ctcccctctc ctgcgccgc caccgggacg 60
gagagcgccc gccggtgcat ttccggcgac acctcgcagt cattcctgcg gcttgcgcgc 120
ccttgtagac agccggggcc ttctgtagaa cgggtgcaggc ctggggtagt ctctgtctcg 180
gacagagaag agaaaaatgc aggacactgg ctcaagagtg cctttgcatt ggtttggctt 240
tggtaccaca gcactgggtg cttctggttg gaattattgc tattgaaaag caagcaagcg 300
tgccgtccct ggctgcaggg ctgctctttt ggaagt 336

```

&lt;210&gt; 265

&lt;211&gt; 487

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 265

```

gaattcggca cgaggtgact gtgggaaact cggaacaag ctacatctt cctgtgggaa 60
accttctagc aacaggatga gtctgcagt gactgcagt gccaccttc tctatgcgga 120
ggtctttgtt gtgttgcttc tctgcattcc cttcatttct cctaaaagat ggcagaagat 180
tttcaagtcc cggctggttg agttgttagt gtccatggc aacaccttct ttgtggttct 240
cattgtcatc cttgtgctgt tggatcatga tgccgtgcgc gaaattcgga agtatgatga 300
tgtgacggaa aaggtgaacc tccagaacaa tcccggggcc atggagcact tccacatgaa 360
gcttttccgt gccagagga atctctacat tgctggcttt tccttgctgc tgctcttct 420
gcttagacgc ctggtgactc tcatttcgca gcaggccacg ctgctggcct ccaatgaagc 480
ctttaaa 487

```

&lt;210&gt; 266

&lt;211&gt; 418

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 266

```

gaattcggca cgagggcgtg acctgctagc tgagcagcgc ttccggggcc gctgtctgcc 60
ctcggacttg gacctgctgt tgcacatgaa caacgcgcgc tacctgcgcg aggccgactt 120
tgccacggta cgcaactga caggtgaggg gctgtcggg gccttcggg cgttgcggg 180
gcaacgggtg ctggcggcct cgtgcgcgc ccaccgcgc tcgctgcgc tgctggagcc 240
cttcgaggtg cgcacccgcc tgcgggctg ggacgaccgc gcgttctacc tggaggcgcg 300
ctttgtcagc ctgcgggacg gtttcgtgtg cgcgctgctg cgttccggc agcacctgct 360
gggcacctca cccgagcgcg tcgtgcagca cctgtgccaa cgcaagggtg aacccct 418

```

&lt;210&gt; 267

&lt;211&gt; 418

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(418)

&lt;223&gt; n = A, T, C or G

&lt;400&gt; 267

```

gaattcggca cgaggtggc tcccaccgt gagttggctc aacagattga ggaagagacc 60
atcaagtgtt ggaaccgct aggtatccgc actgtggctg tcattggtg catctccaga 120
gaagaccagg gcttcaggct gcgcattggg ttgtgagatt tgattgctcc cctgggcgtt 180
tgattgatgt gctggaaaac ccgtnccttg tgcctgaccc gctgtaccta tgtggttctg 240
gatgaggcag ataggatgat tgacatgggc tttagccag atgtccagaa gatcctggag 300
cacatgcctt gtcagcaacc agaagcccaa acacggatga agcttgagga cccctgagaa 360
aatgcttg ccaactttt agtcgggaaa acattaagta cccgcccaa cagtcatt 418

```

&lt;210&gt; 268

&lt;211&gt; 266

98

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 268

```

gaattcggca cgagggcttc tctactgagt cctactttta tgtcctgcct gtggtgagca 60
caaatgttga gcatatcaat ccccatTTTg tagacgaaga gacagagttg agtgacttgc 120
ccaaagacac agggccagtg aggagttgtg caggtttggc ctggcattaa aataataaac 180
attgaaattc agtcgattcc cctatggact cagttataga tctcatcagt tgaaggaaga 240
gagatgcctt ttcctattca accttt

```

266

&lt;210&gt; 269 )

&lt;211&gt; 235

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 269

```

gaattcggca cgagggctcc tgcagccttt tcgctgggac tgcgcgacac cgccccccga 60
ccgggtgccc gctgtgtgcc aggccgggtg ctgggcacag tcccgcgagt gccctataag 120
gactgccagg caataatgaa gttcttttta ctgaaggatg cgaaggaaga tgactgtggc 180
caggatccgt atatcaggga attaggatta tatggacttg aagccacttt gatcc

```

235

&lt;210&gt; 270

&lt;211&gt; 386

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 270

```

gaattcggca cgaggggttc tcgaggggccg ccgggtgctg gtcaccgggg caggcaaagg 60
tatagggcgc ggcacggctcc aggcgctgca cgcgacgggc gcgcgggtgg tggtgtgag 120
ccggactcag gcggatcttg acagccttgc ccgcgagtg ccggggatag aaccctgtg 180
cgtggacctg ggtgactggg aggccaccga gcgggcgctt gggcagcgtg ggccccgtg 240
acctgctggt gaacaacgcc cgtgtgcgcc ctgctgcagc ccttcctgga ggtcaccaag 300
ggcaggggct taatacccg gattcc

```

386

&lt;210&gt; 271

&lt;211&gt; 406

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 271

```

gaattcggca cgaggggctg ctggctggct aagtcctcc cgtcccgcc tctcgctca 60
ctaggagcgg ctctcgggtgc agcgggacag ggcgaagcgg cctgcgcca cggagcgcgc 120
gacactgccc ggaagggaacc gccacccttg cccctcagc tgccactcg tgatttcag 180
cggcctccgc gcgcgcacga tgccctcggc caccagccac agcgggagcg gcagcaagtc 240
gtccggaccg ccaccgccgt cgggttcctc cgggagttag gcggcccgcg gagccggggc 300
cgccgcgcgg gcttctagca ccccgcaacc ggcaccggcg ctgtccagac cgaggccatg 360
aagcagattc tcggggtgat cgacaagaaa cttcggaacc tggaga

```

406

&lt;210&gt; 272

&lt;211&gt; 365

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 272

```

gaattcggca cgaggtcgc ctcactagga gcggctctcg gtgcagcggg acagggcgaa 60
gcggcctgcg cccacggagc gcgcgacact gcccggaagg gaccgccacc cttgccccct 120
cagctgccca ctctgtattt ccagcggcct ccgcgcgcgc acgatgccct cggccaccag 180
ccacagcggg agcggcagca agtcgtccgg accgccaccg ccgtcggggt cctccgggag 240

```

99

tgaggcggcc gcgggagccg gggccgcgcg ccggcttcta gcaccccgca accggcaccg 300  
 gcgctgtcca gaccgaggcc atgaagcaga ttctcggggt gatcgacaag aaacttcgga 360  
 acctg 365

&lt;210&gt; 273

&lt;211&gt; 376

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 273

gaattcggca cgaggctttg gccactcaga gccccggggc cgcggtcgtc gtacgcctga 60  
 aggcgggtcg tgccggcgcc cgctctagtc tccgcctccg ctcaggccgg tcctccgggg 120  
 cttctcaatg gtttcccggt ggcctctcaa tggttttccc ggcggccctt gcgccgacgc 180  
 caggagactt ccggagcttg gtgacgtcac agagcgaagt ttctaccaca aatcgcgggc 240  
 gggggaatag gctcgagggc ggggagcagt gacaattgct aggcggagac agtgcaggga 300  
 agagagacct tataaaggat caggactggc gggaggtatt taactgaaag gaatatctgc 360  
 ttcactgttg caacca 376

&lt;210&gt; 274

&lt;211&gt; 385

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 274

gaattcggca cgaggcttgg gtccgtcgct gcttcggtgt cctgtcggg cttcccagca 60  
 gcggcctagc gggaaaagta aaagatgtct gaatatattc gggtaaccga agatgagaac 120  
 gatgagccca ttgaaatacc atcgggaagac gatgggacgg tgctgctctc cacggttaca 180  
 gccagtttcc caggggcgtg tgggcttcgc tacaggaatc cagtgtctca gtgtatgaga 240  
 ggtgtccggc tggtagaagg aattctgcat gccccagatg ctggctgggg aaatctggtg 300  
 tatgttgtca actatccaaa agataacaaa agaaaaatgg atgagacaga tgcttcatca 360  
 gcagtgaag tgaaaagagc agtcc 385

&lt;210&gt; 275

&lt;211&gt; 395

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(395)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 275

gaattcggca cgagggggag cggagagcgg accccagaga gccctgagca gccccaccgc 60  
 cgccgcgggc ctagttacca tcacaccccg ggaggagccg cagctgccgc agccggcccc 120  
 agtcaccatc accgcaacca tgagcagcga ggcgagacc cagcagccgc ccgcccgc 180  
 ccccgccgcc cccgccctca gcgcgcgcca caccaagccc ggcactacgg gcagcggcgc 240  
 aaggagcggg ggcggggcg gcctcacatt cggcggggcc ttgcccggcg ggacaaagaa 300  
 agggcattcg caacgaaggg ttttgggaaa caagtaaaat gggttcaatt gtaagggaac 360  
 cggatttttg ttttnattca accagggaaa ttgac 395

&lt;210&gt; 276

&lt;211&gt; 282

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 276

gaattcggca cgagggcagg ggtggctctg gctggcattg cctgagccgg cagtgatgaa 60  
 gtggggagct tgcccttgac aggtgggggc tggctggggc cttaatgtga aaagacagtg 120

100

gcaggcagct ggagtagagc gagcccagca gccctaaaag gctgccttca tggccatcta 180  
 gcccagttc agggcagcat ccatagccca caagccagcg tgggtggggc gggggtggtc 240  
 ccacagctgg gttccacctg aagagcctcc gtgcctcgga gc 282

<210> 277  
 <211> 615  
 <212> DNA  
 <213> Homo sapiens

<400> 277  
 gaattcggca cgaggccggt cggcctgggc aacctgcgct gaagatgccg ggaaaactcc 60  
 gtagtgacgc tggtttgaa tcagacaccg caatgaaaaa aggggagaca ctgcgaaagc 120  
 aaaccgagga gaaagagaaa aaagagaagc caaatctga taagactgaa gagatagcag 180  
 aagaggaaaga aactgttttc cccaaagcta aacaagttaa aaagaaagca ggccttctg 240  
 aagttgacat gaattctcct aaatccaaaa aggcacaaaa gaaagaggag ccatctcaaa 300  
 atgacatttc tcctaaaacc aaaagtttga gaaagaaaaa ggagccatt gaaaagaaag 360  
 tggtttcttc taaacccaaa aaagtgcaca aaaatgagga gccttctgag gaagaaatag 420  
 atgctcctaa gcccaagaag atgaagaaag aaaaggaaat gaatggagaa actagagaga 480  
 aaagcccaa actgaagaat ggatttcctc atcctgaacc ggactgtaac cccagtgaag 540  
 ctgccagtga agaaagtaac agtgagatag agcaggaaat cctgtggaac aaaaagaag 600  
 cgctttctct atttt 615

<210> 278  
 <211> 316  
 <212> DNA  
 <213> Homo sapiens

<400> 278  
 gaattcggca cgaggagaaa gggaaaaaag gcgtaaagac agacatgaag caagtgggtt 60  
 tgcaaggaga ccagatccag attctgatga agatgaagat tatgagcgag agaggaggaa 120  
 aagaagtatg ggcggagctg ccattgcccc acccaattct ctggtagaga aagacaaaga 180  
 gttaccccgga gattttcctt atgaagaagg actcaagacc tcgatcacag tctttccaag 240  
 cagcccttcc ttcctccagt gtacagaagg gaaagagaaa agcccgaga atcttccacc 300  
 cggaccctta gcaaac 316

<210> 279  
 <211> 393  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(393)  
 <223> n = A,T,C or G

<400> 279  
 gaattcggca cgagggtgaa accaacttat tgggtcgaat cccatttggc cacaggatac 60  
 tgtacgtatc ttcctttcca gagatttgat atcaccacga caccgccagc atacataaac 120  
 gtgttaccag gtttgcccca gtacaccagc atatatacac ccttgccag cctttctcct 180  
 gaatatcagc taccaagatc agtaccagtg gtgccgtctt ttgtagccaa tgacagagca 240  
 gaaaaaaatg ctggctgcct attttgnggg gcattcattt tgaaatggct tgagaaatgg 300  
 ttggctgggt caccagaat tggccttctt gaaaaccaca agaatccctt tggaaggggg 360  
 cttctttttg gggaaaataa tottggtaaa aag 393

<210> 280  
 <211> 454  
 <212> DNA  
 <213> Homo sapiens

101

&lt;400&gt; 280

```

gaattcggca cgaggcagca atgcggtaga tatgacgtaa acaaattata attaagctag 60
tggtactca gagatcaaaa gaactgcaca ttgcattctg gagcatgaga aatcattttt 120
tttttcatga tgtctaactc tactgaattt attcaatgga gataacagaa agatgattat 180
atatgattaa attacttcca gtattagcag atgcttattt aaatacttgc ttgttctttc 240
tgcaattcca catagaatta aggcaatagt ttaaaagaaa atttaaaaag taacttttct 300
agcattttta tgtagacctg tgaattctaa cacatttgca gtgtagccat cctaagtact 360
aaccagactt gaacaaaatc caacttgcaa aaacgatgca atataaatac caatcaccaa 420
taataggtag tctcactttt aaaaacctgt gtct 454

```

&lt;210&gt; 281

&lt;211&gt; 613

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 281

```

gaattcggca cgagggtgcgc tcttcgttgc ccagtttccg ctcagtggtc gcgtctccgc 60
ccccaccca ccagtcgccg tgcattctcg gccgggctct aggcgccatg gctccccgcg 120
ggaggaagcg taaggctgag gccgcggtgg tcgccgtagc cgagaagcga gagaagctgg 180
cgaacggcgg ggaggggaatg gaggagcgca ccgttggtat cgagcattgc actagctgac 240
gcgtctatgg gcgcaacgcc ccggccctga gccaggcgct gcgcctggag gcccagagc 300
ttccagtaaa ggtgaacccg acgaagcccc ggaggggcag cttcgagggtg acgctgctgc 360
gcccggacgg cagcagtgcg gagctctgga ctgggattaa gaaggggcc ccacgcaaac 420
tcaaattccc tgagcctcaa gaggtggtgg aagagttgaa gaagtacctg tcgtaggagg 480
atttgggtag aagccctcat gctgagcttt gtgtccctgg tgatgttga acattaatga 540
tggaacatgg ccaaacttca gtcatgatcc tgaagccatg gtttcttccc tgccagaaat 600
gaaggttcat tat 613

```

&lt;210&gt; 282

&lt;211&gt; 313

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 282

```

gaattcggca cgaggcgaga acgggcacgg ggagcagcag cctcaaccgc cggcgacgca 60
gcagcaacag cccaacagc agcgcggggc cgccaaggag gccgcgggga agagcagcgg 120
ccccacctcg ctgttcggcg tgacggtggc gccgccgggg gcgaggcagg gccagcagca 180
ggcgggagggt aagaagaagg cggaaggcgg cggaggcggc ggtcgccccg gggctccggc 240
ggcgggggac ggcaaaacag aacagaaagg cggagataaa aagagggggtg ttaaaagacc 300
accacaagat cat 313

```

&lt;210&gt; 283

&lt;211&gt; 557

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 283

```

gaattcggca cgaggcctgg ccggggagac gagttgcatg tggttggttca gctggcgata 60
gcggcgggag cggagccggc ggggcctgtg cgaccgcctg ggtttgtgaa atggctgctg 120
acatttctga atccagcggg gctgactgca aaggagacct aaggaacagt gccaggttag 180
atgccgatta ccacttcca gtcctttatt gtggagtctg ttcattacca acagagtact 240
gtgaatatat gcctgatgtt gctaaatgta gacaatggtt agagaagaat ttccaaatg 300
aatttgcaaa acttactgta gaaaattcac ccaacaaga agctggaatt agtgagggtc 360
aaggaaacag aggggaagaa gaggagaaga aaaaacagaa gagaggtgga aggggtcaaa 420
taaaacaaaa aaagaagacc gtaccacaaa aggttactat agccaaaatt ccagagcaa 480
agaagaata tgtgacaaga gtatgtggcc ttgcaacttt tgaaattgat cttaaagaag 540
cacaagatt ttttgc 557

```

&lt;210&gt; 284



102

&lt;211&gt; 627

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 284

```

gaattcggca cgaggctcac taggagcggc tctcgggtgca gcgggacagg gcgaagcggc 60
ctgcgcccac ggagcgcgcg acactgcccg gaagggaccg ccacccttgc cccctcagct 120
gccactcgt gatttccagc ggccctccgc cgcgcacgat gccctcggcc accagccaca 180
gcgggagcgg cagcaagtgc tccggaccgc caccgcccgc gggttcctcc gggagtgagg 240
cgcccgcggg agccggggcc gccgcgcccg cttctcagca ccccgcaacc ggcaccggcg 300
ctgtccagac cgaggccatg aagcagattc tcgggggtgat cgacaagaaa cttcggaaac 360
tggagaagaa aaagggttaag cttgatgatt accaggaaacg aatgaacaaa ggggaaaggc 420
ttaatcaaga tcagctggat gccgtttcta agtaccagga agtcacaaat aatttggagt 480
ttgcaaaaga attacagagg agtttcatgg cactaagtca agatattcag aaaacaataa 540
agaagacagc acgtcgggag cagcttatga aaaaagaact gaacagaaac gtttaaaaac 600
tgttacttga actacagtat tgttttg 627

```

&lt;210&gt; 285

&lt;211&gt; 474

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 285

```

gaattcggca cgagggcgag aacgaccccc ggaccgacca aagcccgcg cccgctgcat 60
cccgctcca gcacctacgt cccgctcgcg tcgccgccgc caccatgcc cagagaaagg 120
ctgaagggga tgctaaggga gataaagcaa aggtgaagga cgaaccacag agaagatccg 180
cgagggttgc tgctaaacct gctcctccaa agccagagcc caagcctaaa aaggccctg 240
caaagaagg agagaaggta cccaaaggga aaaagggaag agctgatgct ggcaaggagg 300
ggaataacc tgcaaaaaat ggagatgcca aaacagacca ggcacagaaa gctgaagggtg 360
ctggagatgc caagtgaagt gtgtgcattt ttgataactg tgtacttctg gtgactgtac 420
agtttgaaat actatttttt atcaagtttt ataaaaatgc agaatttttg tttta 474

```

&lt;210&gt; 576

&lt;211&gt; 576

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 286

```

gaattcggca cgaggggaat ctgtgaagct cactactgga ccaacaacg ctggagctca 60
aagtagttct tcatgtggga cttctggcct tccagtttct gcacagacag ccttggcaga 120
acaacagcca aaaagcatga aaagcccagc ttctccagag cctggtttct gtgctactct 180
ttgccctatg gtagaaattc cacctaagga tataatggca gaattggagt cagaggatat 240
cttgatccct gaagaatctg taattcagga ggaaattgca gaagaggtag agactagtat 300
ctgtgaatgc caggatgaaa atcataagac aatacctgaa ttttctgagg aggctgaaag 360
tctaaccaat tctcatgaag aaccccaaat agcacctcct gaagataact tggatccctg 420
tggtatgatg aatgatgttt tagaaacttt gcctcatatt gaagttaaga tagaagggaa 480
gtcagaatca ccccaggaag aaatgacagt tgttatcgat cagttagaag tctgtgactc 540
tcttattcct tccacttcat ctatgactca tgtcag 576

```

&lt;210&gt; 287

&lt;211&gt; 514

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 287

```

gaattcggca cgaggcagag aggtttgcc aagagcgag gctgagaata tggagagact 60
atgtggctcc cacagctaat ttggacaaa aggacaagca gtttgttgcc aaggtgatgc 120
aggttctgaa tgctgatgcc attgttgtga agctgaactc aggcgattac aagacgattc 180
acctgtccag catccgacca ccgaggctgg agggggagaa caccaggat aagaacaaga 240

```

103

aactgcgtcc cctgtatgac attccttaca tgtttgaggc ccgggaattt cttcgaaaa 300  
agcttattgg gaagaagggtc aatgtgacgg tggactacat tagaccagcc agcccagcca 360  
cagagacagt gcctgccttt tcagagcgta cctgtgccac tgtcaccatt ggaggaataa 420  
acattgctga ggctcttgtc agcaaagggtc tagccacagt gatcagatac cggcaggatg 480  
atgaccagag atcatcacac tacgatgaac tgct 514

&lt;210&gt; 288

&lt;211&gt; 456

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 288

gaattcggca cgagggggcg ggcaggcggg caggccggca ggcgggtgctg cggagggctg 60  
gtgccccgca gcagggtgggc ggggtgctgg tggcgccggc ggctgggccc ggggctgccc 120  
gctgctgctc ggccgtgctc ggcggccgtg cgggcacgcc atggacttca acatgaagaa 180  
gctggcgtcg gacgcgggca tcttcttcac ccgggctgtg cagttcacgg aggagaaatt 240  
tggccaggct gagaagactg agcttgatgc ccactttgaa aaccttctgg cccgggcaga 300  
cagcaccaag aactggacag agaagatctt gaggcagaca gaggtgctgc tgcagcccaa 360  
ccccagtgc cgagtggagg agttcctgta tgagaagctg gacaggaagg tcccccaag 420  
ggtcaccaac ggggagctgc tggctcagta catggc 456

&lt;210&gt; 289

&lt;211&gt; 262

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 289

gaattcggca cgaggcagaa gcccctagct cctctgagcc tcatggggcc agaggaagca 60  
gtagttcggg cggaagaaa tgctacaagc tggagaatga gaagctgttc gaagagttcc 120  
ttgaactttg taagatgcag acagcagacc accctgaggt ggtccattc ctctataacc 180  
ggcagcaacg tgccactct ctgtttttgg cctcggcgga gttctgcaac atcctctcta 240  
gggtcctgtc tcggggcccg ac 262

&lt;210&gt; 290

&lt;211&gt; 205

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 290

gaattcggca cgaggattta tgggccaactg cacatgcccg ctgcagccct gggatcagct 60  
ggaagctgcc tgtcatctcc tgcccaatcc ccagaaaccc tgattcaggt ctgcaggctc 120  
ctgccccgctc accaggctgc tggctccggt accatgtaaa cctaggaagg taaaggagca 180  
ggcaacctcc tcgtggcctg tgtgt 205

&lt;210&gt; 291

&lt;211&gt; 483

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 291

gaattcggca cgaggcctgg ccgggaccgt gtgggcccgtg aggatgagga cggctgggag 60  
acgcgagggg accgcaaggc ccggaagccc ctggtggaga agaagcggcg cgcgcggatc 120  
aacgagagcc tgcaggagct gcggctgctg ctggcgggag ccgaggtgca ggccaagctg 180  
gagaacgccg aagtgtgga gctgacggtg cggcgggtcc aggggtgtgt gcggggccgg 240  
gcgcgcgagc gcgagcagct gcaggcggaa gcgagcgaac gcttcgctgc cggctacatc 300  
cagtgcagtc acgaggtgca cacgttcgtg tccacgtgcc aggccatcga cgctaccgtt 360  
ctgccgagct cctgaaccat ctgctcagat ccatgccgct gcgtgagggc agcaacttca 420  
ggatctgtg ggggacgccc tgcggggcca cctaaatccc ctggacggaa tggctggctg 480  
cgg 483

104

<210> 292  
 <211> 562  
 <212> DNA  
 <213> Homo sapiens

<400> 292  
 gaattcggca cgagggcgct gcgggttagga gccgggttgc gggagacccc aggttcggtt 60  
 gggattccca gccagaacgg agcttaagcc gggcaggcga gcgaatgacg gaggtagcgag 120  
 ctgcacggcg gcgtgctgcg ctgttgagga cgctgtcccc cgcgctccca ggccgccccg 180  
 aggcttgggg tcttcgaagg ataatcggcg cccggggccg aacagcgggg gcacacgggg 240  
 cgctgccgaa gtgcaaggcc acggccagag ctcgagcccc acgcgctgtc tggagtcgta 300  
 ggttgccgcc gtttggggtc ggggtctgag gcttgggcgc tgcctgggcc gagcggagat 360  
 cggggtttgc ctcccgtccc cgctcaggac cctgacgtgg ctgaagcggc cccgggagca 420  
 tgagcggcag cgcgtggacg tcaaggtggt gatgctgggc aaggagtacg tgggcaagac 480  
 tagcctgggt gagcgctacg tgcacgaccg ctttctgggt gggccttacc agaaccacat 540  
 cggggccgcc ttcgtggcca ag 562

<210> 293  
 <211> 645  
 <212> DNA  
 <213> Homo sapiens

<400> 293  
 gaattcggca cgaggctgag agagagcaca gcctgggtggg ttctggggtc tacggcctag 60  
 gggccgggga agtttgcgcc gccgcgacca gtgctgcgat cccgagccgg gctccagccc 120  
 cgaggaccag gggctgggag ggctgccta cggaaccccc cgggcccagca gcagtcgtct 180  
 cgcgctcctc tgcttgaaaa agtgtttaag cttctaaaaa gtcactctac aagcacctgg 240  
 tttatgcagt tattcgttcc ttacgggaac aaagtcagat ggacacttac acctcggatg 300  
 aacaagaaaag tttggaagtt gcaattcagt gcttggagac agtttttaag atcagcccag 360  
 aagatacaca cctagcagtt tcacagcctt tgacagaaat gtttaccagt tccttctgta 420  
 agaatgacgt tctgccccct tcaaaactcag tgctgaaga tgtgggaaaa gctgaccaat 480  
 tacaagatga aggaattac cacatgagag aagaaatta tgcgtgagaa gtaggttgg 540  
 acacacaggg aatagaattg gatcccaata atgcagttta ctattgcaac agggctgctg 600  
 ctcagagcaa attaggtcac tacacagatg cgataaagga ttgtg 645

<210> 294  
 <211> 521  
 <212> DNA  
 <213> Homo sapiens

<400> 294  
 ctgagcgtct ctgcttagcc gcggtcatga gccggcacag ccggctgcag aggcaggttc 60  
 tgagcctgta ccgcgatctg ctgcgcgccg ggcgtgggaa gccgggcgcc gaggcgcgag 120  
 tgcgggcaga gttccggcag catgcgggcc tgccgcggtc cgacgtgctg cgcacgagt 180  
 acctgtaccg ccgcggggcg cgcagctgc agctgctacg ctccggccac gccaccgcca 240  
 tgggcgcctt cgtacgcccg cgggccccga ccggggagcc tggcggcgctg ggttcccagc 300  
 ctgacgacgg cgacagtcca aggaaccccc acgacagcac gggggcaccg gagaccgcgc 360  
 ccgacgggac gtgacaggcg aagagccgaa ctgcctcgat ggcgtggttg agccaggagg 420  
 ctgcctgac tgcatggggg gactggggaa cccgcctaag gtgagaggtc ttaagagact 480  
 agcttgacga attggggatg tcagagactc ctccctggcg a 521

<210> 295  
 <211> 375  
 <212> DNA  
 <213> Homo sapiens

<400> 295  
 gaattcggca cgaggagaac atgcagtcta ggaaccggca tgcgcataac ctcaggatat 60

## 105

```

aaataatgct gaagcagagt tacgtttttt ttgtttgtgt tttttttgtt tttgtttttt 120
taggtttccg tgtgtttcta ttgagctgct cagtgcccg cttagaagac caggaaaagg 180
agtcacaggt cgtatgctgg aggcttgagc cgcggcaccg tggcgcggt cgcctcgctg 240
cggttggtgg tggcggtgga cattgcagcg cggctggagg gggtccttag acaagggtgca 300
agacaaacag aagagggcac gtgggggtcaa actcctactg cctgcctgat tttctgccac 360
aggacaaatt cacca                                     375

```

&lt;210&gt; 296

&lt;211&gt; 628

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 296

```

gaattcggca cgaggaaaat ggttcgctat tcacttgacc cggagaaccc cacgaaatca 60
tgcaaatcaa gaggttccaa tcttcgtgtt cactttaaga acactcgtga aactgctcag 120
gccatcaagg gtatgcatat acgaaaagcc acgaagtatc tgaaagatgt cactttacag 180
aaacagtgtg taccattccg acgttacaat ggtggagtgt gcagggtgtc gcaggccaag 240
caatggggct ggacacaagg tcggtggccc aaaaagagtgt ctgaattttt gctgcacatg 300
cttaaaaaacg cagagagtaa tgctgaactt aagggttttag atgtagattc tctggtcatt 360
gagcatatcc aagtgaacaa agcacctaag atgcgcgcgc ggacctacag agctcatggt 420
cggattaacc catacatgag ctctccctgc cacattgaga tgatccttac ggaaaaggaa 480
cagattgttc ctaaacacaga agaggaggtt gccagaaga aaaagatatc ccagaagaaa 540
ctgaagaaac caaaacttat ggcacgggag taaattctca ttaaaataaa tgtaattaaa 600
aggaaaaaaa aaaaaaaaaa aactcgag                                     628

```

&lt;210&gt; 297

&lt;211&gt; 645

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 297

```

gaattcggca cgaggagaaa acgaagcagc gttggaaaat ggaattaaaa atgaggaaaa 60
cgcagtcacg ggtgctgaat attctgagaa cgtgatgat ccacacacag ctacacgtga 120
aaacgcagat ggtcaaaagt atgagaacaa ggacgactat acaatcccag atgagtatag 180
aattggacca tatcagccca atgttcctgt tggatagac tatgtgatac ctaaaacagg 240
gttttactgt aagctgtggt cactctttta taaaaatgaa gaagttgcaa agaatactca 300
ttgcagcagc cttcctcatt atcagaaatt aaagaaattt ctgaataaat tggcagaaga 360
acgcagacag aagaaggaaa cttaagatgt gcaaggagat ttaatgattt caaagaaaaat 420
aatggttctt tgtttttaat gttaaccttt tttaaataca atactgatag ttagaagaaa 480
actattgtac tcttttgttt tagtggagaa ataatagatg tctgttcatt tgtaagtgt 540
tatagcaaaa aaaatacaca tatggttaag ttaatgaata gtttttgttt tatcagaatg 600
gcaacagaca gaagtacttt gtagagattg acttcctaag ctctt                                     645

```

&lt;210&gt; 298

&lt;211&gt; 625

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 298

```

gaattcggca cgaggggatt cagcagcctc ccccttgagc cccctcgctt cccgacgttc 60
cgttcccccc tgcccgccct ctcccgccac cgcgcgcgcc gccttcgcga ggcggtttcc 120
accgagggaaa aggaatcgta tcgtatgtcc gctatccaga acctccactc tttcgacccc 180
tttgctgatg caagtaaggg tgatgacctg cttcctgctg gcaactgagga ttatatccat 240
ataagaattc aacagagaaa cggcagggaag acccttacta ctgtccaagg gatcgctgat 300
gattacgata aaaagaaact agtgaaggcg ttttaagaaa agtttgcttg caatgggtact 360
gtaattgagc atccggaata tggagaagta attcagctac agggtgacca acgcaagaac 420
atatgccagt tcctcgtaga gattggactg gctaaggacg atcagctgaa ggttcattgg 480
ttttaagtgc ttgtggctca ctgaagctta agtgaggatt tccttgcaat gtagtagaatt 540
tcccttctct tccttgctac aggttttaaaa acctcacagc ttgtataatg taaccatttg 600

```

106

gggtccgctt ttaacttgga ctagt

625

&lt;210&gt; 299

&lt;211&gt; 545

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 299

```

gaattcggca cgaggagacc caggaggtca aggtacagt gagccgtgat catgccactg 60
cactccagcc tgggtgacag agcgagaccc tgtctcttaa caacaaaacc catgagcggc 120
agccccccag tcctggatgg tggtaaagaa tcctcaagat caaaccacag cagtgtgag 180
agcttgacct gattctaggg ctggggctgg agaaactgct agagatgatg ccgatagcca 240
gtgtgatccc cctgccctga tggtaaggag cagagtgcag actggaaccc tccccctccc 300
aaagattcag acctgtgggg ctgagtgggc tcatagtgtc ccaagtcct gagaggctgg 360
tgtctggctt cagcctccag cttctcaggt tctgatgcag tcagctgagt tccctgccta 420
ttcttgcaag cactaggagg aagggtgggt ggttgctggg aacagcacg agcgccctcc 480
ccaccagat tcacagagca cactccccg ggggatactt taatccggag gccgtgacgc 540
ctgct

```

545

&lt;210&gt; 300

&lt;211&gt; 605

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 300

```

gaattgggca cgaggcgggc cgcagctttt cggttcacag cgggcaggga aagccgcggg 60
aagggtactc caggcgagag gcggacgcga gtcgtcgtgg caggaaaagt gactagctcc 120
ccttcgttgt cagccaggga cgagaacaca gccacgctcc caccggctg ccaacgatcc 180
ctcggcggcg atgtcggccg ccggtgcccg aggcctgcgg gccacctacc accggctcct 240
cgataaagtg gagctgatgc tgcccgagaa attgaggccg ttgtacaacc atccagcagg 300
tcccagaaca gtttttttct gggctccaat tatgaaatgg gggttggtgt gtgctggatt 360
ggctgatatg gccagacctg cagaaaaact tagcacagct caatctgctg ttttgatggc 420
tgctgttaat ttctttgtgg gggcagcagg agcctctcag ctttttcgta ttggagata 480
taaccaagac taaaagctaa agcacacaaa taaaagagtt ctgatcacct gaacaatcta 600
gatgt

```

605

&lt;210&gt; 301

&lt;211&gt; 364

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 301

```

gaattcggca cgaggcgcac acgagaacat gcctctcgca aaggatctcc ttcattccctc 60
tccagaagag gagaagagga aacacaagaa gaaacgcctg gtgcagagcc ccaattccta 120
cttcatggat gtgaaatgcc caggatgcta taaaatcacc acggtcttta gccatgcaca 180
aacggtagtt ttgtgtgttg gctgctccac tgtcctctgc cagcctacag gaggaaaagc 240
aaggcttaca gaaggatggt ccttcaggag gaagcagcac taaaagcact ctgagtcaag 300
atgagtggga aaccatctca ataaacacat tttggataaa aaaaaaaaaa aaaaaaaact 360
cgag

```

364

&lt;210&gt; 302

&lt;211&gt; 545

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 302

```

gaattccggc acgaggggac ccagagagc cctgagcagc cccaccgccc ccgcccgcct 60
agttaccatc acaccccgga aggagccgca gctgccgcag ccggcccccag tcaccatcac 120

```

107

cgcaaccatg agcagcgagg ccgagaccca gcagccgccc gccgcccccc ccgcccggcc 180  
 cgccctcagc gccgcccaga ccaagcccgg cactacgggc agcggcgagc ggagcggtgg 240  
 cccgggcccgc ctcacatcgg cggcgccctgc cggcgggggac aagaagggtca tcgcaacgaa 300  
 ggttttggga acagtaaaat ggttcaatgt aaggaacgga tatggtttca tcaacaggaa 360  
 tgacaccaag gaagatgtat ttgtacacca gactgccata aagaagaata accccaggaa 420  
 gtaccttcgc agtgtaggag atggagagac tgtggagttt gatgttggtg aaggagaaaa 480  
 ggggtgaggag gcagcaaatg ttacagggtcc tgggtggtgtt ccagttcaag gcagtaataa 540  
 tgacag 545

<210> 303  
 <211> 506  
 <212> DNA  
 <213> Homo sapiens

<400> 303  
 gaattcggca cgaggctggt cactccgcca ccgtagaatc gcctaccatt tgggtcaagc 60  
 aaaaagcaat cagcaattgg acaggaaaag aatggcattg aagcagattt ccagcaacaa 120  
 gtgctttggg ggattgcaga aagtttttga acatgacagt gttgaactaa actgcaaaat 180  
 gaaatttgct gtctacttac caccaaaggc agaaacagga aagtgccctg cactgtattg 240  
 gctctcaggt ttaacttgca cagagcaaaa ttttatatca aaatctggtt atcatcagtc 300  
 tgcttcagaa catggtcttg ttgtcattgc tccagatacc agccctcgtg gctgcaatat 360  
 taaagtgaa gatgagagct gggactttgg cactggtgct ggattttatg ttgatgccac 420  
 tgaagatcct tggaaaacca actacagaat gtactcttat gtcacagagg agcttcccca 480  
 actcataaat gcccaattttc cagtgg 506

<210> 304  
 <211> 485  
 <212> DNA  
 <213> Homo sapiens

<400> 304  
 gaattcggca cgaggaggtt gtgggcccag gagccctgcg gctgccggca ggtgaactga 60  
 gctgcccaga gctgcccaga gctgcccaga gctgcccaga gctgcccaga gctgcccaga 120  
 gcatagcctg catagtgtcc tggcgctggg agttccccgt ggacagagcc agagggcagt 180  
 ggcgtccctc gtcagagctg gatcaggccc cccatcgagg agggagggca gacggaggcc 240  
 cgagagcctc cccaggcctc ttcgtgggaa ggccccagta ccactcgtag gaggtctcag 300  
 ctctggcatg gctgcccagg atgtggccga gggggcttca ccctgtgtcc ttaggagggg 360  
 gtggccttga ggcaagagcc gtgcctcact gacccccagg ggccctcatc tccccatgga 420  
 atgggctgta tgtcctgccc caacttgccc cgcagcaggc cagaccccccc tccccccgcc 480  
 cagag 485

<210> 305  
 <211> 615  
 <212> DNA  
 <213> Homo sapiens

<400> 305  
 gaattcggca cgaggcttac aaggaaaatg ctgacttatg accggcgctc tgagcctcag 60  
 gttggggagc gagtgccata cgtcatcatt tatgggaccc ccggagtacc acttatccag 120  
 cttgtaaggc gccagtgga agtctgcag gacccaactc tgagactgaa tgctacttac 180  
 tatattacca agcaaatcct tccacccttg gcaagaatct tctcacttat tggatttgat 240  
 gtcttcagct ggtatcatga attaccaagg atccataaag ctaccagctc ctgcggaagt 300  
 gaacctgaag ggcggaagg cactatttca caatatttta ctaccttaca ctgtcctgtg 360  
 tgtgatgacc taactcagca tggcatctgt agtaaatgac ggagccaacc tcagcatgtt 420  
 gcagtcaccc tcaaccaaga aatccgggag ttggaacgtc aacaggagca acttgtaaaag 480  
 atatgcaaga actgtacagg ttgctttgat cgacacatcc catgtgtttc tctgaactgc 540  
 ccagtacttt tcaaatcttt ccgagtaaat agagaattgt ccaaggcacc atatcttcgg 600  
 cagttattaa accag 615

108

<210> 306  
 <211> 504  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(504)  
 <223> n = A,T,C or G

<400> 306  
 gaattcggca cnaggccaaa acctgtttgg gaagcatatt acagaaatga tttcaagtac 60  
 cctgtattct ggatgctaaa aaacaaaaac aaacaaaaaa acaaaaacaa aaaaacaaaa 120  
 ccagaatcag gtaaacacagc tatgtgatta aaatatttta attcttcagc aattacccgg 180  
 ttttctaaat tgaatcatgc atctatttat aattctaatt attttgtaaa agaagacaaa 240  
 attatgaatc ttaagtattt gctccatctt tttctctgta atggtggaga ggctgcccac 300  
 aattcatctc cacatggagc caagtttaat gtttctagtt cacattttgt acttctgtca 360  
 tgcttatttc aaactccctg agtgatgggt aagaaatcaa acattgcctc agtgggtatca 420  
 agagaacttt ggtggtggtt tcttcagaat catgaagttc ttttgcaga taaatatttt 480  
 gatattattt tcctttttta tata 504

<210> 307  
 <211> 449  
 <212> DNA  
 <213> Homo sapiens

<400> 307  
 gaattcggca cgagggttaa accctgcgtg gcaatccctg acgcaccgcc gtgatgccca 60  
 gggaagacag ggcgacctgg aagtccaact acttccttaa gatcatccaa ctattggatg 120  
 attatccgaa atgtttcatt gtgggagcag acaatgtggg ctccaagcag atgcagcaga 180  
 tccgatgctc ccttcgoggg aaggctgtgg tgctgatggg caagaacacc atgatgcgca 240  
 aggccatccg agggcacctg gaaaacaacc cagctctgga gaaactgctg cctcatatcc 300  
 tggccaataa ggtgccagct gctgccgtgc tgggtgccatt gcccacatgtg aagtcactgt 360  
 gccagcccag aacactggtc tcgggcccg 449

<210> 308  
 <211> 524  
 <212> DNA  
 <213> Homo sapiens

<400> 308  
 gaattcggca cgagggttga ttatggcaag aagtccaagc tggagttctc catttaccca 60  
 gcaccccagc tttccacagc tgtagttgag ccctacaact ccctcctcac caccacacc 120  
 accctggagc actctgattg tgcttcatg gtagacaatg aggccatcta tgacatctgt 180  
 cgtagaaacc tcgatatcga gcgccaacc tacactaacc ttaaccgcct tattagccag 240  
 attgtgtcct ccatcactgc ttccctgaga tttgatggag ccctgaatgt tgacctgaca 300  
 gaattccaga ccaacctggt gccctacccc cgcctccact tccctctggc cacatatgcc 360  
 cctgtcatct ctgctgagaa agcctaccat gaacagcttt ctgtagcaga gatcaccaat 420  
 gcttgctttg agccagccaa ccagatggtg aaatgtgacc ctgcgcatgg taaatacatg 480  
 gcttgctgcc tgttgatccg tggtagcgtg gttcccaaag atgt 524

<210> 309  
 <211> 524  
 <212> DNA  
 <213> Homo sapiens

<400> 309  
 gaattcggca cgagggttgc tcaactgagt cctactttta tgcctgcct gtggtgagca 60

109

```

caaatgttga gcacatcaat ccccatTTTT tagacgaaga gacagagttg agtgacttgc 120
ccaaagacac agggccagtg aggagttgtg caggtttgcc ctggcattaa aataataaac 180
attgaaattc agtcgattcc cctatggact cagttataga tctcatcagt tgaaggaaga 240
gagatgcctt ttcctattca gcctTTTTgc aatccttcca tctagaggag atgtatctta 300
taatatcctc aaaggcactc tgttgctaag agcagccttg atgaggtccc atatagctca 360
ttggaagcag agctagtctt ggaaactgaa aatgttggac cagagtctgc ccattccttt 420
agctctgggt ccagctgtgg tctgggggtg aatggagtct gaccttgcc cacaagggc 480
ctgtctgttc tcattgtggc catccacatc ctggagctgc tcat 524

```

&lt;210&gt; 310

&lt;211&gt; 524

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 310

```

gaattcggca cgaggggaga ctacaaggat agggccagga gtaatggagt ccaaagagaa 60
acgagcagta aacagtctca gcatggaaaa tgccaaccaa gaaatgaag aaaaggagca 120
agttgctaag aaaggggagc ccttggccct ccctttggat gctggtgaat actgtgtgcc 180
tagaggaaat cgtaggcggg tccgcgttag gcagccatc ctgcagtata gatgggatat 240
gatgcatagg cttggagaaac cacaggcaag gatgagagaa gagaatatgg aaaggattgg 300
ggaggagggt agacagctga tggaaaagct gagggaaaag cagttgagtc atagtctgcg 360
ggcagtcagc actgaccccc ctccaccatga ccatcatgat gagttttgcc ttatgccctg 420
aatcctgatg gtttccctaa agttattacg gaaacagacc cctgctttcg aatttacatg 480
ttcatgatgt gcccttgttg taaaccttta cctgtcactt gttt 524

```

&lt;210&gt; 311

&lt;211&gt; 523

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 311

```

gaattcggca cgaggcctcg tgccgtgcc cccgaggat gcgggggtcac tcgctgctcg 60
cccggtctct cactggccga ggtgccacc ccgcagcatt ctgggagtgg tagttttctt 180
ccttcagggt cattcctggc tggccagtgc ccaagactgg cgagactacg attcccagac 240
gcccaagcga gtgcgcggtc acgtggcgc aaggacgctg ggccggtggg cgggggccgg 300
caggtgctcc gcagccgtct gtgccacca gagccggcgg gccgctaggt ccccgagac 360
cctgctatgg tgccgtgccc cgcgtgggg gctcatctcc ccgcgtccg cttggatata 420
ttcggggacc tgaagaagat gaacaagcgc cagctctatt accaggtttt aaacttcgcc 480
atgatcgtgt cttctgcact catgatatgg aaaggcttga tcg 523

```

&lt;210&gt; 312

&lt;211&gt; 524

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 312

```

gaattcggca cgagggtgaa ggtgtgtgtc agcttttgcg tcaactcgagc cctgggcgct 60
gcttgctaaa gagccgagca cgcgggtctg tcatcatgtc gcgttacggg cggtacggag 120
gagaaaccaa ggtgtatgtt ggtaacctgg gaactggcgc tggcaaagga gagttagaaa 180
gggctttcag ttattatggt cttttaagaa ctgtatggat tgcgagaaat cctccaggat 240
ttgcctttgt ggaattcgaa gatcctagag atgcagaaga tgcagtacga ggactggatg 300
gaaaggtgat ttgtggctcc cgagtggagg ttgaactatc gacagggcatg cctcggagat 360
cacgttttga tagaccacct gccgacgtc cctttgatcc aaatgataga tgctatgagt 420
gtggcgaaaa gggacattat gcttatgatt gtcacgttta cagccggcga agaagaagca 480
ggtcacggtc tagatcacat tctcgatcca gaggaaggcg atac 524

```

&lt;210&gt; 313

&lt;211&gt; 523



110

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 313

```

gaattcggca cgaggggtaa caccagaata tttggcaag ggagaaaaa aaagcagcga 60
ggcttcgcct tccccctctc cctttttttt tcctcctctt ccttcctcct ccagccgccc 120
ccgaatcatg tcgatgagtc caaagcacac gactccgttc tcagtgtctg acatcttgag 180
tccccctggag gaaagctaca agaaagtggg catggagggc ggcggcctcg gggctccgct 240
ggcggcgctac aggcagggcc aggcggcacc gccaacagcg gccatgcagc agcacgccgt 300
ggggcaccac ggcgcctgca ccgcgccta ccacatgacg gcggcggggg tgccccagct 360
ctcgactctc gccgtggggg gctactgcaa cggcaacctg ggcaacatga gcgagctgcc 420
gccgtaccag gacacatga ggaacagcgc ctctggcccc ggatggtacg gcgccaaccc 480
agaccgcgcg tccccgcca gttctttttc ttcaggatca ggc 523

```

&lt;210&gt; 314

&lt;211&gt; 525

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 314

```

gaattcggca cgaggggaaa ccagagatag agggaaagcc agagagtga ggagagccag 60
ggagtgaaac aagggctgca ggaaagcgc cagctgagga tgatgtacc aggaaagcca 120
aaagaaaaac taataagggg ctggctcatt acctcaagga gtataaagag gccatacatg 180
atatgaattt cagcaatgag gacatgataa gagaatttga caatatggct aaggtgcagg 240
atgagaagag aaaaagcaaa cagaaattgg ggcgttttt gtggatgcaa agaaatttac 300
aggacccctt ctaccctaga ggtccaaggg aattcagggg tggctgcagg gccccacgaa 360
gggacattga agacattcct tatgtgtagt gtccctggca ggcatttacc aggccatgtg 420
ctttaacgtt cggtaatact ttacttttag catccctcct gttgctagca gccttttgac 480
ctatctgcaa tgcagtgttc tcagtaggaa atgttcatct gttac 525

```

&lt;210&gt; 315

&lt;211&gt; 358

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 315

```

gaattcggca cgaggggggtg gtggagcgtt ggcggccag gctccctggc tggccggttt 60
gggcgtctgg gccgtgaagg tgggacctcc tgttcgggc cgcaagtttc cctctccagc 120
cgcccgcctg tcgtagcatg tccccagaa ctcggggagc gcaggcagga caggcttaga 180
gaagacgcgg tccccagcgc ttgggccacg gacgtccac cccgctcctc tgtcgtgga 240
gaaccgcggg gccgagccac tgggagaagc aggccagagc cttccagggc ctccggcccg 300
tggaccggag gaggatgagc tggctttttc ccctgaccaa gagcgccctc tcctccgc 358

```

&lt;210&gt; 316

&lt;211&gt; 420

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 316

```

gaattcggca cgaggcgttc cttcgcacac tgtgattttg ccctcctgcc cagcagacc 60
tgacgcgggc aaagagctcc cgaggaaagca cagcttgggt caggttcttg cctttcttaa 120
tttttagggac agctaccgga aggaggggaa caaggagttc tcttcgcag cccctttccc 180
cagcccccac ccagctctcc agggaccctt gcctgcctcc taggctggaa gccatggtcc 240
cgaagtgtag ggcaagggtg cctcaggacc ttttggcttt cagcctccct cagcccccag 300
gatctgggtt aggtggcgtt cctcctgctc ctcatgggaa gatgtctcag agccttcatt 360
acctcccctc cccaacccaa tgccaaagtg gacttgggag ctgcacaaag tcagcaggga 420

```

&lt;210&gt; 317

&lt;211&gt; 518

111

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 317

```

gaattcggca cgaggggtgc cggaggggtcg ttttaaaggg cccgcgcgtt gccgccccct 60
cggcccccca tgctgctatc cgtgccgctg ctgctcggcc tcctcggcct ggccgtcgcc 120
gagcctgccg tctacttcaa ggagcagttt ctggacggag acgggtggac ttcccgttg 180
atcgaatcca aacacaagtc agattttggc aaattcgttc tcagttcccg caagttctac 240
ggtgacgagg agaaagataa aggtttgcag acaagccagg atgcacgctt ttatgctctg 300
tcggccagtt tcgagccttt cagcaacaaa ggccagacgc tgggtggtgca gttcacggtg 360
aaacatgagc agaacatcga ctgtgggggc ggctatgtga agctgtttcc taatagtttg 420
gaccagacag acatgcacgg agactcagaa tacaacatca tgtttgggtcc cgacatctgt 480
ggcctgcacc aaaaagggtc atgtcatctt caactaca                    518

```

&lt;210&gt; 318

&lt;211&gt; 401

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(401)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 318

```

aacaccaagg tggacaagag agttgagtcc aaatatggtc ccccatgccc atcatgcccc 60
gcacctgagt tcctgggggg accatcagtc ttcctgttcc ccccaaaacc caaggacact 120
ctcatgatct cccggacccc tgaggtcacg tgcgtggtgg tggacgtgag ccaggaagac 180
cccgaggtcc agttcaactg gtacgtggat ggcgtaggag tgcataatgc caagacaaag 240
ccgcgggagg agcagttcaa cagcacgtac cgtgtgggtc gcgtcctcac cgtcctgcac 300
caggactggc tgaacggcaa ggagtacaag tgcaagggtc ccaacaaagg cctcccgccc 360

```

&lt;210&gt; 319

&lt;211&gt; 401

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 319

```

accgtgtact attagccatg gtcaacccca ccgtgttctt cgacattgcc gtcgacggcg 60
agcccttggg ccgcgtctcc tttgagctgt ttgcagacaa ggtcccaaag acagcagaaa 120
attttcgtgc tctgagcact ggagagaaag gatttgggta taagggttcc tgcttcaca 180
gaattattcc agggtttatg tgtcagggtg gtgacttcac acgccataat ggcactggtg 240
gcaagtccat ctatggggag aaatttgaag atgagaactt catcctaag catacgggtc 300
ctgcatcttg tccatggcaa atgctggacc caacacaaat ggttccagc ttttcatctg 360
cactgccaag actgagtggt tggatggcaa gcatgtggtg t                    401

```

&lt;210&gt; 320

&lt;211&gt; 471

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 320

```

tagagtccca caaaccttg gcatgcctta atgtttgaga attcattct atttctcatt 60
aatctcttga aagcaaagat atttataaa tctttttgga ccagtgtttt agatggtagt 120
ggctgtggca gtgactttta attagccatc ctgaacccat catttaaaat atttattttt 180
gctttcagaa attttgaaat aagtaaggga aaaaaccaa ttatttacag atacacataa 240
ccaacccaaa ataaaagcaa aataactaat taggcacaca gaaagactaa aagtaaattc 300

```

112

actaggaaag acactcctca aagatagaat gttaaattttg tgaatccaga gtgtcctaaac 360  
 cagaataacg cttgtcctta taccctaaag gacttgccaa gaaagataaa aagtatttta 420  
 ttatcccaga aagaatgcaa ggtcttcat ttcagttggc ttataacacc a 471

<210> 321  
 <211> 471  
 <212> DNA  
 <213> Homo sapiens

<400> 321  
 attactcaac agatttggac acaacggaaa gacaacagtt gatatttcta cttggtgtga 60  
 gcagtttgca actttttgtt cagagcaact ggacggggcc ccctgttgac ttacaccctc 120  
 aggacttttt gtcactgtt ttgttcagc aattcagtg ggtaaagga ctggatgcat 180  
 ttgttctgag cctgctcact ctatggtgtg aatcaatcta cagcctgacc tcgaagccta 240  
 tactactgtt attagcacgc attatcctag tgaatgtaag acataaactg acagctattc 300  
 agagcttgcc atggtggact ttgagatgtg tgaatattca tcagcatttg cttgaggaac 360  
 gctcacctct gctttttact cttgcccgaact actgtattga tcaagtgatg aaactacaga 420  
 atctgtttgt agatgattca ggtcgatatt tggctattca attccatctg g 471

<210> 322  
 <211> 601  
 <212> DNA  
 <213> Homo sapiens

<400> 322  
 tgaaggagca gttgccgcg ttggcggcg cccgagcagt tttcgtgct gctacggctg 60  
 ttgccatgag gogaggctag ggaggacctc acttccccgg ggtgtaataa tgtaactga 120  
 ggccagtcta tccatatggg gatggggaag ccttggcatt gtcctttttc tgataacctt 180  
 tggacccttt gtaatatttt atttgacatt ttatatctc tgctttgttg gtgggggttt 240  
 agtggttact ctcctgtttg gaaaaacaaa ctcagagaag tacctagaac agtgtgaaca 300  
 ctcatttctt cctccaacat cacctggggt tcctaagtgc ttagaagaaa tgaaacggga 360  
 agccaggact attaagattg atagaagatt gacgggtgcc aatataattg atgaacctct 420  
 agcgaaggtc atccagtttt ccttgggga ttctgtccag tttgtgatt atacactaag 480  
 cgatgatgaa tcttttcttc ttgaaattag gcagactctt caaacgcac tcattcagtt 540  
 tgctactagg tcaaaagaaa tagactggca acctatttt actacacgca ttgtagatga 600  
 c 601

<210> 323  
 <211> 601  
 <212> DNA  
 <213> Homo sapiens

<400> 323  
 gatgaggtag cagaggctca acgggcagag tttagccctg cccagttctc tggccttaag 60  
 aagatcaacc tgaaccactt gttgaatttc acttttgaa cccgtggcca gacgggtcac 120  
 tttgaaggca gtggacatgg tagctgggga aagaggaaca agtggggaca taagcctttt 180  
 aacaaggaac tctttttaca ggccaactgc caatttgtg tgtctgaaga ccaagactac 240  
 acagctcatt ttgctgatcc tgatacatga gtttaactgg actttgtgga acaagtgcgc 300  
 atttgtagcc atgaagtgcc atcttgccc atatgcctct atccacctac tgcagccaag 360  
 ataaccggtt gtggacacat cttctgctgg gcatgcatcc tgcactatct ttcactgagt 420  
 gagaagacgt ggagtaaatg tccatctgtg tacagttctg tgcataagaa ggatctcaag 480  
 agtggtgttg ccacagagtc acatcagtat gttgttggg ataccattac gatgcagctg 540  
 atgaagaagg agaaaggggt ggtggtggct ttgcccgaat ccaaatggat gaatgtagac 600  
 c 601

<210> 324  
 <211> 461  
 <212> DNA  
 <213> Homo sapiens

113

&lt;400&gt; 324

```

catctttcttc ctttcgcggg gtcctccgta gttctggcac gagccaggcg tactgacagg 60
tggaccagcg gactggtgga gatggcgacg ctctctctga ccgtgaattc aggagaccct 120
ccgctaggag ctttctgggc agtagaacac gtgaaagacg atgtcagcat ttccgttgaa 180
gaagggaag agaatttct tcatgtttct gaaaatgtga tattcacaga tgtgaattct 240
atacttcgct acttggctag agttgcaact acagctgggt tatatggctc taatctgatg 300
gaacatactg agattgatca cttggttgga gttcagtgtc acaaaattat cttcatgtga 360
ttcctttact tctacaatta atgaactcaa tcattgcctg tctctgagaa catacttagt 420
tggaaactcc ttgagtttag cagatttatg tgtttgggcc a 461

```

&lt;210&gt; 325

&lt;211&gt; 461

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 325

```

tcacttttga accccgtggc cagacgggtc actttgaagg cagtggacat ggtagctggg 60
gaaagaggaa caagtgggga cataagcctt ttaacaagga actcttttta caggccaact 120
gccaatattg ggtgtctgaa gaccaagact acacagctca ttttctgat cctgatacat 180
tagtttaactg ggactttgtg gaacaagtgc gcattttag ccatgaagtg ccatcttgcc 240
caatatgcct ctatccacct actgcagcca agataaccg ttgtggacac atcttctgct 300
gggcatgcat cctgcactat ctttctactg gtgagaagac gtggagtaaa tgtcccatct 360
gttacagttc tgtgcataag aaggatctca agagtgtgt tgccacagag tcacatcagt 420
atgttgttgg tgataccatt acgatgcagc tgatgaagaa g 461

```

&lt;210&gt; 326

&lt;211&gt; 451

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

<221> ~~catctttcttc~~

&lt;222&gt; (1)... (451)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 326

```

ctgtggaggc cagttctgga gctattgcag cctcggttgc ccggccgggg acccgagccg 60
aaaagtattc gtcagaatgt cgggcaaaga ccgaattgaa atctttccct cgcgaatggc 120
acagaccatc atgaangctc gtttaaaggg agcacagaca ggtcgaaacc tcctgaagaa 180
aaaatctgat gccttaactc ttcgatttgc acagatccta aagaagataa tagagactaa 240
aatgttgatg ggcgaagtga tgagagaagc tgccctttca ctagtgaag ccaagttcac 300
agcaggtgac ttcagcacta cagttatcca aaatgtcaat aaagcgcaag tgaagattcg 360
agcgaagaaa gataatgtag caggtgttac tttgccagta tttgaacatt accatgaagg 420
aactgacagt tatgaactga ctggttttagc c 461

```

&lt;210&gt; 327

&lt;211&gt; 601

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 327

```

gaggggaggc cagcgaagcc gagtaaaacc gccgccgggg agaagactga aggagcagtt 60
gccgccgttg gcggcgggcc gagcagtttt cgctgtgct acggctgttg ccatgaggcg 120
aggctaggga ggacctcact tcccgggggt gtaataatgt taactgaggc cagtctatcc 180
atatggggat ggggaagcct tggcattgtc ctttttctga taaccttttg accctttgta 240
atattttatt tgacatttta tatcctctgc tttgtgggtg ggggttttagt gggtactctc 300
ctgttttgaa aaacaaactc agagaagtac ctagaacagt gtgaacactc atttcttcc 360
ccaacatcac ctgggggttc taagtgttta gaagaaatga aacgggaagc caggactatt 420

```

114

aagattgata gaagattgac ggggtgccaat ataattgatg aacctctcca gcaagttatc 480  
 cagttttcct tgagggatta tgtccagtat tggattata cactaagcga tgatgaatct 540  
 tttcttcttg aaattaggca gactcttcaa aacgcactca ttcagtttgc tactagggtca 600  
 a 601

<210> 328  
 <211> 601  
 <212> DNA  
 <213> Homo sapiens

<400> 328  
 ccggaatgat caccaagaca cacaaagtag accttgggct cccagagaag aaaaagaaga 60  
 agaaagtggc caaagaacca gagactcgat actcagtttt aaacaatgat gattactttg 120  
 ctgatgttcc tcccttaaga gctacatccc cctctaagag tgtggcccat gggcaggcac 180  
 ctgagatgcc tctagtgaag aaaaagaaga agaaaaagaa ggggtgtcagc accctttgcg 240  
 aggagcatgt agaacctgag accacgctgc ctgctagacg gacagagaag tcaccagacc 300  
 tcaggaagca ggtgtttggc cacttggagt tcctcagtgg ggaaaagaaa aataagaagt 360  
 cacctctagc catgtcccat gcctctgggg tgaaaacctc cccagaccct agacaggggtg 420  
 aggaggaaac cagagttggc aagaagctca aaaaacacaa gaaggaaaaa aagggggccc 480  
 aggaccccac agccttctcg gtccaggacc cttggttctg tgaggccagg gaggccaggg 540  
 atgttgggga cacttgctca gtggggaaga aggatgagga acaggcagcc ttggggcaga 600  
 a 601

<210> 329  
 <211> 501  
 <212> DNA  
 <213> Homo sapiens

<400> 329  
 agcagcttcc gctccaagct gcatcttcta gacctcgtg gatcagaaag acagaagaaa 60  
 accaaggctg aaggggatcg tctaaaagag ggtattaata ttaaccgagg cctcctatgc 120  
 ttgggaaatg taatcagtgc tcttggagat gacaaaaagg gtggctttgt gccctacaga 180  
 gatttcaagc tgaatcagct gcttcaagc tctctaggag gtaacagccc tctctctatg 240  
 atagcctgtg tyagtcctgc tgactccaat cttagggaaa cattaaatac ccttcgctat 300  
 gctgacagag caagaaaaat caagaacaaa cctattgtta atattgatcc ccagacagct 360  
 gaacttaatc atctaaagca acaggtacaa cagctacaag tcttgttget acaggcccat 420  
 ggaggtagcc tgccctggatc tataactgtg gaaccatcag agaattctaca atccctgatg 480  
 gagaagaatc agtccctggg a 501

<210> 330  
 <211> 451  
 <212> DNA  
 <213> Homo sapiens

<400> 330  
 cgcgaggcgc gcgccatgga acagcgggta gctgagtttc gggcggcgcg gaaacgggag 60  
 ggtctggcgc cccaaccccc tgctgccagt cagggcgcac aaaccccagg agagaaggcg 120  
 gaagcagcag cgactctaaa ggcagcccca ggtgggctaa agcggttcct ggtatggaaa 180  
 cctaggcccc cgagtgcctg gcccagccc gccctagtgc aggaagcggc tcagccccag 240  
 ggcagcacat cagagacacc atggaacaca gccattcctc tgccgtcgtg ctggggaccag 300  
 tctttcctga ccaatatcac cttcttgaag gttcttctct ggttggtcct gctgggactg 360  
 tttgtggaac tggaatttgg cctgcatatt ttgtcctgtc cttgttctat tggatgtacg 420  
 tcgggacacg aggccttgaa gagaagaaa a 451

<210> 331  
 <211> 331  
 <212> DNA  
 <213> Homo sapiens

115

&lt;400&gt; 331

```

cgttggtcct gtgcggtcac ttagccaaga tgcctgagga aaccagacc caagaccaac 60
cgatggagga ggaggaggtt gagacgttcg cctttcaggc agaaattgcc cagttgatgt 120
cattgatcat caatactttc tactcgaaca aagagatctt tctgagagag ctcatattcaa 180
attcatcaga tgcattggac aaaatcccgt atgaaagctt ggacagaatc caataaatta 240
aaacttcttg ggaaaagaag cttgcattat taacccttta taccgaacca aaccaaagaa 300
tccgaaactt cttcacttat ttggtgggga a

```

331

&lt;210&gt; 332

&lt;211&gt; 401

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 332

```

tccttcttga tcctgaactg ggtaggtgac cgctgttgct gctcgtgttg aatctagaac 60
cgtagccaga catgggactg gaggacgagc aaaagatgct taccgaatcc ggagatcctg 120
aggaggagga agaggaagag gaggaaattg tggatcccct aacaacagtg agagagcaat 180
gcgagcagtt ggagaaatgt gtaaaggccc gggagcggct agagctctgt gatgagcgtg 240
tatcctctcg atcacatata gaagaggatt gcacggagga gctctttgac ttcttgcattg 300
cgagggacca ttgcgtggcc cacaactctt ttaacaactt gaaataaatg tgtggactta 360
attcacccca gtcttcatca tctgggcatc agaattattc c

```

401

&lt;210&gt; 333

&lt;211&gt; 331

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 333

```

gatccctgca gaggcctcat ccccgacag cgagccagtc ctagagaagg atgacctcat 60
ggacatggat gcctctcagc agaatttatt tgacaacaag tttgatgaca tctttggcag 120
ttcattcagc agtgatccct tcaatttcaa cagtcaaaat ggtgtgaaca aggatgagaa 180
ggaccactta attgagcgac tatacagaga gatcagtgga ttgaaggcac agctagaaaa 240
catgaagact gggagcagc ggcgtgtgct gcagctgaag ggcagctga ggcagctgga 300
agcagatctg gccgagcagc agcacctgcg g

```

331

&lt;210&gt; 334

&lt;211&gt; 551

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 334

```

agcgggactg gctgggtcgg ctgggctgct ggtgcgagga gccgcggggc tgtgctcggc 60
ggccaagggg acagcgcgtg ggtggccgag gatgctgcgg ggcggtagct ccggcgcccc 120
tagctggtga ctgctgcgcc gtgcctcaca cagccgaggc gggctcggcg cacagtcgct 180
gctccgcgcg cgcgcggcgc ggcgctccag gtgctgacag cgcgagagag cgcggccctc 240
aggagcaagg cgaatgtatg acaacatgtc cacaatggtg tacataaagg aagacaagtt 300
ggagaagctt acacaggatg aaattatttc taagacaaag caagtaattc aggggctgga 360
agctttgaag aatgagcaca attccatttt acaaagtttg ctggagacac tgaagtgttt 420
gaagaaagat gatgaaagta atttgggtga ggagaaatca aacatgatcc cggaagtcac 480
tgagatggtt ggagctcggc ctgagtgagg cacaggttat gatggctttg tcaaatacacc 540
tgaatgcttg t

```

551

&lt;210&gt; 335

&lt;211&gt; 501

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 335

```

caggcggcgg agcgggactg gctgggtcgg ctgggctgct ggtgcgagga gccgcggggc 60

```

116

```

tgtgctcggc ggccaagggg acagcgcgtg ggtggccgag gatgctcggg ggcggtagct 120
ccggcgcccc tagctggtga ctgctgcgcc gtgcctcaca cagccgaggg gggctcggcg 180
cacagtgcgt gctccgcgcg cgcgcgccgg ggcgtccag gtgctgacag cgcgagagag 240
cgcgccctc aggagcaagg cgaatgtatg acaacatgtc cacaatgggtg tacataaagg 300
aagacaagtt ggagaagctt acacaggatg aaattatttc taagacaaag caagtaattc 360
aggggctgga agctttgaag aatgagcaca attccatttt acaaagtgtg ctggagacac 420
tgaagtgttt gaagaaagat gatgaaagta atttggtgga ggagaaatca aacatgatcc 480
ggaagtcact ggagatgttg g 501

```

&lt;210&gt; 336

&lt;211&gt; 521

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 336

```

cctcggcggc ggcgcggttg cttacagcct gagaagagcg tctcggccgg gagcggcggc 60
ggccatcgag acccaaccaa ggcggtccc cctcggcctc ccagcgctcc caagccgcag 120
cgcccgcgcc ccttcagcta gctcgtcgc tgcctctgct tccctgctgc cggctcggcc 180
atggcggttg cgttggcggc gctggcgcg gtgcagccgg cctcggcgag ccggtaccag 240
cagttgcaga atgaagaaga gtctggagaa cctgaacagg ctgcaggtga tgcctctcca 300
ccttacagca gcatttctgc agagagcgca gcatattttg actacaagga tgagtctggg 360
tttccaaagc ccccatctta caatgtagct acaacactgc ccagttatga tgaagcggag 420
aggaccaagg ctgaagctac tatccctttg gttcctggga gagatgagga ttttgtgggt 480
cgggatgatt ttgatgatgc tgaccagctg aggataggaa a 521

```

&lt;210&gt; 337

&lt;211&gt; 521

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 337

```

aaaggaggaa aatacacgga agagaattgc tgcctggct gagtccagag agataactga 60
gagtgaggaa agaggatcaa agagacgga ttggatctca gaggcagagg ttccacttgg 120
gagtgggtct cctcctagaa agactttctg gaggagaccc ccctactgtg taacagagga 180
ggacttttgg attaagaaaa gcattccagg aagccgacag tgtcagcaaa cgtggaggtg 240
agatccttca aagtgagtggt tgtggaggtt tccagaattt tctgagcctg aaggggaagg 300
tgagagcgag acctgcccct ttggaggctt gacttagccc tgagggcacc ctgtagccag 360
ggtgggcaga tgccaatatg gtagagacga agactgagta gggagccagc cacagtgcct 420
gtggtctcag gcagggagtg aagaccagag tggagcaggc tagaaacctg ggaaggaagc 480
aggttcccca gtataagccc atgatgtgtg aagaatgagc c 521

```

&lt;210&gt; 338

&lt;211&gt; 581

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 338

```

atactgcttg cttggagatg tctcgggaga ccattcttgc tatgacaagg cctgggagtt 60
gtcccgttac cgcagtgtct gtgctcagcg ctccaaagcc ctcccttcac ttcggaacaa 120
ggagtttcaa gagtgtgtag agtgcttcga acgctcgggt aagattaatc ccatgcagct 180
cggggtgttg tttctctcgc gttgtgccta tttggccttg gaagactatc aaggttcagc 240
aaaggcattt cagcgtgtgt tgactctaga acccgataat gctgaagctt ggaacaattt 300
gtcaacttcc tatatccgat taaaacaaaa agtaaaagct tttagaactt tacaagaagc 360
tctcaagtgt aactatgaac actggcagat ttgggaaaac tacatctca ccagcactga 420
cgttggggaa ttttcagaag ccattaaagc ttatcaccgg ctcttggact tacgtgacaa 480
atacaagat gttcaggtcc ttaaaattct agtcagggca gtgattgatg ggatgactga 540
tcgaagtgga gatgttgcaa ctggcctcaa aggaaagctg c 581

```

&lt;210&gt; 339

117

<211> 581  
<212> DNA  
<213> Homo sapiens

<400> 339  
aagaagaaga agctcgcgtt cgtgaagaag cagagaggggt cgggcaggaa cgagagaagc 60  
atttccagag agaagagcaa gagcgcctgg agagaaagaa gcgacttgag gagattatga 120  
aaagaaccag gagaacagaa gctacagata agaaaaccag tgatcagaga aacgggtgata 180  
tagccaaggg agctctcact ggaggaacag aggtgtctgc acttccatgt acaacaaacg 240  
ctccgggaaa tggaaagcca gttggcagcc cacatgtgggt tacctcacac cagtcaaaag 300  
aaaaaaaaaa gcgtgatgga atagctattg gatcagggtta caaaaaacaa tttttaaaaa 360  
taagctaaca tctaagaaac atcattttgc ctatactgcc tccccaaaaa tcctgttttt 420  
actcagtga cactaagcc cactcagaaa tgttctggat tgtcattttc tccatccttt 480  
agcaccttct tattttgggg ggagctctga agccttgcaa gaagtgggag agaaaaggac 540  
caggtgtgac agaaggagc atttaagtta ttacaataaa c 581

<210> 340  
<211> 571  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(571)  
<223> n = A,T,C or G

<400> 340  
ggtggcaaat tcaagtccctg ttaaccccgt ggtgttcttt gatgtcagta ttggcgggtca 60  
ggaagtggc cgcatgaaga tcgagctctt tgcagacgtt gtgcctaaga cggccgagaa 120  
ctttaggcag ttctgcaccg gagaattcag gaaagatggg gttccaatag gatacaaaag 180  
aagcaccttc cacagggtca taaaggattt catgattcag ggtggagatt ttgttaatgg 240  
agatgggtact ggagtcgcca gtatttaccg ggggccattt gcagatgaaa atttttaaact 300  
tcagttcttt atcacctgct ctaagtgcga ttggctggat gggaagcatg tgggtgtttg 420  
aaaaatcatc gatggacttc tagtgaagaa aaagattgag aatgttccca caggccccaa 480  
caataagccc aagctacctg tgggtgatctc cagtgtgggg agatgtagtc cagacaaaga 540  
ctgaatcagt atacttgctc gacttcaagg n 571

<210> 341  
<211> 581  
<212> DNA  
<213> Homo sapiens

<400> 341  
taatgagacc aaagtgttga agggcaggac gagcccgtgc taacagagaa agtgttgttt 60  
cctcaatttg gttttagact gtcttgcct atgggggaga aaagatctgc ccttgggaga 120  
ggtgccaact ttatagatct attaataaaa gaactggcag gcttacagtt cttgccaatg 180  
aggaaacttg aatgagagaa gccagggtca accttgccca acagactgga gcccatcacc 240  
ctaacttcac cccgcttctc cttacccaac cgtcaaaggc taggcagcac ccaccagca 300  
gcttccacct ggctgaagcc tgcacctgct tcagaccaag ggttagatgg aaatttgca 360  
tggaagaga gggctcacct gtgggcagga tagactctat ccaagaagga gaactgaaaa 420  
atgaaaacct atgagacaag ggtgatcct gaagcaggca ggagaaaggg ctggagggag 480  
aggcactggg gaatttttcc tgggtgaatac tgaagtact agatgttttg tcttgcaaaa 540  
ctcaagggaa aactctcaaa ctctaattgt tggcctattc t 581

<210> 342  
<211> 451  
<212> DNA  
<213> Homo sapiens



118

&lt;400&gt; 342

```
gcagaccaga cttcgctcgt actcgtgcgc ctcgcttcgc ttttcctccg caaccatgtc 60
tgacaaaccc gatatggctg agatcgagaa attcgataag tcgaaactga agaagacaga 120
gacgcaagag aaaaatccac tgccttccaa agaaacgatt gaacaggaga agcaagcagg 180
cgaatcgtaa tgaggcgtgc gccgccaata tgcactgtac attccacaag cattgccttc 240
ttattttact tcttttagct gtttaacttt gtaagatgca aagagggttg atcaagttta 300
aatgactgtg ctgccccttt cacatcaaag aactactgac aacgaagccg cgcctgcctt 360
tcccatctgt ctatctatct ggctggcagg gaaggaaaga acttgcattg ttggtgaagg 420
aagaagtggg ggggtgaaga aatgggggtg g 451
```

&lt;210&gt; 343

&lt;211&gt; 601

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 343

```
tgacctcatg gacatggatg cctctcagca gaatttattt gacaacaagt ttgatgacat 60
ctttggcagt tcattcagca gtgatccctt caatttcaac agtcaaatg gtgtgaacaa 120
ggatgagaag gaccacttaa ttgagcgact atacagagag atcagtggat tgaaggcaca 180
gctagaaaac atgaagactg agagccagcg ggttgtgctg cagctgaagg gccacgtcag 240
cgagctggaa gcagatctgg ccgagcagca gcacctgcgg cagcaggcgg ccgacgactg 300
tgaattcctg cgggcagaac tggacgagct caggaggcag cgggaggaca ccgagaaggc 360
tcagcggagc ctgtctgaga tagaaaggaa agctcaagcc aatgaacagc gatatagcaa 420
gctaaaggag aagtacagcg agctggttca gaaccacgct gacctgctgc ggaagaatgc 480
agaggtgacc aaacagggtg ccatggccag acaagcccag gtagatttgg aacgagagaa 540
aaaagagctg gagggattcg ttggagccgc tcagtgaccc agggccagcg ggaagactca 600
a 601
```

&lt;210&gt; 344

&lt;211&gt; 571

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 344

```
gcgacccggg gagcgagcac gtcgctccgc accgctcttc ctccagccgc tgagccgtcc 60
cttctcgcca tgtccagag caggcaccgc gccgaggccc cgccgctgga gcgcgaggac 120
agtgggacct tcagtttggg gaagatgata acagctaagc cagggaaaac accgattcag 180
gtattacacg aatacggcat gaagaccaag aacatcccag tttatgaatg tgaagatct 240
gatgtgcaaa tacacgtgcc cactttcacc ttacagagtaa ccgttgggtg cataacctgc 300
acaggtgaag gtacaagtaa gaagctggcg aaacatagag ctgcagaggc tgccataaac 360
atthtgaag ccaatgcaag tatthgtctt gcagttcctg accccttaat gcctgaccct 420
tccaagcaac caaagaacca gcttaatcct attggttcat tacaggaatt ggctattcat 480
catggctgga gacttcctga atataccctt tcccaggaag gaggacctgc tcataagaga 540
gaatatacta caatttgtag gctagagtca t 571
```

&lt;210&gt; 345

&lt;211&gt; 551

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 345

```
gacctggcgc tttgtgcggc tccaggcctc cgagtggact ccagaaagcc tgaaaagcta 60
tcatggcagc aaggcccaag ctccactatc ccaacggaag aggcgggatg gagtccgtga 120
gatgggtttt agctgccgcc ggagtgcagt ttgatgaaga atttctggaa acaaaagaac 180
agttgtacaa gttgcaggat ggtaaccacc tgctgttcca acaagtgcgc atggttgaaa 240
ttgacgggat gaagtgtgta cagacccgaa gcattctcca ctacatagca gacaagcaca 300
atctctttgg caagaacctc aaggagagaa ccctgtactg tggcccctct cgagtgttgt 360
cacttgcagc ottactgatg ccttagctga ttagcaacct ctgtagcaca ccacatttac 420
```

119

tttatgtctt acatagttag tgagatcagg gaacaaaaac ccaagaaggt cacgaagacc 480  
 agttggaact tcagtagaga gagtctgagt aaaacaaaag aatagggatt cagatattga 540  
 atactatac t 551

<210> 346  
 <211> 501  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)... (501)  
 <223> n = A,T,C or G

<400> 346  
 tatgggaaac tgctctttat ttagaccttt gggacaaaat taacttttgt cacatattac 60  
 ttaaaaaaaa atccagtttt acatattttt aaatagatag aactaaatga tcagagaatt 120  
 tcttctgtaa aaattggcca aattttatca aaaatctaac atacgataca atccaaatta 180  
 taaaaagact acttgggatc ataattttcc aaatgtatga cagttataac tccatcttaa 240  
 caagngtgaa aagtacttgc tctcatgttg ctttgggtcca aaagagtaga gctaactcag 300  
 taacaggcaa ctaagtaccc aatcttttgc caaaattaat ttanattgtg actggcagca 360  
 gaaatatcca taatgaacag ctctactata acaaagaata attaaagaat acttttcgtg 420  
 aacatatcac agtatcaa atcatttttat aagagaaaaa tatgaaggaa atgataaaat 480  
 agctatcaca acaaaaaaga a 501

<210> 347  
 <211> 621  
 <212> DNA  
 <213> Homo sapiens

<400> 347  
 gcccgggaga agactgaagg agcagttgcc gccgttggcg gcggcccgag cagttttcgc 60  
 ataatgrtaa ctgaggccag tctatccata tggggatggg gaagccttgg cattgtcctt 120  
 tttctgataa cctttggacc ctttgaata ttttatttga cttttatat cctctgcttt 240  
 gtgggtgggg gtttagtggt tactctcctg tttggaaaaa caaactcaga gaagtaccta 300  
 gaacagtgtg aacactcatt tcttctccca acatcacctg gggttcctaa gtgcttagaa 360  
 gaaatgaaac ggggaagccag gactattaag attgatagaa gattgacggg tgccaatata 420  
 attgatgaac ctctccagca agttatccag ttttcttga gggattatgt ccagtattgg 480  
 tattatacac taagcgatga tgaatctttt cttcttgaaa ttaggcagac tcttcaaaac 540  
 gcactcattc agtttgctac taggtcaaaa gaaatagact ggcaacctta ttttactacc 600  
 cgcattgtag atgactttgg c 621

<210> 348  
 <211> 511  
 <212> DNA  
 <213> Homo sapiens

<400> 348  
 cggcgggcgg cggcgggcga tggcgggcgc ggagggcggg ggcgacgacg cccgctgcgt 60  
 gcggctgagc gccgagcggg cacaggcgcg gctggccgac gtggacacgc tgctgttcga 120  
 ctgcgacggc gtgctgtggc gcggggagac cgccgtgcct ggcgcgcccg aggcctgcg 180  
 ggcgctgcga gcccgcgga agcgctggg cttcatcacc aacaacagca gcaagaccg 240  
 cgctgcctac gccgagaagc tgcggcgctt gggcttcggc ggcccccgcg gggcgggcgc 300  
 cagcctggag gtcttcggca cggcctactg caccgcgctc tacctgcgcc agcgctggc 360  
 cggcgcccc gcgccaagg cctacgtgct gggcagccca gccctggccg cggagctgga 420  
 gccgtggcg tcgccagcgt gggcggtggg cccgaccact gcaggcgag ggtcccgcg 480  
 actggctgca cgcccggttg agcgactgc g 511

120

<210> 349  
<211> 521  
<212> DNA  
<213> Homo sapiens

<400> 349  
gctcaggcgc ctgcggctgg gtgagcgcac gcgaggcggc gaggcggcag cgtgtttcta 60  
ggtcgtggcg tcgggcttcc ggagctttgg cggcagctag gggaggatgg cggagtcttc 120  
ggataagctc tatcgagtcg agtacgccaa gagcgggcgc gcctcttgca agaatgcag 180  
cgagagcatc cccaaggact cgctccggat ggccatcatg gtgcagtcgc ccatgtttga 240  
tggaaaagtc ccacactggt accacttctc ctgcttctgg aagggtggcc actccatccg 300  
gcaccctgac gttgaggtgg atgggttctc tgagcttcgg tgggatgacc agcagaaagt 360  
caagaagaca gcggaagctg gaggagtac aggcgaaggc caggatggaa ttggtagcaa 420  
ggcagagaag actctgggtg actttgcagc agagtatgcc aagtccaaca gaagtacgtg 480  
caagggggtg tatggagaag aatagaaaaa gggccagggtg c 521

<210> 350  
<211> 451  
<212> DNA  
<213> Homo sapiens

<400> 350  
gccggcgggc ggcgatggcg gcggcggagg ccggtggcga cgacgcccgc tgcgtgcggc 60  
tgagcgccga gcgggcacag gcgctgctgg ccgacgtgga cagcgtgctg ttcgactgcg 120  
acggcgtgct gtggcgcggg gagaccgcgc tgcttgccgc gcccgaggcc ctgcgggcgc 180  
tgcgagcccgc cggcaagcgc ctgggcttca tcaccaacaa cagcagcaag acccgcgctg 240  
cctacgccga gaagctgcgg cgcctgggct tcggcgggccc cgcgggggccc ggcgccagcc 300  
tggaggtctt cggcacggcc tactgcaccg cgctctacct gcgccagcgc ctggccggcg 360  
ccccgcgcgc caaggcctac gtgctgggca gccagccctt ggccgcgagg ctggagccgt 420  
gggcgtcgcc agcgtgggcy tggggcccga c 451

<210> 351  
<211> 581  
<212> DNA  
<213> Homo sapiens

<400> 351  
agagagagag agagagagag agagagagag agagagacct cgtgccgaat tcggcacgag 60  
gcctcgtgcc ggaaacttag tgatggacaa gttggtggtt tcataaatta tcgagatagc 120  
aagttaacac gaattctcca gaattccttg ggaggaaatg caaagacacg tattatctgc 180  
acaattactc cagtatcttt tgatgaaaca cttactgctc tccagtttgc cagtactgct 240  
aaatatatga agaatactcc ttatgttaat gaggtatcaa ctgatgaagc tctcctgaaa 300  
aggtatatga aagaaataat ggatcttaaa aaacaattag aggaggtttc tttagagacg 360  
cgggctcagg caatggaaaa agaccaattg gcccaactttt ggaagaaaaa gatttgcttc 420  
agaaagtaca gaatgagaaa attgaaaact taacacggat gctggtgacc tcttcttccc 480  
tcacgttgca ccaggaatta aaggctaaaa gaaaacgaag agttacttgg tgccttgcaa 540  
aattaccaaa tgaagaactc aacttttcag atcattttat t 581

<210> 352  
<211> 461  
<212> DNA  
<213> Homo sapiens

<400> 352  
aaaggcgatg aggtggatgg agtggatgaa gtggcgaaga agaaatctaa aaaagaaaaa 60  
gacaaggata gtaagcttga aaaagcccta aaggctcaga acgacctgat ctggaacatc 120  
aaggacgagc taaagaaaagt gtgttcaact aatgacctga aggagctact catcttcaac 180  
aagcagcaag tgcttcttgg ggagtcggcg atcttgacc gagtagctga tggcatggtg 240  
ttcgtgcccc tccttccctg cgaggaatgc tcgggtcagc tggcttcaa gagcgatgcc 300

121

tattactgca ctggggacgt cactgcctgg accaagtgt tggtaagac acagacaccc 360  
 aaccggaagg agtgggtaac cccaaaggaa ttccgagaaa tctcttacct caagaaattg 420  
 aaggttaaaa agcaggaccg tatattcccc ccagaaccag c 461

<210> 353  
 <211> 491  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(491)  
 <223> n = A,T,C or G

<400> 353  
 atggcggcgg cggaggccgg tggcgacgac gcccgctgcg tgcggctgag cggcgagcgg 60  
 gcacaggcgc tgctggccga cgtggacacg ctgctgttcg actgcgacgg cgtgctgtgg 120  
 cgcggggaga ccgcccgtgc tggcgcgccc gaggccctgc gggcgctgcg agcccgcggc 180  
 aagcgcttgg gcttcatcac caacaacagc agcaagaccc gcgctgccta cggcgagaag 240  
 ctgcggcgcc tgggcttggg cggccccgcg gggcccgggc ccagcctgga ggtcttcggc 300  
 acggcctact gcaccgcgct ctacctgcgc cagcgcttgg ccggcgcccc cgcgccaag 360  
 gctactgtgc tgggcaaccc agccctggcc gcgganctgg agccgtgggc gtcgccagcg 420  
 tgggcgtggg gcccgaccac tgcaagggca gggccccgcg gactggctga cggccccgctg 480  
 gaaccgact g 491

<210> 354  
 <211> 401  
 <212> DNA  
 <213> Homo sapiens

<400> 354  
 ggcgtcccgg tgtggctgtg ccgttggtcc tgtgcgggtca cttagccaag atgcctgagg 60  
 aagccagagc ccagagacaa cggatggagg agcaggcgtt tggcgcttgc gcttthcagg 120  
 cagaaattgc ccagttgatg tcattgatca tcaatacttt ctactogaac aaagagatct 180  
 ttctgagaga gctcatttca aattcatcag atgcatttga caaaatccgg tatgaaagct 240  
 tgacagatcc cagtaaatta gactctggga aagagctgca tattaacctt ataccgaaca 300  
 aacaagatcg aactctcact attgtggata ctggaatttg aatgaccaag gctgacttga 360  
 tcaataacct tgggtactatc gccaaagtctg ggaccaaagc g 401

<210> 355  
 <211> 451  
 <212> DNA  
 <213> Homo sapiens

<400> 355  
 tcttcagcgc atcagaagta tccagaatgt tcctgaaagc tcaggggctg tggaaactgt 60  
 tccagcattt caagaaatta cttctatgaa agaacgatgc aacaagcttc ttcagaaaagt 120  
 tcagaaaaat aaagaattgg tgcagactga aatccaagaa agacattcct tcacaaaaga 180  
 gataattgct ttgaagaatt tctttcaaca gaccacaact tcattccaaa atatggcatt 240  
 ccaggatcac ccagaaaagt cagaacaatt tgaggagcct caaagcatcc ttaagaaaagg 300  
 gaaactaact tttgagaata ttatggaaaa actgcgaatc aagtattccg aaatgtacac 360  
 catagtccct gcagagattg aatcccaggt ggaagaatgc agaaaagctt tagaagacat 420  
 agatgagaag attagccaat gaagtcttaa a 451

<210> 356  
 <211> 441  
 <212> DNA  
 <213> Homo sapiens

122

<220>  
<221> misc\_feature  
<222> (1)...(441)  
<223> n = A,T,C or G

<400> 356  
gtcgcgcac cggcgcccca tgaacgcctt catggtgtgg gcaaaggacg agcgcaagcg 60  
gctggctcag cagaacccgg acctgcacaa cgcggtgctc agcaagatgc tgggcaaagc 120  
gtggaaggag ctgaacgcgg cggagaagcg gcccttcgtg gaggaagccg aacggctgcg 180  
cgtgcagcac ttgcgcgacc accccaacta caagtaccgg ccgcgcgcga agaagcagcg 240  
gcgcaaggcc cggcggtctg agcccggctc tgctcccggg attagcgccc ccgcagccac 300  
cgccgacctt tcccgcggcg tctggctcgn tcgcgccttc cgcgagctgc cccgctgggc 360  
gccgagttca cggctggggc tgccaccccg agcgtcgctc tgacggctga cccgggagct 420  
gcttttccac gccgcgcgc a 441

<210> 357  
<211> 451  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(451)  
<223> n = A,T,C or G

<400> 357  
gcggcgccgg agggcgggtg cgacgacgcc cgctgcgtgc ggctgagcgc cgagcgggca 60  
caggcgctgc tggccgacgt ggacacgctg ctgttcgact gcgacggcgt gctgtggcgc 120  
ggggagaccg ccgtgcctgg cgcgcgcgag gccctgcggg cgtgcgagc ccgcggcaag 180  
cgctgggctt tcatcaccac caacagcagc aagaccgcgc ctgcctacgc cgagaagctg 240  
cggcgcttgg gcttcggcgg ccccgcgggg cccgcgcgca gcctggaggt ctctggcagc 300  
gcctactgca ccgcgctcta cctgcgccag cgctggcgg gcgccccgc gcccaagcct 360  
acgtgcctgg cagcccgagg ctggagcgg ccctggagc cgtggcgctc gccagagc 420  
gcgtggggcc cgaaccactt gcagggcgag g 451

<210> 358  
<211> 571  
<212> DNA  
<213> Homo sapiens

<400> 358  
gcggcgatgg cggcgcgcca ggccggtggc gacgacgccc gctgcgtgcg gctgagcgcc 60  
gagcgggac aggcgctgct ggccgacgtg gacacgctgc tgttcgactg cgacggcgtg 120  
ctgtggcgcg gggagaccgc cgtgcctggc gcgcccagg ccctgcgggc gctgcgagcc 180  
cgcggcaagc gcctgggctt catcaccac aacagcagca agaccgcgc tgcctacgcc 240  
gagaagctgc ggcgcctggg ctctggcgcc cccgcggggc ccgcgcgcag cctggaggtc 300  
ttcggcacgg cctactgcac cgcgctctac ctgcgccagc gcctggccgg cgcgcccgcg 360  
cccaagccta cgtgctgggc agcccagccc tggccgcgga gctggaggcc gtgggcgtcg 420  
ccagcgtggg cgtggggccc gaccactgca gggcgagggt cccggcgact ggctgcacgc 480  
gccgctggag cccgacgtgc gcgcggtggt ggtgggcttt gaccgcgact tagctacatg 540  
aagctacca agcccttgcg ctacttgaag a 571

<210> 359  
<211> 511  
<212> DNA  
<213> Homo sapiens

<400> 359  
cgctgctgtt atggccgcct ccttgaggta gtatccgcac atggaattct agggccgcag 60

123

```

gtgtatttac ggtaactgtc gccactagat ttcagcgcct ttggactctc ctgttttcac 120
tttcttttgt tgactcccgt gtggccctcg tgggagcctg ttttggtgc agcgggtgtct 180
ggggtgatgt ggaccccgga gctggcaatt ctgaggggat tccccactga ggctgagcgg 240
cagcaatgga aacaggaggg ggtcgtcggg tcagagagtg gatctttcct acaattgctg 300
ctggaaggga actatgaagc catattctta aattcaatga ctcaaaatat ttttaattca 360
acaacaaccg ctgaagaaaa gattgatagc tacctggaga agcaggtagt aacattcctg 420
gattactcaa cagatttggg cacaacggaa agacaacagt tgatatttct acttggtgtg 480
agcagtttgc aactttttgt tcaaagcaac t 511

```

&lt;210&gt; 360

&lt;211&gt; 481

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 360

```

gcgttctcgg ggagctgctg ccgtagctgc cgccgccgct accacgcgct tcgggtgtag 60
aatttggaa ccttcgcgcg cgtaacaat gaagcagagt tcgaacgtgc cggctttcct 120
cagcaagctg tggacgcttg tggaggaaac ccacactaac gattcatca cctggagcca 180
gaatggccaa agttttcttg tottgatga gcaacgattt gcaaaagaaa ttcttcccaa 240
atatttcaag cacaataata tggcaagctt tgtgaggcaa ctgaatatgt atggtttccg 300
taaagtagta catatogact ctggaattgt aaagcaagaa agagatgggt ctgtagaatt 360
tcagcatcct tacttcaaac aaggacagga tgacttggtg gagaacatta aaaggaaggt 420
ttcatcttca aaaccagaag aaaataaaat tcgtcaggaa gatttaacaa aaattataag 480
t 481

```

&lt;210&gt; 361

&lt;211&gt; 551

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 361

```

cgtagaggaa gacactgtgg aggccagttc tggagctatt gcagcctcgg ttgcccgcc 60
gggggtgagc ggggagaggt tctctcaga atctcggga ccggccgcat tgaactctgt 120
ccttcgcgaa tggcacagac catcatgaag gctcgtttaa agggagcaca gacaggtcga 180
aacctcctga agaaaaaatc tgatgcctta actcttcgat ttgcacagat cctaaagaag 240
ataatagaga ctaaaatggt gatggggcga gtgatgagag aagctgcctt ttcactagct 300
gaagccaagt tcacagcagg tgacttcagc actacagtta tccaaaatgt caataaagcg 360
caagtgaaga ttcgagcgaa gaaagataat gtagcagggt ttactttgcc agtatttgaa 420
cattaccatg aaggaactga cagttatgaa ctgactgggt tagccagagg tggggaacag 480
ttggctaaat taaagaggaa ttatgcccaa agcagtggaa ctactggtgg aactagcttc 540
tcttcagac t 551

```

&lt;210&gt; 362

&lt;211&gt; 481

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(481)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 362

```

gggttacatt ttggattaaa cctgtttccc gggtatgtgt agggaaacagc aaagngatgc 60
acnaactttt aacattcgtt atggggaaaa catcctttaa cttcgggggtc gtctgccaaa 120
gcaggggtctg ggaggttcca tgcagttccc gntgggtgtg agggaaatgc cctggtctgg 180
cctccgagcc ccaggtcca ccgtctccc tccctcatt tgtaanaata gctacacact 240
aacatttttg gaaggagagg cacataactt tttttaacat ttggttaacta gggtatgggc 300
tctacattgt cagctacttg ggatatatat ttaattttct taaattcccc tttaactcta 360

```

124

ttttatggtt ttgatttcag attgcaaaca tgtaaaacct gcatagcagc gagttctcgg 420  
 ttttgcggtt tcttttagtgc tttactgtca ctgtcatgta atcagctaata tctcttctgg 480  
 a 481

<210> 363  
 <211> 461  
 <212> DNA  
 <213> Homo sapiens

<400> 363  
 ggaaccaggga cctcggcgtg gcctagcgag ttatggcgac gaaggccgtg tgcgtgctga 60  
 agggcgacgg cccagtgacg ggcacatca atttcgagca gaaggaaagt aatggaccag 120  
 tgaaggtgtg gggaagcatt aaaggactga ctgaaggcct gcatggattc catgttcacg 180  
 agtttggaga taatacagca ggctgtacca gtgcaggtcc tcaactttaat cctctatcca 240  
 gaaaacacgg tgggccaaag gatgaagaga ggcatgttgg agacttgggc aatgtgactg 300  
 ctgacaaaga tgggtgtggc gatgtgtcta ttgaagattc tgtgatctca ctctcaggag 360  
 accattgcat cattggccgc acactgggtg tccatgaaaa acagatgact tgggcaaagg 420  
 tggaaatgaa gaaagtacaa agacaggaaa cgcttgaagt c 461

<210> 364  
 <211> 531  
 <212> DNA  
 <213> Homo sapiens

<400> 364  
 ggttctactt totgcacgtc agaaatcaat tccatgtcag ctcgagtcc tctcttctgt 60  
 gtgtgtccag gccatctgat tttcttctac atcatctacc tgggtggagg tcagtcagtc 120  
 ataaacagcc agacctttgt ggtgctctac ctgctggcag gcctgatcca ggtgacaatc 180  
 ctgctgtacc tcgcagaagt gatggttcgg ctgacttggc accaggccct ggatcctgac 240  
 aacctgca tcccctacct tacagggtcg ggggacctgc tcggtactgg cctcctggca 300  
 ctctgctttt tcaactgact gctactgaag agcaaggcag agctgggtgg catctcagaa 360  
 ctggcatctg gacctcccta actgggcccc gctgggtcca tttgctcatt agaatttcc 420  
 cctctgcctc tgcagtaacc ttttctgagt cttgctaagg tagctctcac a 531

<210> 365  
 <211> 4834  
 <212> DNA  
 <213> Homo sapiens

<400> 365  
 gatgtggagc tggggtcctt gcaagtcacg aacaaaacga gaaagattat ggaacatggg 60  
 ggggccacct tcatcaatgc ctttctgact acacccatgt gctgcccgtc acggtcctcc 120  
 atgctcaccg ggaagtatgt gcacaatcac aatgtctaca ccaacaacga gaactgctct 180  
 tccccctcgt ggcaggccat gcatgagcct cggacttttg ctgtatatct taacaacact 240  
 ggctacagaa cagccttttt tggaaaatac ctcaatgaat ataatggcag ctacatcccc 300  
 cctgggtggc gagaatggct tggattaatc aagaattctc gcttctataa ttacactgtt 360  
 tgtcgcaatg gcatcaaaaga aaagcatgga tttgattatg caaaggacta cttcacagac 420  
 ttaatcacta acgagagcat taattacttc aaaatgtcta agagaatgta tccccatagg 480  
 ccggttatga tgggtgatcag ccacgctgcy cccacggccc ccgaggactc agccccacag 540  
 ttttctaaac tgtaccccaa tgcctcccaa cacataactc ctagtataaa ctatgcacca 600  
 aatatggata aacactggat tatgcagtac acaggacca tgcgtcccat ccacatggaa 660  
 ttacaaaaca ttctacagcg caaaaggctc cagacttga tgcagtga tgattctgtg 720  
 gagaggctgt ataactgct cgtggagacg ggggagctgg agaatactta catcatttac 780  
 accgcccacc atggttacca tattggcag tttggactgg tcaaggggaa atccatgcca 840  
 tatgactttg atattcgtgt gccttttttt attcgtggtc caagtgtaga accaggatca 900  
 atagtcccaac agatcgttct caacattgac ttggcccca cgatcctgga tattgctggg 960  
 ctgcacacac ctctgatgt ggacggcaag tctgtctca aacttctgga cccagaaaag 1020

ccaggttaaca	ggtttcgaac	aaacaagaag	gccaaaattt	ggcgtgatac	attcctagtg	1080
gaaagaggca	aattttctacg	taagaaggaa	gaatccagca	agaatatcca	acagtcaaat	1140
cacttgccca	aatatgaacg	ggtcaaagaa	ctatgccagc	aggccaggta	ccagacagcc	1200
tgtgaacaac	cggggcagaa	gtggcaatgc	attgaggata	catctggcaa	gcttcgaatt	1260
cacaagtgt	aaggacccag	tgacctgctc	acagtcgggc	agagcacgcg	gaacctctac	1320
gctcgcggct	tccatgacaa	agacaaagag	tgcagttgta	gggagtcctg	ttaccgtgcc	1380
agcagaagcc	aaagaaagag	tcaacggcaa	ttcttgagaa	accaggggac	tccaaagtac	1440
aagcccagat	ttgtccatac	tcggcagaca	cgttccttgt	ccgtcgaatt	tgaaggtgaa	1500
atatatgaca	taaatctgga	agaagaagaa	gaattgcaag	tgttgcaacc	aagaaacatt	1560
gctaagcgtc	atgatgaagg	ccacaagggg	ccaagagatc	tccaggcttc	cagtgggtggc	1620
aacaggggca	ggatgctggc	agatagcagc	aacgccgtgg	gcccacctac	caactgtccga	1680
gtgacacaca	agtggtttat	tcttcccaat	gactctatcc	attgtgagag	agaactgtac	1740
caatcggcca	gagcgtggaa	ggaccataag	gcatacattg	acaaagagat	tgaagctctg	1800
caagataaaa	ttaaagaattt	aagagaagtg	agaggacatc	tgaagagaag	gaagcctgag	1860
gaatgtagct	gcagtaaaca	aagctattac	aataaagaga	aaggtgtaaa	aaagcaagag	1920
aaattaaaga	gccatcttca	cccattcaag	gaggctgctc	aggaagtaga	tagcaaaactg	1980
caacttttca	aggagaacaa	ccgtaggagg	aagaaggaga	ggaaggagaa	gagacggcag	2040
aggaaggggg	aagagtgcag	cctgcctggc	ctcacttgct	tcacgcata	caacaaccac	2100
tgccagacag	ccccgttctg	gaacctggga	tctttctgtg	cttgacagag	ttctaacaat	2160
aacacctact	ggtgtttgct	tacagttaat	gagacgcata	atcttctttt	ctgtgagttt	2220
gctactggtc	ttttggagta	ttttgatatg	aatacagatc	cttatcagct	cacaaataca	2280
gtgcacacgg	tagaacgagg	cattttgaat	cagctacacg	tacaactaat	ggagctcaga	2340
agctgtcaag	gatataagca	gtgcaaccca	agacctaaga	atcttgatgt	tggaaataaa	2400
gatggaggaa	gctatgacct	acacagagga	cagttatggg	atggatggga	aggttaatca	2460
gccccgtctc	actgcagaca	tcaactggca	aggcctagag	gagctacaca	gtgtgaatga	2520
aaacatctat	gagtagacag	aaaactacag	acttagtctg	gtggactgga	ctaattactt	2580
gaaggattta	gatagagtat	ttgactgctc	gaagagtcac	tatgagcaaa	ataaaacaaa	2640
taagactcaa	actgctcaaa	gtgacgggtt	cttggtgtgc	tctgctgagc	acgctgtgtc	2700
aatggagatg	gcctctgctg	actcagatga	agacccaagg	cataagggtt	ggaaaacacc	2760
tcatttgacc	ttggcagctg	accttcaaac	cctgcatttg	aaccgaccaa	cattaagtcc	2820
agagagttaa	cttgaattga	ataacgacat	tccagaagtt	aatcatttga	attctgaaca	2880
ctggagaaaa	accgaaaaat	ggacggggca	tgaagagact	aatcatctgg	aaaccgattt	2940
caggaacccg	aaagaacttc	cccagtatgg	tggtcctgga	aaggacattt	ttgaagatca	3000
actatatctt	cctgtgcatt	ccgatggaat	ttcagttcat	cagatgttca	ccatggccac	3060
cgcagaacac	cgaagtaatt	ccagcatagc	ggggaagatg	ttgaccaagg	tggagaagaa	3120
tcacgaaaag	gagaagtcac	agcacctaga	aggcagcgcc	tcctcttcac	tctcctctga	3180
ttagatgaaa	ctgttacctt	accctaaca	cagtatctct	ttttaacttt	tttatttgta	3240
aactaataaa	ggtaatcaca	gccaccaaca	ttccaagcta	ccctgggtac	ctttgtgcag	3300
tagaagctag	tgagcatgtg	agcaagcggt	gtgcacacgg	agactcatcg	ttataattta	3360
ctatctgcc	agagtagaaa	gaaaggctgg	ggatatttgg	gttggcttgg	ttttgatttt	3420
ttgcttgttt	gtttgttttg	tactaaaaca	gtattatctt	ttgaatatcg	tagggacata	3480
agtatatata	tggtatccaa	tcaagatggc	tagaatgggt	cctttctgag	tgtctaaaac	3540
ttgacacccc	tggtaaatct	ttcaacacac	ttccactgcc	tgcgtaatga	agttttgatt	3600
catttttaac	cactggaatt	tttcaatgcc	gtcattttca	gttagatgat	tttgcacttt	3660
gagattaaaa	tgccatgtct	atttgattag	tottattttt	ttatttttac	aggcttatca	3720
gtctcactgt	tggtgtcat	tgtgacaaag	tcaaataaac	ccccaggac	gacacacagt	3780
atggatcaca	tattgtttga	cattaagcct	ttgccagaaa	atgttgcatg	tgttttacct	3840
cgacttgcta	aaatcgatta	gcagaaggcc	atggctaata	atgttggtgg	tgaataataa	3900
taataaagta	aacaaaatga	agattgcctg	ctctctctgt	gcctagcctc	aaagcgttca	3960
tcatacatca	tacctttaag	attgctatat	tttgggttat	tttcttgaca	ggagaaaaag	4020
atctaaagat	cttttatttt	catctttttt	ggttttcttg	gcatgactaa	gaagcttaaa	4080
tgttgataaa	atatgactag	ttttgaattt	acaccaagaa	cttctcaata	aaagaaaatc	4140
atgaatgctc	cacaatttca	acataccaca	agagaagtta	atttcttaac	attgtgttct	4200
atgattattt	gtagacacct	ccaccaagttc	tgatatcttt	taaagacata	gttcaaaatt	4260
gcttttgaaa	atctgtattc	ttgaaaatat	ccttggtgtg	tattaggttt	ttaaatacca	4320
gctaaaggat	tacctcactg	agtcacagct	accctcctat	tcagctcccc	aagatgatgt	4380
gtttttgctt	accctaagag	aggttttctt	cttattttta	gataattcaa	gtgcttagat	4440
aaattatgtt	ttctttaagt	gtttatggta	aactctttta	aagaaaattt	aatatgttat	4500
						4560



126

agctgaatct ttttggtaac tttaaatott tatcatagac tctgtacata tgttcaaatt 4620  
 agctgcttgc ctgatgtgtg tatcatcggt gggatgacag aacaaacata tttatgatca 4680  
 tgaataatgt gctttgtaaa aagatttcaa gttattagga agcatactct gttttttaat 4740  
 catgtataat attccatgat acttttatag aacaattctg gcttcaggaa agtctagaag 4800  
 caatatttct tcaaataaaa ggtgtttaaa cttt 4834

&lt;210&gt; 366

&lt;211&gt; 818

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 366

Asp Val Glu Leu Gly Ser Leu Gln Val Met Asn Lys Thr Arg Lys Ile  
                                   5                                  10                                  15  
 Met Glu His Gly Gly Ala Thr Phe Ile Asn Ala Phe Val Thr Thr Pro  
                                   20                                  25                                  30  
 Met Cys Cys Pro Ser Arg Ser Ser Met Leu Thr Gly Lys Tyr Val His  
                                   35                                  40                                  45  
 Asn His Asn Val Tyr Thr Asn Asn Glu Asn Cys Ser Ser Pro Ser Trp  
                                   50                                  55                                  60  
 Gln Ala Met His Glu Pro Arg Thr Phe Ala Val Tyr Leu Asn Asn Thr  
                                   65                                  70                                  75                                  80  
 Gly Tyr Arg Thr Ala Phe Phe Gly Lys Tyr Leu Asn Glu Tyr Asn Gly  
                                   85                                  90                                  95  
 Ser Tyr Ile Pro Pro Gly Trp Arg Glu Trp Leu Gly Leu Ile Lys Asn  
                                   100                                  105                                  110  
 Ser Arg Phe Tyr Asn Tyr Thr Val Cys Arg Asn Gly Ile Lys Glu Lys  
                                   115                                  120                                  125  
 His Gly Phe Asp Tyr Ala Lys Asp Tyr Phe Thr Asp Leu Ile Thr Asn  
                                   130                                  135                                  140  
 Glu Ser Ile Asn Tyr Phe Lys Met Ser Lys Arg Met Tyr Pro His Arg  
                                   145                                  150                                  155                                  160  
 Pro Val Met Met Val Thr Ser His Ala Ala Pro His Gly Pro Glu Tyr  
                                   165                                  170                                  175  
 Ser Ala Pro Gln Phe Ser Lys Leu Tyr Pro Asn Ala Ser Gln His Ile  
                                   180                                  185                                  190  
 Thr Pro Ser Tyr Asn Tyr Ala Pro Asn Met Asp Lys His Trp Ile Met  
                                   195                                  200                                  205  
 Gln Tyr Thr Gly Pro Met Leu Pro Ile His Met Glu Phe Thr Asn Ile  
                                   210                                  215                                  220  
 Leu Gln Arg Lys Arg Leu Gln Thr Leu Met Ser Val Asp Asp Ser Val  
                                   225                                  230                                  235                                  240  
 Glu Arg Leu Tyr Asn Met Leu Val Glu Thr Gly Glu Leu Glu Asn Thr  
                                   245                                  250                                  255  
 Tyr Ile Ile Tyr Thr Ala Asp His Gly Tyr His Ile Gly Gln Phe Gly  
                                   260                                  265                                  270  
 Leu Val Lys Gly Lys Ser Met Pro Tyr Asp Phe Asp Ile Arg Val Pro  
                                   275                                  280                                  285  
 Phe Phe Ile Arg Gly Pro Ser Val Glu Pro Gly Ser Ile Val Pro Gln  
                                   290                                  295                                  300  
 Ile Val Leu Asn Ile Asp Leu Ala Pro Thr Ile Leu Asp Ile Ala Gly  
                                   305                                  310                                  315                                  320  
 Leu Asp Thr Pro Pro Asp Val Asp Gly Lys Ser Val Leu Lys Leu Leu  
                                   325                                  330                                  335  
 Asp Pro Glu Lys Pro Gly Asn Arg Phe Arg Thr Asn Lys Lys Ala Lys  
                                   340                                  345                                  350  
 Ile Trp Arg Asp Thr Phe Leu Val Glu Arg Gly Lys Phe Leu Arg Lys  
                                   355                                  360                                  365  
 Lys Glu Glu Ser Ser Lys Asn Ile Gln Gln Ser Asn His Leu Pro Lys

127

370 375 380  
 Tyr Glu Arg Val Lys Glu Leu Cys Gln Gln Ala Arg Tyr Gln Thr Ala  
 385 390 395 400  
 Cys Glu Gln Pro Gly Gln Lys Trp Gln Cys Ile Glu Asp Thr Ser Gly  
 405 410 415  
 Lys Leu Arg Ile His Lys Cys Lys Gly Pro Ser Asp Leu Leu Thr Val  
 420 425 430  
 Arg Gln Ser Thr Arg Asn Leu Tyr Ala Arg Gly Phe His Asp Lys Asp  
 435 440 445  
 Lys Glu Cys Ser Cys Arg Glu Ser Gly Tyr Arg Ala Ser Arg Ser Gln  
 450 455 460  
 Arg Lys Ser Gln Arg Gln Phe Leu Arg Asn Gln Gly Thr Pro Lys Tyr  
 465 470 475 480  
 Lys Pro Arg Phe Val His Thr Arg Gln Thr Arg Ser Leu Ser Val Glu  
 485 490 495  
 Phe Glu Gly Glu Ile Tyr Asp Ile Asn Leu Glu Glu Glu Glu Leu  
 500 505 510  
 Gln Val Leu Gln Pro Arg Asn Ile Ala Lys Arg His Asp Glu Gly His  
 515 520 525  
 Lys Gly Pro Arg Asp Leu Gln Ala Ser Ser Gly Gly Asn Arg Gly Arg  
 530 535 540  
 Met Leu Ala Asp Ser Ser Asn Ala Val Gly Pro Pro Thr Thr Val Arg  
 545 550 555 560  
 Val Thr His Lys Cys Phe Ile Leu Pro Asn Asp Ser Ile His Cys Glu  
 565 570 575  
 Arg Glu Leu Tyr Gln Ser Ala Arg Ala Trp Lys Asp His Lys Ala Tyr  
 580 585 590  
 Ile Asp Lys Glu Ile Glu Ala Leu Gln Asp Lys Ile Lys Asn Leu Arg  
 595 600 605  
 Glu Val Arg Gly His Leu Lys Arg Arg Lys Pro Glu Glu Cys Ser Cys  
 610 615 620  
 Ser Lys Gln Ser Tyr Tyr Asn Lys Glu Lys Gly Val Lys Lys Gln Glu  
 625 630 635 640  
 Lys Leu Lys Ser His Leu His Pro Phe Lys Glu Ala Ala Gln Glu Val  
 645 650 655  
 Asp Ser Lys Leu Gln Leu Phe Lys Glu Asn Asn Arg Arg Arg Lys Lys  
 660 665 670  
 Glu Arg Lys Glu Lys Arg Arg Gln Arg Lys Gly Glu Glu Cys Ser Leu  
 675 680 685  
 Pro Gly Leu Thr Cys Phe Thr His Asp Asn Asn His Trp Gln Thr Ala  
 690 695 700  
 Pro Phe Trp Asn Leu Gly Ser Phe Cys Ala Cys Thr Ser Ser Asn Asn  
 705 710 715 720  
 Asn Thr Tyr Trp Cys Leu Arg Thr Val Asn Glu Thr His Asn Phe Leu  
 725 730 735  
 Phe Cys Glu Phe Ala Thr Gly Phe Leu Glu Tyr Phe Asp Met Asn Thr  
 740 745 750  
 Asp Pro Tyr Gln Leu Thr Asn Thr Val His Thr Val Glu Arg Gly Ile  
 755 760 765  
 Leu Asn Gln Leu His Val Gln Leu Met Glu Leu Arg Ser Cys Gln Gly  
 770 775 780  
 Tyr Lys Gln Cys Asn Pro Arg Pro Lys Asn Leu Asp Val Gly Asn Lys  
 785 790 795 800  
 Asp Gly Gly Ser Tyr Asp Leu His Arg Gly Gln Leu Trp Asp Gly Trp  
 805 810 815  
 Glu Gly

&lt;210&gt; 367

128

<211> 361  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(361)  
 <223> n = A,T,C or G

<400> 367  
 ttnggnttta anaagtacca atttaataat gaataacttan aaatatggna cncagatacc 60  
 atagtaatat aaaatgcata caattttaaa ttattttctt ataaactctn tacatgaatg 120  
 gctggcggct tccaacanat aaacttttgg acaaaggnac aanatatattt tgggcattca 180  
 ttttaataac catctagtta tccaattagg aggnctctaa aaaaataaat atgacaaata 240  
 tatggatttc tgaagtataa actgacatac aaatctatat attttcttaa tacttttcat 300  
 taaagcatct ttaaagcatt ctgtaacatg aagttganag ttcaaattan atgtaatgaa 360  
 a 361

<210> 368  
 <211> 558  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(558)  
 <223> n = A,T,C or G

<400> 368  
 ccagtgtggt ggaattcgac tcgtctcagg ccagtgcag ccttctcagc caaacgccga 60  
 ccaaggaaaa ctcaactacca tgagaattgc agtgatttgc ttttgcctcc taggcatcac 120  
 ctgtgccata ccagttaaac aggtgattc tggaagtctt gaggaaaagc agctttacaa 180  
 cctagcccca cagaatgctg tgtcctctga agaaaccaat gactttaaac aagagaccct 240  
 tccaagtaag tccaacgaaa gccatgacca catggatgat atggatgatg aagatgatga 360  
 tgaccatgtg gacagccagg actccattga ctcgaaacgac tctgatgatg tagatgacac 420  
 tgatgattct caccagtctg atgagtctca ccattctgat gaatctgatg aactggtcac 480  
 tgattttccc acggacctgc cagcaaccga agttttcact ccagttgtcc ccacagtaga 540  
 cacatatgat ggccgagg 558

<210> 369  
 <211> 1021  
 <212> DNA  
 <213> Homo sapiens

<400> 369  
 tttttacaac atatattcttt aattaaattt atattggkgg gtttaaaaaa cattaagtca 60  
 ggagatgata gctagggaaa taaggatatcc tgtgagtatt tataacaaaa tatttaaaat 120  
 ttaaaaagaa taagaaacat caattggctt tttgtaactt aaaagagact aaccaagtgt 180  
 tgtttccag ttctgtacaa gcagaggcca caggaggatt ctacataag aagcacaggg 240  
 aaaagaattg ttaattctgc gtgtgtgtt ttgtttctca gaattgtttg gaagaacttt 300  
 gtccagtcag aaatgagtaa aaacaagatg taagaaacat taaaacaggg gccatatggt 360  
 cttaagagat aatcttgag aatatagcaa aagacaaatt gctccattag atattataat 420  
 ttggtatgta acatgaacat ttaaaattct gattaaagtg actaaaaggg tttgtttttt 480  
 aaaaaaaatc aaacagaaac ttacgggata aaactcaaaa taaatttact ctcatgtagta 540  
 acttgatgta ggaatataag tcctctcact ttgataaaca tgaatataaa atattgctgt 600  
 ctgtattcta gggtttctta cattttctgt aaagagtgt tcatgctatg tcatatgtaa 660  
 atgactcaac attttgagct aaaaggctgt tcacaatata cacattcttt acttacaag 720  
 caaaataagc ttaacacctt tatattaaaa acccgggata cagcaggatt agtagaccg 780

129

```

tgaaaaataa ttcttccac aaactgcagt cttttatctt actcaatgtg actcttctct 840
taattgaatt tttaagtac catttttagta actgggcaaa atatataatt ttcattctat 900
aattcttgga gaaagtcatt ctggacccaa aaagtaaatt cacttcctta tttcttttagt 960
agaaaaataa tagagacttt gctctggcgc attgctgagg tacatctgaa tcttcattggt 1020
t                                                    1021

```

```

<210> 370
<211> 204
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(204)
<223> n = A,T,C or G

```

```

<400> 370
ggaaagcgga agancaggtc ttgatgtgtc ctagaatctt gccatttctg agattgagcc 60
attgaaggca ttccatttct aaagcttatt tagccgggtg ttctaaagaa ttccacacta 120
acgtgataac atggtttttg taacaataaa tgtaggatat ttccctggcac atgcaataaa 180
acctaatacat tgtttcttta aaaa                                204

```

```

<210> 371
<211> 628
<212> DNA
<213> Homo sapiens

```

```

<400> 371
gtgatttcta atcctccctt ttttgattta gttggatgtg cttttaaatg tcotttgcct 60
gcttgaggta gaaaggggac ctttttgagt tgtcattttg cactttcaaa acttattttc 120
ttggaaaaca atatttatag ggcttaaagc ccattttcat ttctaactta aattatgtgt 180
gcctatctga aaactttggg ctctttcttg tttctttccc aaaattcaga agttaatggg 240
cttctaggtg gctttatctt ttttttattt cactgatttg gctgtctctt gttaggctta 300
aaaataaacct tgtgtatgct accaacttaa agtgcattat tttgtgtcac tttttttttt 360
cttgtaaaaa tgacttggat tgaaaatatg tggtagcctt tttatttcta cattaagtgc 420
tacctaggat atttccaagg actgccacaa aaccatattg tgcagtactt tactactttg 480
ggaaagctgc atctttctac cacattttta catctaatat atttaatttc tttgaagagg 540
gttctgtgta cgttattgta gttcccagtt taatatagtt ctttgtatct ctttaacaggg 600
tggaagttat tgcaaacacac tctggaaa                                628

```

```

<210> 372
<211> 473
<212> DNA
<213> Homo sapiens

```

```

<400> 372
ccagtgtggt ggaattcctg ccgccctgcc gccctgccgc cctgccgcgc gtggtcgtcg 60
cccgtggtgc tccgtcgcgc ccgccacctc acgtcctccc gtgcgtcggg agcgtctcgg 120
ctacaacatg ttgggcatga tcaagaactc gctgttcgga agcgtagaga cgtggccttg 180
gcaggtccta agcaaagggg acaaggaaga agttgcctat gaagaaaggg cctgtgaagg 240
cggcaaatat gccacagtag aagtgcagga taagcctgtg gatgaggttc tacgggaagg 300
aatgcccaag gtgcgaaagt atgcaggggg caccaatgac aagggaattg ggatggggat 360
gacagtccct atttcttttg ctgtgttccc caatgaagat ggctctctgc agaagaaatt 420
aaaagctctg ttccggattc caaaccaatt tcaaagcgac ccaccagctc cca          473

```

```

<210> 373
<211> 283
<212> DNA
<213> Homo sapiens

```

130

<220>  
<221> misc\_feature  
<222> (1)...(283)  
<223> n = A,T,C or G

<400> 373  
tttaagtcaa tgccttttat ttttagtttt tctgaagaca aagctcttat aagaatcaca 60  
gatgaaagat caggcacaaa tcacattttc ccccttaata acaaaataca aatccaataa 120  
ttttagaaaa tcagttttta gtgaccana tgctggaga aaagctgcca ggatttttct 180  
ggtctatcgc agaattttct acatcaatga gaaggatgct gcatatcttg gctgtattat 240  
ttcctaccgn gagaaaagaa acttaatatata tggaacatgc ttt 283

<210> 374  
<211> 529  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(529)  
<223> n = A,T,C or G

<400> 374  
tccagngtgg tgggaattccg cgcgcggggc gctgctgctg gcgctgctgc tggctcgggc 60  
tggactcagg aagccggagt cgcaggaggc ggcgccctta tcaggaccat gcggccgacg 120  
ggtcatcacg tcgcgcacg tgggtggaga ggacgcgaa ctogggcgtt ggccgtggca 180  
ggggagcctg cgcctgtggg attcccacgt atgcggagtg agcctgctca gccaccgctg 240  
ggcactcacg gcggcgacact gctttgaaac tgacctagt gatccctccg ggtggatggt 300  
ccagtttggc cagctgactt ccattgccatc cttctggagc ctgcaggcct actacacccg 360  
ttacttcgta tcgaatatct atctgagccc tcgctacctg ggaattcac cctatgacat 420  
tgcccttggtg aagctgtctg cacctgtcac ctacactaaa cacatccagc ccactctgtct 480  
ccacggcctc acatttgagt ttgaccccg ggcagactgc tgggtgact 529

<210> 375  
<211> 519  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (1)...(519)  
<223> n = A,T,C or G

<400> 375  
tttgaattta naccaagaac ttctcaataa aagaaaatca tgaatgctcc acaatttcaa 60  
cataccacaa gagaagttaa tttcttaaca ttgtgttcta tgattatttg taagaccttc 120  
accaagtctt gatattcttt aaagacatag ttcaaaattg cttttgaaaa tctgtattct 180  
tgaaaatata cttgttgtgt attaggtttt taaataccag cttaaaggatt acctactga 240  
gtcatcagta ccctcctatt cagctcccca agatgatgtg tttttgctta ccctaagaga 300  
ggttttcttc ttatttttag ataattcaag tgcttagata aattatgttt tctttaagtg 360  
tttatggtaa actcttttaa agaaaattta atatgttata gctgaatctt tttgtaact 420  
ttaaaatctt atcatagact ctgtacatat gttcaaatta gctgcttgcc tgatgtgtgt 480  
atcatcgggtg ggatgacaga acaaacatat ttatgatca 519

<210> 376  
<211> 171  
<212> DNA  
<213> Homo sapiens

131

<400> 376  
 tcaagattta gccaaaggctg tggcaaagggt gtaacttgta aacttgagtt ggagtactat 60  
 atttacaat aaaattggca ccatgtgcca tctgtacata ttactgttgc atttactttt 120  
 aataaagctt gtggcccctt ttactttttt atagcttaaa aaaaaaaaaa a 171

<210> 377  
 <211> 270  
 <212> DNA  
 <213> Homo sapiens

<400> 377  
 ccagtgtggt ggaattaatc aggcctccca aatttagcag gtgctgggga ggaccctagg 60  
 gagtggttta tgggggctag ctggtgaaac tgccctttcc tttctgttct atgagtgtga 120  
 tgggtgtttga gaaaatgtgg ggctatggtt caggcgcaact tcacatgtgc aaagatggag 180  
 aaagcactca cctacacgtt taggctcaga atattgattg aaacattttg aatgatcaaa 240  
 aataaaatgt tattttttaa gtttcaaaaa 270

<210> 378  
 <211> 416  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)... (416)  
 <223> n = A,T,C or G

<400> 378  
 ccagtgtggt ggaattcgcc actgctaggg tttacaggtc atccctggat taaataagtg 60  
 atattgtggt ttttttttct ttgacacaaa gtaaaattat aattaatatt gaataaagta 120  
 aaaatgaact ccagtgnngn ggaattcggc actcaggaaa tattagttgc atgaacgaag 180  
 gcttctctct atcacaagag agatgtggtt cagcccttgc atgtttcaat gaggttctca 240  
 atnccaanag ggctatgcta tcatcctgga gcccaactctg ctaacaatta gcanaacgga 300  
 agccttaatt tccanattct agtgaacttg atgagtcaan actattgcaa ttggaaatct 360  
 gttctctctct gctgctgcat tccctgctta atactcaagc canaaaccag gaaggt 416

<210> 379  
 <211> 576  
 <212> DNA  
 <213> Homo sapiens

<400> 379  
 ttcctatgat cattaaactc attctcaggg ttaagaaagg aatgtaaatt tctgcctcaa 60  
 tttgtacttc atcaataagt ttttgaagag tgcagatttt tagtcagggtc ttaaaaataa 120  
 actcacaaat ctggatgcat ttctaaattc tgcaaatggt tccctggggtg acttaacaag 180  
 gaataatccc acaatatacc tagctaccta atacatggag ctggggctca acccactgtt 240  
 ttttaaggatt tgcgcttact tgtggctgag gaaaaataag tagttcgagg aagtagtttt 300  
 taaatgtgag cttatagata gaaacagaat atcaacttaa ttatgaaatt gttagaacct 360  
 gttctcttgt atctgaatct gattgcaatt actattgtac tgatagactc cagccattgc 420  
 aagtctcaga tatcttagct gtgtagtgat tcttgaaatt ctttttaaga aaaattgagt 480  
 agaaagaaat aaacccttg taaatgaggc ttggcttttg tgaaagatca tccgcaggct 540  
 atgttaaaag gatcttagct cactaaaagt gtaata 576

<210> 380  
 <211> 347  
 <212> DNA  
 <213> Homo sapiens

132

&lt;400&gt; 380

```
ccagtgtgtg ggaattcggg gagaaggaag cctggggccc agccgaggaa gcgaaaaacc 60
aaacaagcag ttcccatgtt ggaaccccaa gaacctgaga tcaaaactaaa atatgccacc 120
cagccactgg ataaaactga tgccaagaac aagtcttttt acccttacat ccatgtagta 180
aataagtgtg aacttggagc cgttttgtaca atcatcaatg ctgaggaaga agaacagacc 240
aaattagtga ggggcaggaa ggggtcagagg tcaactgacce ctccacctag cagcactgaa 300
agcaaggcgc tcccgccctc gtcctttatg ctgcaggagc ctgttgt 347
```

&lt;210&gt; 381

&lt;211&gt; 258

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 381

```
gacaagctcc tggctcttgag atgtcttctc gttaaggaga tgggcctttt ggaggtaaag 60
gataaaatga atgagttctg tcatgattca ctattctaga acttgcatga cctttactgt 120
gttagctctt tgaatgttct tgaaatttta gactttcttt gtaaacaat gatatgtcct 180
tatcattgta taaaagctgt tatgtgcaac agtgtggaga ttccttgtct gatttaataa 240
aataacttaaa cactgaaa 258
```

&lt;210&gt; 382

&lt;211&gt; 580

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 382

```
gccgtaggga gtacctgtcg cccagctga ctgtggcccc ctccgtgac catccatctc 60
caggagcaaa gacagagacg caggaatgga aagcggagtt cctaacagga tgaaagttcc 120
cccatcagtt cccccagtac ctccaagcaa gtagctttcc acatttgtca cagaaatcag 180
aggagagatg gtgttgggag ccctttggag aacgccagtc tcccaggccc cctgcatcta 240
tcgagtttgc aatgtcacia cctctctgat cttgtgctca gcatgattct ttaatagaag 300
ttttattttt tctgtcactc tgctaatacat gtgggtgagc cagtggaaac gcgggagacc 360
tctgttagtt ttacagatcg cctcttactc cccgggtctc aagggaaacc agtggtaag 420
gagttgtttc tgaccactcg atctctacta ccacaaggaa aatagtttag gagaaaccag 480
cttttactgt ttttgaaaaa ttacagcttc accctgtcaa gttaacaagg aatgcctgtg 540
ccaataaaag gtttctccaa cttgaagtct actctgaaaa 580
```

&lt;210&gt; 383

&lt;211&gt; 608

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 383

```
gtgctagatg aaaagcgtgc aatatgyttt aaagctatca acaaaaactg aatattataa 60
gcaagcaata tcatagtaat tggcagatta gctcatattc tatacagcat cgtttaaata 120
ggaaaaatgt aatgctagca aaaaataaat ttagaatat ggcatgacat gaaaatacaa 180
tcttatattt acaccagctt ttcactaata ttttgtacct aagggtgatgg ggaactccat 240
tcagataata aaattctctt tcagctagag aagttaacag gaataaatat atgaacaaaa 300
aagctgcaag gataaatgtg gagaaaatga tgagaattag ctaacatttt taagtttttt 360
taaaactttct tcccctcact tagttgtact taatatttag tggaaagtaa taattttttt 420
aattttctat caactaatag tatagtaact atgattaact tgtttacttt ttctgaggat 480
tagtaaatca attttttttt tatttcaa attttggattt acacttgagg gtaaattaaa 540
tctggtaaac tgaatttcct agttaataa aattagttgc agtatatgat gaacagtgtg 600
tgactcaa 608
```

&lt;210&gt; 384

&lt;211&gt; 585

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

133

<400> 384  
 ttatttcctt aaatattgct acaaaaggaa gatgcggtg taagccctga ttttttttc 60  
 tccaagaaa aatcttaaag gaccacttta gataatattt gattcctact gtaaaattta 120  
 gaaaatgatg aattcttgct catTTTTgtA atcaagattt taggaaaaac agaagtacat 180  
 ctatctttat gaaatttttg gcaggTTTT gtgtatcaat attttgtagt tttagggaat 240  
 attttatttt ttagttattt gtgtcaaat ataattataa aaggtacagc agaaaatata 300  
 ccatgttttt atataggttc acacctgtac ttaggaggga ccctgtccat ctatatactt 360  
 tttgtataaa attttaaaat gttaaagatc cacaaggtct taataaaatg attctatagc 420  
 tagaaaaaca tttaccttcc cagtgtcttg cactaaaaa tactgtgaaa ggaaactaga 480  
 aagactgtaa ctattgctgg aaatgttcta tattgaatgt acatgctctt gttggaaaaa 540  
 tgtctatatg tgatggaaat aaaccagaat cgaagttatt tcaaa 585

<210> 385  
 <211> 511  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(511)  
 <223> n = A,T,C or G

<400> 385  
 atattgtaca gtatttatcg agataaacat ggtwatcaaa atgtccattg tttataagct 60  
 gagaatttgc caatattttt caaggagagg cttcttgctg aattttgatt ctgcagctga 120  
 aatttaggac agttgcaaac gtgaaaagaa gaaaattatt caaatttga catTTtaatt 180  
 gtttaaaaaat tgtacaaaag gaaaaaatta gaataagtag tggcgaaacca tctctgtggt 240  
 cttgtttaaa aaggggcaaaa gtttttagact actaaatttt ttaacagtaa gttataaaat 300  
 ttagtagtct aaaacttata acttactgtt aaaagcaaaa atggccatgc aggttgacac 360  
 cgttggtaat ttataatagc ttttgttcga tcccaacttt ccattttgtt cagataaaaa 420  
 aaaccatgaa attactgngt ttgaaatatt ttcttatggt ttgtaaatatt tctgtaaatt 480  
 attttgtata ttttaaggtat tttccctttt 512

<210> 386  
 <211> 311  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(311)  
 <223> n = A,T,C or G

<400> 386  
 gtggaattcc atgaatntag ttcccatcat gacttanaag gtgctgtagg tgggtactac 60  
 ccagaaccga gtnagctttg tcacttggtat caaagtgatt ctgatttcca tggagatctt 120  
 acatttcaac acgtatttca taaccacact taccacttac agccaactgc accagaatct 180  
 acttctgaac cttttccgtg gcctgggaag tcacagaaga taaggagtag ataccttgaa 240  
 gacacagata gaaacttgag ccgtgatgaa cagcngcta aagctttgca tatccctttt 300  
 tctgtagatg a 311

<210> 387  
 <211> 461  
 <212> DNA  
 <213> Homo sapiens

<400> 387  
 -cacagatagc aagacttcat ttcaggagtt gggagtggga agtaggaagt gtttaatccc 60



134

```

aagttttggt gccctaaaat ggctagtagt atagttaatt ctcaattctc tagctgtgat 120
cttctgtgcc ttctatctct tcctaaggaa aaccacatta gatgaaccca gggctcagtc 180
attttaggga gaggggttgag acaacactgc cagcaacaca gctggaatca cccgagtcgg 240
gaacattaaa gttcctgaga gaatatgaaa caactatcaa cataatattt ctccctactt 300
ttacagtaaa atattggag taaataaata tagggaatgc aacaactggc taggagtgtt 360
ttacattcag ttgtttggaa gcataacaca ttcagctcct ttgaatcttc ccgttagaaa 420
atacagaatt actctatcac cttttaaggt acagtaaaaa a 461

```

<210> 388  
 <211> 555  
 <212> DNA  
 <213> Homo sapiens

```

<400> 388
ggataaaggc cagggatgct gctcaacctc ctaccatgta caggacgtct cccattaca 60
actacccaat ccgaagtgtc aactgtgtca ggactaagaa accctggttt tgagtagaaa 120
agggcctgga aagaggggag ccaacaaatc tgtctgtctc ctcacattag tcattggcaa 180
ataagcattc tgtctctttg gctgctgcct cagcacagag agccagaact ctatcgggca 240
ccaggataac atctctcagt gaacagagtt gacaaggcct atgggaaatg cctgatggga 300
ttatcttcag cttgttgagc ttctaagttt ctttcccttc attctaccct gcaagccaag 360
ttctgtaaga gaaatgcctg agttctagct caggttttct tactctgaat ttagatctcc 420
agacccttcc tggccacaat tcaaattaag gcaacaaaca tataccttcc atgaagcaca 480
cacagacttt tgaaagcaag gacaatgact gcttgaattg aggccttgag gaatgaagct 540
ttgaaggaaa agaatt 555

```

<210> 389  
 <211> 563  
 <212> DNA  
 <213> Homo sapiens

```

<400> 389
ttattttggt cagctgagta ccatcaggat atttaaccct ttaagtgtct ttttgggagt 60
agcaaatata agcaaatata attgctcttg acagcttttg ttggaatgg gttattgagt 120
cattcacctt ggtcctacac tttttaggat gcttgggtgaa cataacacca cttataatga 180
acatcccttg ttcttatatt ttgggctatg tgggtaggaa ttgttacttg ttactgcagc 240
agcagcccta gaaagtaagc ccagggtctc agatctaagt tagtccaaaa gctaaatgat 300
ttaaagtcaa gttgtaatgc taggcataag cactctataa tacattaaat tataggccga 360
gcaattaggg aatgtttctg aaacattaaa cttgtattta tgtcactaaa attctaacac 420
aaacttaaaa aatgtgtctc atacatatgc tgtactaggc ttcatcatgc atttctaaat 480
ttgtgtatga tttgaatata tgaaagratt tatacaagag tggtatttaa aattattaaa 540
aataaatgta tataatttga aaa 563

```

<210> 390  
 <211> 278  
 <212> DNA  
 <213> Homo sapiens

```

<400> 390
gaacattatg ttttagatgg gtagtactag ctactcatct gtccccccaga aaccaagct 60
aagcatggac atattgaaga gaatgtcagc accattaaaa aaactctaga aaaatcacat 120
gtgatgactg aggttaattc agtctgtcaa ttacatcagt ataattgcct tcttgtaacc 180
ctaagtatgg tgaagcagaa ttgaattcta caaaagtctt tcatctgttt tcctatggaa 240
taattaacaa acccaataaa tgtataataa gcatgaaa 278

```

<210> 391  
 <211> 578  
 <212> DNA  
 <213> Homo sapiens

135

<400> 391  
 cgggcgctcg ctcgcaggat ggatcccgt cccgggacag actcggcgcc gctggctggc 60  
 ctggcctggg cgctggcctc tgcacccccg ccgcgggggg tcagcgcgat ctctgcacc 120  
 gtcgaggggg caccgccag ctttggaag agcttcgcgc agaaatctgg ctacttcctg 180  
 tgccttagtt ctctgggcag cctagagaac ccgcaggaga acgtgggtggc cgatatccag 240  
 atcgtggtgg acaagagccc cctgccgctg ggcttctccc ccgtctgcga ccccatggat 300  
 tccaaggcct ctgtgtccaa gaagaaacgc atgtgtgtga agctgttgcc cctgggagcc 360  
 acggacacgg ctgtgtttga tgcgggctg agtggaaga ccaagacagt gcctggatac 420  
 cttcgaatag gggacatggg cggctttgcc atctggtgca agaaggccaa ggccccgagg 480  
 ccagtgccca agccccgagg tctcagccgg gacatgcagg gcctctctct ggatgcagcc 540  
 agccagccaa gtaagggcgg cctcctggag cggacagc 578

<210> 392  
 <211> 439  
 <212> DNA  
 <213> Homo sapiens

<400> 392  
 ttcaacaaac cttgtatagt gtatgttttg ccatatttaa tattaatagc agaggaagac 60  
 tccttttttc atcactgtat gaatttttta taatgttttt ttaaaatata tttcatgtat 120  
 acttataaac taattcacac aagtgtttgt cttagatgat taaggaagac tatatctaga 180  
 tcatgtctga ttttttattg tgacttctcc agccctggtc tgaatttctt aagggtttat 240  
 aaacaaatgc tgcattttat tagctgcaag aatgcacttt agaactattt gacaattcag 300  
 actttcaaaa taaagatgta aatgactggc caataataac catttttagga aggtgttttg 360  
 aattctgtat gtatatattc actttctgac atttagatat gccaaaagaa ttaaaatcaa 420  
 aagcactaag aaataaaaa 439

<210> 393  
 <211> 544  
 <212> DNA  
 <213> Homo sapiens

<400> 393  
 tttgaattta caccaagaac ttctcaataa aagaaaaatca tgaatgctcc acaatttcaa 60  
 cataccacaa gagaagttaa tttcttaaca ttgtgttcta tgattatttg taagaccttc 120  
 accaagtctt gatattcttt aaagacatag ttcaaaattg cttttgaaaa tctgtattct 180  
 tgaataatgc cttgttgtgt attagggttt taaataccag cttaaaggatt acctcactga 240  
 gtcacagta cctctctatt cagctcccca agatgatgtg tttttgctta ccctaagaga 300  
 ggttttcttc ttatttttag ataattcaag tgcttagata aattatgttt tctttaagtg 360  
 tttatggtaa actcttttaa agaaaattta atatgttata gctgaatctt tttggtaact 420  
 ttaaatcttt atcatagact ctgtacatat gttcaaatga gctgcttgcc tgatgtgtgt 480  
 atcatcggtg ggatgacaga acaaacatat ttatgatcat gaataatgtg ctttgtaaaa 540  
 agat 544

<210> 394  
 <211> 424  
 <212> DNA  
 <213> Homo sapiens

<400> 394  
 aaacatcatt tagcagcaat gaacctgtca acacatggaa ataagggtta cagtcatgca 60  
 aatgtccatt taactttgtt tgagccaaac aaatataaca gtaaaactaat tagactggct 120  
 tacatccccg tagacagtga aaccaattat ttcttaaga aggggttgct tgtttttact 180  
 ctagggcaaa ggtgcataac ttcttgtaat actcctgaat agttcttcaa atcaggacag 240  
 ataaagttag caactgatgg aatagctacc ttgatgtgca aatgggtggg tctttaatta 300  
 ggttcattta tataattgag aaagaagcca gggaatgcat ttgtgcaagg atgattttaa 360  
 aagaagaggg atggtctgcc ttttaattct gtatgggagg aaaattcata aaaaactgaa 420  
 aaaa 424

136

<210> 395  
 <211> 279  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> misc\_feature  
 <222> (1)...(279)  
 <223> n = A,T,C or G

<400> 395  
 ttcctatgat nattaaactc attctcaggg ttaagaaagg aatgtaaatt tctgcctcaa 60  
 tttgcacttc atcaataagt ttttgaagag tgccagatttt tagtcaggtc ttaaaaaataa 120  
 actcacaatc ctggatgcat ttctaaattc tgcaaatgtt tccctggggtg acttaacaag 180  
 gaataatccc acaatatacc tagctaccta atacatggag ctggggctca acccactgtt 240  
 ttttaaggatt tgcgcttact tgtggctgan gaaaaataa 279

<210> 396  
 <211> 3293  
 <212> DNA  
 <213> Homo sapiens

<400> 396  
 cagccccggg ccaggccgag gccggggcag gagcgcaggg gctttgttat gcacctaaag 60  
 ccatattgga agctccagaa gaaagagcac cccccggaag tcagcaggga aacgcagaga 120  
 actcctatga accaccaaaa ggctgttaaatt gatgaaacat gcaaaagctag ccacataaca 180  
 tcaagtgtct ttcccttcagc ctctctcggt aaagcatcat ctcgaaagcc atttggggtc 240  
 ctttctocaa atgttctgtg cagtatgagt ggggaagagtc ctgtagagag cagcttgaat 300  
 gttaaaacca aaaagaatgc accatctgca acgatccacc agggcgaaga agaaggacca 360  
 cttgatattct gggctgttgt gaaacctgga aataccaagg aaaaaattgc attctttgca 420  
 tcccaccagt gtagtaacag gataggatct atgaaaaataa aaagttcctg ggatattgat 480  
 gggagagcta ctgagagag gaaaaaatca gggatctta aaaaagccca ggttaagggtg 540  
 gaaagggatga gggagggttaa cagcagggtgc taccaacctg agccttttgc atgtggcatt 600  
 gagcactgtt ctgtgcaacta tgtgagtgc agtggggatg gagtctatgc tgggaggcct 660  
 ctgtcagtta tacagatggt tgcttctctg gagcaagag ccagtgctct gctagctagc 720  
 tgttcaaaaa actgcacaaa ctacacctgca attgtgaggt tttctggcca atccagaggt 780  
 gtgcctgcag tgtctgagtc ctattctgcc ccaggagctt gtgaagaacc cacagaaagg 840  
 ggaatctctg aggttggtga accacagagc gaaccagtc gtgtccttga catggtagcc 900  
 aagttggagt ctgagtgcct gaagcggcag ggccagcgtg agcctgggag cctctcaagg 960  
 aataacagct tccgtcgaaa tgtgggcaga gtattgcttg caaatagcac tcaggctgat 1020  
 gaaggcaaaa caaagaagg cgtcttgag gcacctgaca ctccagtgaa tccctgtggg 1080  
 tctgtatctg tggattgttg cccttcaaga gctgacgtt gttctcctaa ggaggaccag 1140  
 gcctgggacg gtgcttctca ggactgccc ccattgccag caggagttag tttccacata 1200  
 gacagtgcag agttagagcc gggttcgcaa actgcccgtg aaaaacagca cagatatgat 1260  
 gtggaaatga cagatgaact cgttgggtta cctttttcct ctcatacctt tcccaagcc 1320  
 tctgaattgc ccacagatgc tgttgattgt atgagcagag agcttgtgtc ccttactagc 1380  
 cgaatctctg atcaaaagaa agaattcttg tgcattagta tcaactgtgc caaggtagac 1440  
 aaagaccagc cttccatttt aaactcctgt gaagaccag ttccagggat gttgtttttt 1500  
 ttgccacctg gtcagcactt gtcagactat tcccagttga atgaaagcac aacaaaagag 1560  
 tcttcagagg ccagccagct tgaagatgct gctgggggtg acagtgcatc tgaggaaaaa 1620  
 agtgggtctg ctgagccatt tgtactgcca gcctcttctg tggaaagtac attaccagt 1680  
 cttgagcagc ccagttggaa gaagcagggt tgcagtgact tccctggagac cagggtttaa 1740  
 atccagcagc ttttggagcc tcagcagtag atggcttttc tgccccacca cattatggt 1800  
 aaaatcttca ggttacttcc caccaagagt ttagtggtcc ttaaagtac ctgctgctat 1860  
 ttcaagttta tcaattagta ctacaatatc aggcagcagc attctcgtg ggttcagat 1920  
 ccacgctata gagaggatcc ttgcaaacag tgcaagaaaa agtatgtgaa aggggatgtg 1980  
 tccctgtgcc gatggcacc caagccctat tgccaggcat tgccctatgg gccagggtat 2040  
 tggatgtgct gccaccggtc tcagaaagga ttccctggct gtaagctggg gcttcatgac 2100

137

```

aatcactggg ttctgcctg ccacagcttt aatcgggcaa tccataagaa agcaaaaggg 2160
actgaagctg aagaggaata cttaaagtcca tgtgagaggc aacaaaagga ccggtttcta 2220
aagctgcaaa acacctagat acaccgttca aatgagcgta gccccctgag tcatcactct 2280
agaagaatct gtacatcatc aggactgcat tgctcaggca ttttctaaac tctaaattta 2340
cgagctgtac aaaaaaattg gtcttggtgt ttatagtggc atctcatgtt tgaacccggg 2400
tggtatccca cagttggatt cagttggctg tgaataactg cctgttttcc taaatcaaac 2460
ccatcctcaa aggatgaaga ctcaccacca tccaggacat tcagaagagt tcactgcaga 2520
tgctgcaggt agtcctcaaa aatgggttcc agaaatgttt tgagcactgg caacatattt 2580
gaataaagtg aatattgtcc tgtgaaaaga atagcaggac ttttagatga aaagtattct 2640
taaaaagaaa agtcaggcac cccaccttag acctcgtag cttgatcctg tgagattgat 2700
gtttgtggct ggaggtggat ttcatgccct gtggtgttta cagtgtatat aatggttgtg 2760
ttttcatggg gctatgaaag tgcacgttaa acctgagcgc ctttaccttt agatgagtg 2820
tttggccct ctgtgaatag cacgattaaa atccagttgt atataatgga cagctaaccg 2880
aacaatataa tcaccacaat gcagctagga tagtgttgcg gctataattt tgtgtttttt 2940
tttttaatt gtctagtctt aaatttgtag atcttgata aaatatgaat gtttcccaa 3000
taaatatga atgtttcctg tataatatat gaatgtttct gagaagaaac tctaaatagt 3060
tgaaggcta acctgtcaa aggataccaa ataatggttt aactggacaa cctgaaaatt 3120
agcatagaaa acaatccttt gttatatttt agtgatccac aagattgaga aaatattata 3180
tagttagata ataacattct tgtctacttt atcctgtctg gttacaaaat tttttaaacc 3240
ttaataaaaa acatgcatct taaatggaag aaaaaaaa aaaaaaactc gag 3293

```

&lt;210&gt; 397

&lt;211&gt; 727

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 397

```

Gln Pro Arg Ala Arg Pro Arg Pro Gly Gln Glu Arg Arg Gly Phe Val
      5              10              15
Met His Leu Lys Pro Tyr Trp Lys Leu Gln Lys Lys Glu His Pro Pro
      20              25              30
Glu Val Ser Arg Glu Thr Gln Arg Thr Pro Met Asn His Gln Lys Ala
      35              40              45
Val Asn Asp Glu Thr Cys Lys Ala Ser His Ile Thr Ser Ser Val Phe
      50              55              60
Pro Ser Ala Ser Leu Gly Lys Ala Ser Ser Arg Lys Pro Phe Gly Ile
      65              70              75              80
Leu Ser Pro Asn Val Leu Cys Ser Met Ser Gly Lys Ser Pro Val Glu
      85              90              95
Ser Ser Leu Asn Val Lys Thr Lys Lys Asn Ala Pro Ser Ala Thr Ile
      100             105             110
His Gln Gly Glu Glu Glu Gly Pro Leu Asp Ile Trp Ala Val Val Lys
      115             120             125
Pro Gly Asn Thr Lys Glu Lys Ile Ala Phe Phe Ala Ser His Gln Cys
      130             135             140
Ser Asn Arg Ile Gly Ser Met Lys Ile Lys Ser Ser Trp Asp Ile Asp
      145             150             155             160
Gly Arg Ala Thr Lys Arg Arg Lys Lys Ser Gly Asp Leu Lys Lys Ala
      165             170             175
Lys Val Gln Val Glu Arg Met Arg Glu Val Asn Ser Arg Cys Tyr Gln
      180             185             190
Pro Glu Pro Phe Ala Cys Gly Ile Glu His Cys Ser Val His Tyr Val
      195             200             205
Ser Asp Ser Gly Asp Gly Val Tyr Ala Gly Arg Pro Leu Ser Val Ile
      210             215             220
Gln Met Val Ala Phe Leu Glu Gln Arg Ala Ser Ala Leu Leu Ala Ser
      225             230             235             240
Cys Ser Lys Asn Cys Thr Asn Ser Pro Ala Ile Val Arg Phe Ser Gly
      245             250             255

```

138

Gln Ser Arg Gly Val Pro Ala Val Ser Glu Ser Tyr Ser Ala Pro Gly  
 260 265 270  
 Ala Cys Glu Glu Pro Thr Glu Arg Gly Asn Leu Glu Val Gly Glu Pro  
 275 280 285  
 Gln Ser Glu Pro Val Arg Val Leu Asp Met Val Ala Lys Leu Glu Ser  
 290 295 300  
 Glu Cys Leu Lys Arg Gln Gly Gln Arg Glu Pro Gly Ser Leu Ser Arg  
 305 310 315 320  
 Asn Asn Ser Phe Arg Arg Asn Val Gly Arg Val Leu Leu Ala Asn Ser  
 325 330 335  
 Thr Gln Ala Asp Glu Gly Lys Thr Lys Lys Gly Val Leu Glu Ala Pro  
 340 345 350  
 Asp Thr Gln Val Asn Pro Val Gly Ser Val Ser Val Asp Cys Gly Pro  
 355 360 365  
 Ser Arg Ala Asp Arg Cys Ser Pro Lys Glu Asp Gln Ala Trp Asp Gly  
 370 375 380  
 Ala Ser Gln Asp Cys Pro Pro Leu Pro Ala Gly Val Ser Phe His Ile  
 385 390 395 400  
 Asp Ser Ala Glu Leu Glu Pro Gly Ser Gln Thr Ala Val Lys Asn Ser  
 405 410 415  
 Asn Arg Tyr Asp Val Glu Met Thr Asp Glu Leu Val Gly Leu Pro Phe  
 420 425 430  
 Ser Ser His Thr Tyr Ser Gln Ala Ser Glu Leu Pro Thr Asp Ala Val  
 435 440 445  
 Asp Cys Met Ser Arg Glu Leu Val Ser Leu Thr Ser Arg Asn Pro Asp  
 450 455 460  
 Gln Arg Lys Glu Ser Leu Cys Ile Ser Ile Thr Val Ser Lys Val Asp  
 465 470 475 480  
 Lys Asp Gln Pro Ser Ile Leu Asn Ser Cys Glu Asp Pro Val Pro Gly  
 485 490 495  
 Met Leu Phe Phe Leu Pro Pro Gly Gln His Leu Ser Asp Tyr Ser Gln  
 500 505 510  
 Leu Asn Glu Ser Thr Thr Lys Glu Ser Ser Gln Ala Ser Gln Asn Glu  
 515 520 525  
 Asp Ala Ala Gly Gly Asp Ser Ala Ser Glu Glu Lys Ser Gly Ser Ala  
 530 535 540  
 Glu Pro Phe Val Leu Pro Ala Ser Ser Val Glu Ser Thr Leu Pro Val  
 545 550 555 560  
 Leu Glu Ala Ser Ser Trp Lys Lys Gln Val Ser His Asp Phe Leu Glu  
 565 570 575  
 Thr Arg Phe Lys Ile Gln Gln Leu Leu Glu Pro Gln Gln Tyr Met Ala  
 580 585 590  
 Phe Leu Pro His His Ile Met Val Lys Ile Phe Arg Leu Leu Pro Thr  
 595 600 605  
 Lys Ser Leu Val Ala Leu Lys Cys Thr Cys Cys Tyr Phe Lys Phe Ile  
 610 615 620  
 Ile Glu Tyr Tyr Asn Ile Arg Pro Ala Asp Ser Arg Trp Val Arg Asp  
 625 630 635 640  
 Pro Arg Tyr Arg Glu Asp Pro Cys Lys Gln Cys Lys Lys Lys Tyr Val  
 645 650 655  
 Lys Gly Asp Val Ser Leu Cys Arg Trp His Pro Lys Pro Tyr Cys Gln  
 660 665 670  
 Ala Leu Pro Tyr Gly Pro Gly Tyr Trp Met Cys Cys His Arg Ser Gln  
 675 680 685  
 Lys Gly Phe Pro Gly Cys Lys Leu Gly Leu His Asp Asn His Trp Val  
 690 695 700  
 Pro Ala Cys His Ser Phe Asn Arg Ala Ile His Lys Lys Ala Lys Gly  
 705 710 715 720  
 Thr Glu Ala Glu Glu Glu Tyr

139

725

<210> 398  
<211> 403  
<212> DNA  
<213> Homo sapiens

<400> 398  
ccagtgtggt ggaattccag cctcgtgccg ggagtcgcgc catttgtgtc cgcttctctg 60  
cactatgtcg ggtggcctcc tgaaggcgct gcgcagcgac tcctacgtgg agctgagcca 120  
gtaccgggac cagcacttcc ggggtgacaa tgaagaacaa gaaaaattac tgaagaaaag 180  
ctgtacgtta tatgttgaa atctttcttt ttacacaact gaagaacaaa tctatgaact 240  
cttcagcaaa agtgggtgaca taaagaaaat cattatgggt ctggataaaa tgaagaaaac 300  
agcatgtgga ttctgttttg tggaatatta ctcacgcgca gatgcggaaa acgccatgcg 360  
gtacataaat gggacgcgtc tggatgaccg aatcattcgc aca 403

<210> 399  
<211> 403  
<212> DNA  
<213> Homo sapiens

<400> 399  
ttttgatgct ttctttcatg ggaatagtca cttttttatt tagtaaactg cattgctgga 60  
accaccaagg agtgtggaat gtccttgagt gtattattta tgcaagtcac agtcacgttg 120  
ccatcatggc agctatgtga aacactaata aatgtgtttt tactttttat tcccgtaaa 180  
actgatgtaa aacaggataa aggccttgta tagtcaacta taagtatctg ggtctaagta 240  
atttccttag atgttttctaa agaaacattt tcagctttgc tcccattatg attccaataa 300  
ggaacgcttt cctagtgcaa ttttaggagt aaagtttgaa gagataaaaa tagccaaaga 360  
taggagacgt ctgaattttg aatgataaac agtcatgttt taa 403

<210> 400  
<211> 383  
<212> DNA  
<213> Homo sapiens

<400> 400  
ttatttttcc cctcaaattc atgattttta cgtctgttac aaagggaatt ttgctgatag 60  
ctctttgggt cccactgttc catthttatgc taatagattc cattctaggg cccagccgtc 120  
tcttgactga tgggtgtccc ttttaaccctt ggcattgtata atagaatttt ggtgaatgaa 180  
agaacccaaa taggccagat agtcccccca ggccttgata tccataaaaag gcttggggaat 240  
gcattatgta attgtcctta gtctttttgt tgttttagaa aaa 283

<210> 401  
<211> 303  
<212> DNA  
<213> Homo sapiens

<400> 401  
cataaagggt gtgcgcgtct tcgacgtggc ggtcttgccg ccactgctgc gagaccgcgc 60  
cctggacctc aaggtcatcc acttgggtgc tgatccccgc gcggtggcga gttcacggat 120  
ccgctcgcgc caccgcctca tccgtgagag cctacaggtg gtgcgcagcc gagaccgcgc 180  
agctcaccgc atgcccttct tggaggccgc gggccacaag cttggcgcca agaaggaggg 240  
cgtgggcggc cccgcagact accacgctct gggcgctatg gaggtcatct gcaatagtat 300  
ggc 303

<210> 402  
<211> 473  
<212> DNA

140

&lt;213&gt; Homo sapiens

&lt;400&gt; 402

```

ccaacacagt cagaacatt gttttgaatc ctctgtaaac caaggcatta atcttaataa 60
accaggatoc atttaggtac cacttgatat aaaaaggata tccataatga atattttata 120
ctgcatcctt tacattagcc actaaatacg ttattgcttg atgaagacct ttcacagaat 180
cctatggatt gcagcatttc acttggctac ttcataccca tgccttaaag aggggcagtt 240
tctcaaaagc agaaacatgc cgccagttct caagttttcc tcctaactcc atttgaatgt 300
aagggcagct ggccccaat gtggggaggt ccgaacattt tctgaattcc cattttcttg 360
ttcgcggtta aatgacagtt tctgtcatta cttagattcc gatctttccc aaagggtgtg 420
atttacaag aggccagcta atagcagaaa tcatgaccct gaaagagaga tga 473

```

&lt;210&gt; 403

&lt;211&gt; 513

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 403

```

ggcattaact tttagaattt gggctggtga gattaatttt ttttaatatc ccagctagag 60
atatggcctt taactgacct aaagagggtgt gttgtgattt aattttttcc cgttcctttt 120
tcttcagtaa acccaacaat agtctaacct taaaaattga gttgatgtcc ttatagggtca 180
ctacccctaa ataaacctga agcaggtggt ttctcttgga catactaaaa aatacctaaa 240
aggaagctta gatggtctgt gacacaaaaa attcaattac tgtcatctaa tgccagctgt 300
taaaagtgtg gccactgagc atttgatttt ataggaaaaa atagtatttt tgagaataac 360
atagctgtgc tattgcacat ctgttgaggg acatcccaga tttgcttata ctcagtgcct 420
gtgatattga gttaaaggat ttgaggcagg ggtaattatt aaacatattg cttctattct 480
tggaaaaata gaagtgtaaa atgttaataa tac 513

```

&lt;210&gt; 404

&lt;211&gt; 533

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 404

```

ccagtgtggt ggaattcgcg gtaggtggtg accataacac aagcatgact atatgaagga 60
agaggaaagg tttcctgaag atgaggcgac tgaatcggaa aaaaacttta agtttggtta 120
aagagttgga tgcctttccg aaggttcctg agagctatgt agagacttca gccagtggag 180
gtacagtttc tctaatagca tttacaacta tggctttatt aaccataatg gaattctcag 240
tatatcaaga tacatggatg aagtatgaat acgaagtaga caaggatttt tctagcaaat 300
taagaattaa tatagatatt actgttgcca tgaagtgtca atatgttgga gcggatgtat 360
tggatttagc agaaacaatg gttgcatctg cagatggttt agtttatgaa ccaacagtat 420
ttgatctttc accacagcag aaagagtggc agaggatgct gcagctgatt cagagtaggc 480
tacaagaaga gcattcactt caagatgtga tatttaaaag tgcttttaaa agt 533

```

&lt;210&gt; 405

&lt;211&gt; 513

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(513)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 405

```

ccagnngngt ggaattcctt agacatattc tgagcctaca gcagaggaac ctccagtctc 60
agcaccatga atcaaaactgc cattctgatt tctgtcctta tctttctgac tctaagtggc 120
attcaaggag tacctctctc tagaactgta cgctgtacct gcacagcat tagtaatcaa 180
cctgttaatc caaggtcttt agaaaaactt gaaattattc ctgcaagcca attttgtcca 240

```

141

```

cgtgttgaga tcattgctac aatgaaaaag aagggtgaga agagatgtct gaatccagaa 300
tcgaaggcca tcaagaatct actgaaagca gttagcaagg aaaggctctaa aagatctcct 360
taaaaccaga ggggagcaaa atcgatgcag tgcttccaag gatggaccac acagaggctg 420
cctctcccat cacttccta catggagtat atgtcaagcc ataattgttc ttagtttgca 480
gttacctaa aagggtgacca atcatgggtca cca 513

```

```

<210> 406
<211> 483
<212> DNA
<213> Homo sapiens

```

```

<400> 406
atataccatt taatacatct acactttctt atttaagaag atattgaatg caaaataatt 60
gacatataga actttacaaa catatgtcca aggactctaa attgagactc ttccacatgt 120
acaatctcat catcctgaag cctataatga agaaaaagat ctagaactg agttgtggag 180
ctgactctaa tcaaatgtga tgattggaat tagaccattt ggcctttgaa ctttcatagg 240
aaaaatgacc caacatttct tagcatgagc tacctcatct ctagaagctg ggatggactt 300
actattcttg tttatatttt agatactgaa aggtgctatg cttctgttat tattccaaga 360
ctggagatag gcagggctaa aaagggtatta ttatttttcc tttaatgatg gtgctaaaat 420
tcttctata aaattcctta aaaataaaga tggtttaatc actaccattg tgaaaacata 480
act 483

```

```

<210> 407
<211> 241
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(241)
<223> n = A,T,C or G

```

```

<400> 407
tcacaaagnc cactttactc aaattggtga acagngnata ggaagaagcc agcaggagct 60
ctgactaagg ttgacataat angtccacct cccattactt tgatatctga tcaaatgtat 120
agactnggct ttgttttttg tgctattagg aaattctgat gagcattact attcactgat 180
gcagaagac gttcttttgc ataaaagact ttttttaaca ctttggactt ctctgaaata 240
t 241

```

```

<210> 408
<211> 213
<212> DNA
<213> Homo sapiens

```

```

<400> 408
ccagtgtggt ggaattcaca tgatacagcc actgggctta tacagtatgc attggaccag 60
ggcgtgaacg tcaccagggt attcgtggac accgtaggga tgccagagac ataccaggcg 120
cggttgacgc aaagtcttcc cgggattgag gggaccggcc aaggccaaag cagatgccct 180
ctaccgggtg gttagtgtcg ccagcatctg tgc 213

```

```

<210> 409
<211> 413
<212> DNA
<213> Homo sapiens

```

```

<400> 409
tcagatgagt ggctgctgaa ggggccccct tgtcattttc attataaccc aatttccact 60
tatttgaact cttaagtcac aaatgtataa tgacttatga attagcacag ttaagttgac 120
actagaaact gcccatctct gtattacact atcaaatagg aaacattgga aagatgggga 180

```



142

```

aaaaaatctt attttaaaat ggcttagaaa gttttcagat tactttgaaa attctaaact 240
tctttctgtt tccaaaactt gaaaatatgt agatggactc atgcattaag actgttttca 300
aagctttcct cacattttta aagtgtgatt ttccttttaa tatacatatt tattttcttt 360
aaagcagcta tatcccaacc catgactttg gagatatacc tataaaacca ata 413

```

```

<210> 410
<211> 153
<212> DNA
<213> Homo sapiens

```

```

<220>
<221> misc_feature
<222> (1)...(153)
<223> n = A,T,C or G

```

```

<400> 410
gcaaaccacg actgaagaaa gacgaaaagt gggaaataac ttgcaacgtc tgtagagat 60
ggttgctaca catgttgggt ctgtaganaa acatcttgag gagcagattc cttaaagtga 120
taganaatat gaagaatgca tgtcaaaaga tct 153

```

```

<210> 411
<211> 253
<212> DNA
<213> Homo sapiens

```

```

<400> 411
cagtgtgggt gaattcgtcg gcgaaagcgg cggaagttc gtactgggca gaacgcgacg 60
ggtctgcggc ttagtgaaa atgcctcgtg taaaagcagc tcaagctgga agacagagct 120
ctgcaaagag acatcttgca gaacaatttg caagttggag agataataac tgacatggca 180
aaaaaggaat ggaaagtagg attaccatt ggccaaggag gctttggctg tatatatctt 240
gctgatatga att 253

```

```

<210> 412
<211> 3079
<212> DNA
<213> Homo sapiens

```

```

<400> 412
gaagtgagta gtgggggtgc cagaccaggt gcgtctgccg ctggattgtg ataggaagca 60
gagtgttcgt gtgaaagatg gatactatga tgctgaatgt gcggaatctg tttgagcagc 120
ttgtgcgcgg ggtggagatt ctcaagtgaag gaaatgaagt ccaatttatc cagttggcga 180
aggactttga ggatttccgt aaaaagtggc agaggactga ccatgagctg gggaaatata 240
aggatctttt gatgaaagca gagactgagc gaagtgcctc ggatgttaag ctgaagcatg 300
cacgtaatca ggtggatgta gagatcaaac ggagacagag agctgaggct gactgcgaaa 360
agctggaacg acagattcag ctgattcgag agatgctcat gtgtgacaca tctggcagca 420
ttcaactaag cgaggagcaa aaatcagctc tggcttttct caacagaggc caaccatcca 480
gcagcaatgc tgggaacaaa agactatcaa ccattgatga atctggttcc attttatcac 540
atatcagctt tgacaagact gatgaatcac tggattggga ctcttctttg gtgaagactt 600
tcaaactgaa gaagagagaa aagaggcgct ctactagccg acagtttgtt gatgggtccc 660
ctggacctgt aaagaaaact cgttccattg gctctgcagt agaccagggg aatgaatcca 720
tagttgcaaa aactacagtg actgttccca atgatggcgg gcccatcgaa gctgtgtcca 780
ctattgagac tgtgccatat tggaccagga gccgaaggaa aacaggtact ttacaacctt 840
ggaaacagtga ctccaccctg aacagcaggc agctggagcc aagaactgag acagacagtg 900
tgggcacgcc acagagtaat ggagggatgc gcctgcatga ctttgtttct aagacggtta 960
ttaaacctga atcctgtgtt ccattgtgaa agcggataaa atttggcaaa ttatctctga 1020
agtgtcgaga ctgtcgtgtg gtctctcatc cagaatgtcg ggaccgctgt ccccttccct 1080
gcattccctac cctgatagga acacctgtca agattggaga gggaaatgctg gcagactttg 1140
tgtcccagac ttctccaatg atccctcca ttgttgtgca ttgtgtaaat gagattgagc 1200
aaagaggtct gactgagaca ggcctgtata ggatctctgg ctgtgaccgc acagtaaaag 1260

```

143

```

agctgaaaga gaaattcctc agagtgaaaa ctgtaccctt cctcagcaaa gtggatgata 1320
tccatgctat ctgtagcctt ctaaaagact ttcttcgaaa cctcaaagaa cctcttctga 1380
cctttgcct taacagagcc tttatggaag cagcagaaat cacagatgaa gacaacagca 1440
tagctgccat gtaccaagct gttggtgaac tgccccaggc caacaggac acattagctt 1500
tcctcatgat ccacttgcag agagtggctc agagtccacq tactaaaatg gatgttgcca 1560
atctggctaa agtctttggc cctacaatag tggcccatgc tgtgccaat ccagaccag 1620
tgacaatggt acaggacatc aagcgtcaac ccaaggtggt tgagcgcctg ctttccttgc 1680
ctctggagta ttggagtcag ttcattgatgg tggagcaaga gaacattgac cccctacatg 1740
tcattgaaaa ctcaaatgcc ttttcaacac cacagacacc agatattaaa gtgagtttac 1800
tgggacctgt gacctcctt gaacatcagc ttctcaagac tccttcatct agttccctgt 1860
cacagagagt ccgttccacc ctcaccaaga acactcctag atttgggagc aaaagcaagt 1920
ctgccactaa cctaggacga caaggcaact tttttgcttc tccaatgctc aagtgaagtc 1980
acatctgcct gttacttccc agcattgact gactataaga aaggacacat ctgtactctg 2040
ctctgcagcc tcctgtactc attactactt ttagcattct ccaggctttt actcaagttt 2100
aattgtgcat gagggtttta ttaaaactat atatatcttc ccttccctct cctcaagtca 2160
cataatatca gcactttgtg ctgggtcattg ttgggagctt ttagatgaga catctttcca 2220
ggggtagaag ggttagtatg gaattggtt tgattctttt tggggaaggg ggttattgtt 2280
cctttggctt aaagccaaat gctgctcata gaatgatctt tctctagttt catttagaac 2340
tgatttccgt gagacaatga cagaaaccct acctatctga taagattagc ttgtctcagg 2400
gtgggaagtg ggagggcagg gcaaagaaag gattagacca gaggatttag gatgcctcct 2460
tctaagaacc agaagtctc attccccatt atgaactgag ctataatatg gagctttcat 2520
aaaaatggga tgcattgagg acagaactag tgatgggagt atgcgtagct ttgatttgya 2580
tgattaggtc tttaatagtg ttgagtggca caaccttgta aatgtgaaag tacaactcgt 2640
atttctctct gatgtgccgc tggctgaact ttgggttcat ttgggttcaa agccagtttt 2700
tcttttaaaa ttgaattcat tctgatgctt ggccccata ccccaacct tgtccagtgg 2760
agcccaactt ctaaaggtea atatatcatc ctttggcatc ccaactaaca ataaagagta 2820
ggctataagg gaagattgtc aatattttgt ggtaagaaaa gctacagtca ttttttctt 2880
gcactttgga tgctgaaatt tttcccatgg aacatagcca catctagata gatgtgagct 2940
ttttcttctg ttaaaattat tcttaatgtc tgtaaaaacg attttcttct gtagaatgtt 3000
tgacttcgta ttgacctta tctgtaaaac acctatttg gataatattt ggaaaaaagt 3060
aaatagcttt ttcaaaatg 3079

```

&lt;210&gt; 113

&lt;211&gt; 632

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 413

```

Met Asp Thr Met Met Leu Asn Val Arg Asn Leu Phe Glu Gln Leu Val
      5              10              15
Arg Arg Val Glu Ile Leu Ser Glu Gly Asn Glu Val Gln Phe Ile Gln
      20              25              30
Leu Ala Lys Asp Phe Glu Asp Phe Arg Lys Lys Trp Gln Arg Thr Asp
      35              40              45
His Glu Leu Gly Lys Tyr Lys Asp Leu Leu Met Lys Ala Glu Thr Glu
      50              55              60
Arg Ser Ala Leu Asp Val Lys Leu Lys His Ala Arg Asn Gln Val Asp
      65              70              75              80
Val Glu Ile Lys Arg Arg Gln Arg Ala Glu Ala Asp Cys Glu Lys Leu
      85              90              95
Glu Arg Gln Ile Gln Leu Ile Arg Glu Met Leu Met Cys Asp Thr Ser
      100             105             110
Gly Ser Ile Gln Leu Ser Glu Glu Gln Lys Ser Ala Leu Ala Phe Leu
      115             120             125
Asn Arg Gly Gln Pro Ser Ser Ser Asn Ala Gly Asn Lys Arg Leu Ser
      130             135             140
Thr Ile Asp Glu Ser Gly Ser Ile Leu Ser His Ile Ser Phe Asp Lys
      145             150             155             160
Thr Asp Glu Ser Leu Asp Trp Asp Ser Ser Leu Val Lys Thr Phe Lys

```

[illegible]

<210> 414  
<211> 3061  
<212> DNA  
<213> Homo sapiens

<400> 414  
cggcacgagg cgacttttgg ggaggtagtt ctttggcagc gggcatggcg ggtaccgtgg 60  
tgctggacga tgtggagctg cgggaggctc agagagatta cctggacttc ctggacgacg 120  
aggaagacca ggaatttat cagagcaaag ttcgggagct gatcagtac aaccaatacc 180  
ggctgattgt caatgtgaat gacctgcgca ggaaaaacga gaagagggtt aaccggcttc 240  
tgaacaatgc ctttgaggag ctggttgccct tccagcgggc cttaaaggat tttgtggcct 300  
ccattgatgc tacctatgcc aagcagtagt aggagttcta cgtaggactg gaaggcagct 360  
ttggctccaa gcacgtctcc ccgcggactc ttacctctg cttctcagc tgtgtggtct 420  
gtgtggaggg cattgtcact aaatgttctc tagttcgtcc caaagtcgtc cgcagtgtcc 480  
actactgtcc tgcactaag aagaccatag agcgcgtta tctgatctc accaccctgg 540  
tggcctttcc ctccagctct gtctatccta ccaaggatga ggagaacaat ccccttgaga 600  
cagaatatgg cctttctgtc tacaaggatc accagaccat caccatccag gagatgccgg 660  
agaaggcccc agcggccag ctccccgct ctgtggacgt cattctggat gatgacttgg 720  
tggataaagc gaagcctggg gaccgggttc aggtggtggg aacctaccgt tgccttctg 780  
gaaagaaggg aggtacacc tctgggacct tcaggactgt cctgattgcc tgaatgtta 840  
agcagatgag caaggatgct cagccctctt tctctgtga ggatatagcc aagatcaaga 900  
agttcagtaa aaccgatcc aagtatatct ttgaccagct ggccaagtca ttggcccaa 960  
gtatccatgg gcatgactat gtcaagaaag caatcctctg cttgctcttg ggaggggtgg 1020  
aacgagacct agaaaatggc agccacatcc gtggggacat caatattctt ctaataggag 1080  
accatccgt tgcgaagtct cagcttctgc ggtatgtgct ttgcaactga ccccgagcta 1140  
tccccaccac tggccggggc tctctggag tgggtctgac ggtgctgtc accacagacc 1200  
aggaacacag agagcgccgt ctggaagcag ggccatggg cctggctgac cgaggcgtgg 1260  
tttgcattga tgaatttgac aaaatgtctg acatggatcg cacagccatc catgaagtga 1320  
tggagcaggg tgcagtgacc attgccaagg ctggcatcca tgcctggctg aatgcccgt 1380  
gcagtgtttt ggcagctgcc aaccctgtct acggcaggta tgaccagtat aagactccaa 1440  
tgggagacct tgggtacag gactcactgc tctcagatt tgacttgctc ttcctcatga 1500  
tggatcagat ggatcctgag caggatcggg agatctcaga ccatgtcctt cggatgcacc 1560  
gttacagagc acctggggag caggatggcg atgctatgcc cttgggtagt gctgtggata 1620  
tcttggccac agatgatccc aactttagcc aggaagatca gcaggacacc cagatttatg 1680  
agaagcatga caaccttcta catgggacca agaagaaaaa ggagaagatg gtgagtgcag 1740  
cattcatgaa gaagtacatc catgtggcca aaatcatcaa gcctgtcctg acacaggagt 1800  
cgccacccta cattgcagaa gattattcac gcctgcgcag ccaggatagc atgagctcag 1860  
acaccgccag gacatctcca gttacagccc gaacactgga aactctgatt cgactggcca 1920  
cagcccatgc gaaggccgc atgagcaaga ctgtggacct gcaggatgca gaggaagctg 1980  
tggagttggt ccagtatgct tactttaaga aggttctgga gaaggagaag aaacgtaaga 2040  
agcgaagtga ggatgaatca gagacagaag atgaagagga gaaaagccaa gaggaccagg 2100  
agcagaagag gaagagaagg aagactcgcc agccagatgc caaagatggg gattcatacg 2160  
acccctatga cttcagtgc acagaggagg aaatgcctca agtgaggatt gattgaatcc aggttgaagg 2220  
cagactcaca ggagaccaag gaatcccaga aagtgaggat gattgaatcc aggttgaagg 2280  
cattcaaggt ggcctcttg gatgtgttcc ggaagctca tgcgcagtca atcggcata 2340  
atcgccctac agaattccatc aaccgggaca gcgaagagcc cttctcttca gttgagatcc 2400  
aggctgctct gagcaagatg caggatgaca atcaggtcat ggtgtctgag ggcatactct 2460  
tctctatctg aggagccctc gtctctgaac ttgggttgty ccgagagagt ttgttctgtg 2520  
tttcccaccc tctccctgac ccaagtcttt gcctctactc ccttaacagt gttgaattca 2580  
actgaaggcg aggaatgttg gtgatgaagc tgagttcagg actcgggtgga ccctttggga 2640  
atgggtcatg aaagctgcca tggggtgagg aaagaggaga cagtgggaga ggacaatgac 2700  
tattgcatct tcattgcaaa agcactggct catccgccct acttcccac ccacacaaac 2760  
ccaattgtaa ataacatatg acttctgagt acttttggg gcacaactgt tttctgtttg 2820  
ctgttttttt gttttgtttt ttttctccag agcacttttg tctagactag gctttgggtg 2880  
gttccaattg gtggagagaa gctctgaggc agtcatgca ggtcaagaaa gctttctttg 2940  
cagtagcacc agttaagggt aatatgtatt gtatcacaaa acaaacccaa tatccagatg 3000  
aatatccgag atgttgaata aacttagcca tttcgtacaa aaaaaggggg gcccggtaaa 3060

146

3061

c

<210> 415  
 <211> 732  
 <212> DNA  
 <213> Homo sapiens

<400> 415  
 tgctgcgaac cacgtgggtc ccggggcgct ttcgggtgct ggccggctgca gccggagtgc 60  
 aaacctaaagc agctgggaag aacctgggcc aactgtgagc gtaccttcat tgcgatcaaa 120  
 ccagatgggg tccagcgggg tcttgtggga gagattatca agcgttttga gcagaaaagga 180  
 ttccgccttg ttggtctgaa attcatgcaa gcttccgaag atcttctcaa ggaacactac 240  
 gttgacctga aggacctcc attctttgcc ggctgtgga aatacatgca ctcagggccg 300  
 gtagttgcca tggctctggga ggggctgaat gtggtgaaga cgggcccagat catgctcggg 360  
 gagaccaacc ctgcagactc caagcctggg accatccgtg gagacttctg catacaagtt 420  
 ggcaggaaca ttatacatgg cagtgattct gtggagagtg cagagaagga gatcggcttg 480  
 tggtttcacc ctgaggaact ggtagattac acgagctgtg ctcagaactg gatctatgaa 540  
 tgacaggagg gcagaccaca ttgcttttca catccatttc cctccttcc catgggcaga 600  
 ggaccaggct taggaaaatc tagttattta caggaaacttc atcataattt ggagggaagc 660  
 tcttgagct gtgagttctc cctgtacagt gttaccatcc ccgacctct gattaaaatg 720  
 cttctccca gc 732

<210> 416  
 <211> 2846  
 <212> DNA  
 <213> Homo sapiens

<400> 416  
 gactgagcga agtgcctctg atgttaagct gaagcatgca cgtaatcagg tggatgtaga 60  
 gatcaaacgg agacagagag ctgaggctga ctgcgaaaag ctggaacgac agattcagct 120  
 gattcgagag atgctcatgt gtgacacatc tggcagcatt caactaagcg aggagcaaaa 180  
 atcagctctg gcttttctca acagaggcca accatccagc agcaatgctg ggaacaaaag 240  
 tgaatcaact agtgcgaat ctggttccat tttatcagat atcagcttgc ccaggactga 300  
 gaggcgctct actagccgac agtttgttga tgggtccctt ggacctgtaa agaaaactcg 360  
 ttccatttgc tctgcagtag accaggggaa tgaatccata gttgcaaaaa ctacagtgc 420  
 tgttcccaat gatggcgggc ccacgaagc tgtgtccact attgagactg tgccatattg 480  
 gaccaggagc cgaaggaaaa caggtaactt acaaccttgg aacagtgcct ccacctgaa 540  
 cagcaggcag ctggagccaa gaactgagac agacagtgtg ggcacgccac agagtaattg 600  
 agggatgcgc ctgcatgact ttgtttctaa gacggttatt aaacctgaat cctgtgttcc 660  
 atgtggaaag cggataaaat ttggcaaat atctctgaag tgtcgagact gtcgtgtggt 720  
 ctctcatcca gaatgtcggg accgctgtcc ccttccctgc attcctaccc tgataggaa 780  
 acctgtcaag attggagagg gaatgctggc agactttgtg tccagactt ctccaatgat 840  
 cccctccatt gttgtgcatt gtgtaaatga gattgagcaa agaggtctga ctgagacagg 900  
 cctgtatagg atctctggct gtgaccgcac agtaaaagag ctgaaagaga aattcctcag 960  
 agtgaaaact gtacccctcc tcagcaaggt ggatgatatc catgctatct gtacgcttct 1020  
 aaaagacttt cttcgaacc tcaaagaacc tcttctgacc tttcgcctta acagagcctt 1080  
 tatggaagca gcagaaatca cagatgaaga caacagcata gctgccatgt accaagctgt 1140  
 tgggtgaact cccagggcca acagggacac attagcttcc ctcatgattc acttgacag 1200  
 agtggctcag agtccacata ctaaaatgga tgttgccaat ctggctaaag tctttggccc 1260  
 tacaatagtg gcccatgctg tgcccaatcc agaccagtg acaatgttac aggacatcaa 1320  
 gcgtaacccc aaggtggttg agcgcctgct ttccttgccct ctggagtatt ggagtcagtt 1380  
 catgatgggt gagcaagaga acattgaccc cctacatgtc attgaaaact caaatgcctt 1440  
 ttcaacacca cagacaccag atattaaagt gattttactg ggacctgtga ccaactcctga 1500  
 acatcagctt ctcaagactc cttcatctag ttccctgtca cagagagtcc gttccacct 1560  
 caccaagaac actcctagat ttgggagcaa aagcaagtct gccactaacc taggacgaca 1620  
 aggaactttt tttgcttctc caatgctcaa gtgaagtcac atctgcctgt tacttccag 1680  
 cattgactga ctataagaaa ggacacatct gtactctgct ctgcagcctc ctgtactcat 1740  
 tactactttt agcattctcc aggcctttac tcaagtttaa ttgtgcatga gggttttatt 1800

147

```

aaaactatat atatctcccc ttcccttctcc tcaagtcaca taatatcagc actttgtgct 1920
ggtcattggt gggagctttt agatgagaca tctttccagg ggtagaaggg ttagtatgga 1980
attggttggt attctttttt ggggaagggg ttattgttcc ttgggcttaa agccaaatgc 2040
tgctcataga atgatctttc tctagtttca tttagaactg atttccgtga gacaatgaca 2100
gaaaccctac ctatctgata agattagctt gtctcagggt gggaagtggg agggcagggc 2160
aaagaaagga ttagaccaga ggatttagga tgcctccttc taagaaccag aagttctcat 2220
tccccattat gaactgagct ataatatgga gctttcataa aaatgggatg cattgaggac 2280
agaactagtg atgggagtat gcgtagcttt gatttggatg attaggtctt taatagtgtt 2340
gagtggcaca accttgtaaa tgtgaaagta caactcgtat ttatctctga tgtgccgctg 2400
gctgaacttt ggggtcattt ggggtcaaaag ccagtttttt ttttaaaatt gaattcattc 2460
tgatgcttgg ccccatatac cccaaccttg tccagtggag cccaactctt aaaggtcaat 2520
atatcatcct ttggcatccc aactaacaat aaagagtagg ctataaggga agattgtcaa 2580
tattttgtgg taagaaaagc tacagtcatt ttttctttgc actttggatg ctgaaatttt 2640
tcccatggaa catagccaca tctagataga tgtgagcttt ttcttctgtt aaaattattc 2700
ttaatgtctg taaaaacgat tttcttctgt agaattgttg acttcgtatt gacccttattc 2760
tgtaaaaacac ctatttggga taatatttgg aaaaaaagta aatagctttt tcaaatgaa 2820
aaaaaaaaaa aaaaaaaaaa ctcgag 2846

```

&lt;210&gt; 417

&lt;211&gt; 1602

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 417

```

atgctcctgg acgcgggtcc gcagttcccg gccatcgggg tgggcagctt cgcgcgccac 60
catcaccact ccgcgcgggc ggcggcgggc gctgccgcgg agatgcagga ccgtgaactg 120
agcctggcgg cggcgagaaa cggcttcgtt gattccgcgg ccgcgcacat gggagccttc 180
aagctcaacc cggcgcgcca cgagctgtcc ccgggcccaga gctcggcggt cactgcgcag 240
ggccccggcg cctaccccgg ctccgctgcg gctgccgctg cggcgcgagc gctcggggcc 300
cacgcgcgcg acgttggctc ctactctggg ccgcccttca actccaccgg ggacttctct 360
ttccgcagcg cgcggcttcc ggggacttcg gcgcggggcg gcgggcagca cgggctgttc 420
gggcggggcg cggcgggcct gcaccacggc caactcggag cgcaggggca cctcctcttc 480
cggcgcttga cagagagcca cggcggggag gctcgcaga atgtgctcaa cggcgagctg 540
cgcctcgggc tgcccggcga ggtgttcggg cgctcggagc aataccgcca ggtggccagc 600
ccgcggaccg acccctactc ggcgcgcaa ctccacaacc agtacggccc catgaatatg 660
aacatgggta tgaacatggc agcagccggc gccaccacc accaccacca ccaccaccac 720
cccgtgtcct ttttcgcta tatgcggcag cagtgcacat agcaggagct aatctgcaag 780
tggatcgacc ccgagcaact gagcaatccc aagaagagct gcaacaaaac tttcagcacc 840
atgcacgagc tggtagacaca cgtctcgtg gagcacgtcg gcggcccgga gcagagcaac 900
cacgtctgct tctgggagga gtgtccgcgc gagggcaagc ccttcaaggc caaatacaaa 960
ctggtcaacc acatccgctg gcacacaggg gagaaacct tcccctgccc cttcccgggc 1020
tgtggcaaa gttctcgcgg ctccgagaa ctcaagatcc acaaaaggac ccacacaggg 1080
gagaagccgt tccagtgtga gtttgagggc tgcgaccggc gcttcgccaa cagcagcgac 1140
aggaagaagc acatgcacgt ccacacctcc gataagccct atctctgcaa gatgtgcgac 1200
aagtccatca cgcaccccag ctgcgtgcgg aagcacatga aggtccatga gtccctcccg 1260
cagggttctg aatcctcccc ggccgcccagc tccggctatg agtcgtccac gccccggggg 1320
ctggtgtccc ccagcgccga gccccagagc agctccaacc tgtcccagc ggcggcgga 1380
ggcgcgcgcg cggctgcggc ggccggcgcc gcggtgtccg cgggtgcacc ggcgggaggg 1440
tcgggcagtg gcggcgcggg aggcggctca ggcggcgga cgggcagtg cggggcgggc 1500
ggcgggcgcg gcggcggggg cggcgcgagc tctggcgggg gcagcgggac agccgggggt 1560
cacagcgccc tctcctccaa cttcaatgaa tggtagctgt ga 1602

```

&lt;210&gt; 418

&lt;211&gt; 2910

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 418

```

gggggagccc ctgcaagttt cccgggcccgc gcgcgcgct cgctcgcctc ccagcccgcg 60

```

148

```

gcccagagccg ccgcccgcgc cgcctatgcc tcggccaaac aaaggggctc caagggcggc 120
cacggcgccg cgagcccctc ggagaagggt gccaccccg cgggcggcgc ggatgacgtg 180
gcgaagaagc cgcgcgcgcg gccgcagcag ccgcccgcgc cgcgcgcgcg gcacccgcag 240
cagcaccgcg agcagcaccg gcagaaccag gcgcacggca agggcggcga ccgcccgcgc 300
ggcgccgcgc gcggcaagtc ctctcctccc tcctccgcct ccgcccgcgc tgcccgcgcg 360
gccgectcgt cctcggcgtc ctgctcgcgc aggtcgcgca gggcgctcaa ctttctcttc 420
tacctcgcgc tgggtggcggc ggccgctttc tcgggctggt gcgtccacca cgtcctggag 480
gaggtccagc aggtccggcg cagccaccag gacttctccc ggcagaggga ggagctgggc 540
cagggccttc agggcgctga gcagaagggt cagtctttgc aagccacatt tggaaacttt 600
gagtccatct tgagaagctc ccaacataaa caagacctca cagagaaagc tgtgaagcaa 660
ggggagagtg aggtcagccg gatcagcgaa gtgctgcaga aactccagaa tgagattctc 720
aaagacctct cggatgggat ccatgtggtg aaggacgccc gggagcggga cttcacgtcc 780
ctggagaaca cgggtggagga gcggctgacg gagctcacca aatccatcaa cgacaacatc 840
gccatcttcc cagaagtcca gaagaggagc cagaaggaga tcaatgacat gaaggcaag 900
gttgccctcc tggaagaatc tgaggggaaac aagcaggatt tgaaagcctt aaagggaagc 960
gtgaaggaga tacagacctc agccaagtc agagagtggg acatggaggc cctgagaagt 1020
acccttcaga ctatggagtc tgacatctac accgaggttc gcgagctggt gagcctcaag 1080
caggagcagc aggtcttcaa ggaggcgccg gacacggagc ggctcgccct gcaggccctc 1140
acggagaagc ttctcaggtc tgaggagtcc gtctcccgcg tcccggagga gatccggaga 1200
ctggaggaag agctccgcca gctgaagtcc gattcccacg ggccgaagga ggacggaggc 1260
ttcagacact cggaaagcctt tgaggcactc cagcaaaaga gtcagggact ggactccagg 1320
ctccagcagc tggaggatgg ggtgctctcc atgcagggtg cttctcgcgg ccagaccgag 1380
agcctggagt ccctcctgtc caagagccag gagcacgagc agcgctggc ccctgcaggg 1440
gcctggaag gcctcgggtc ctccagggca gaccaggatg gcctggccag cacggtgagg 1500
agcctgggag agaccagct ggtgctctac ggtgacgtg aggagctgaa gaggagtgtg 1560
ggcgagctcc ccagcaccgt ggaatcactc cagaagggtc aggagcagg gcacacgctg 1620
ctcagtcagg accaagccca ggccgcccgt ctgcctcctc aggacttctt ggacagactt 1680
tcttctctag acaacctgaa agcctcagtc agccaagtgg aggcggactt gaaaatgctc 1740
aggactgctg tggacagttt ggttgcatc tcggtcaaaa tagaaaccaa cgagaacaat 1800
ctggaatcag ccaagggttt actagatgac ctgaggaatg atctggatag gttgtttgtg 1860
aaagtggaga agattcacga aaaggtctaa atgaattgcg tgtgcagggc gcgatttaa 1920
agtccaattt ctcatgacca aaaaatgtgt ggttttttcc catgtgtccc ctacccccca 1980
atctctctg agctcttcaa agcagttgtt cactacgtgc acaccaggc attgtatttt 2040
catgcccagt taacttattt acaatattta agttctctgc ttctgcattt ggttggtttc 2100
ctgaagcgca gccctgtgta ataacagggt gcttttcatg gatgtctcta gtcagagaaa 2160
aatgataaag gcttaaatg aggattaaca gaagcagatt aacctcagaa atcctgtctg 2220
gctggcagat ttcaagtaaa aaaaaaaaaa aggtgggttg gggggaccct tttctttcta 2280
gttgctctta aggaaaatta attttacttt ttttttgtt ctggccgaaa tttttatgag 2340
atatctctca cttgtcttcc actttgaacc ggttaaagct catagctgtc agctctgaat 2400
gaggagggga gaagcccctg ggtctttctt tgaaaggaa ccgctgcttg agggctgcct 2460
ccctcatggt gtgcgtgtcg ttctcttctt gacgcactg tgatatcaga ggtaactatg 2520
caaagcatcc aggcggttct gaagtgtgaag cactacaccc agcagagtcc cggtgccctc 2580
tgtccccact gccggcccat gtctctctc cggaggtcac caaggaatgc acaggtttcg 2640
actaccagaa aggggagtc ttgggttctt tcaaaaaatt cgtgaggaga gctgtctaca 2700
gtggaatagg ggtctccct gggaatgca ggccaagtcc ttttatttta acatgatgtc 2760
catgaagagg tttgcgctc ggcagccct gtcggcaagg agcgtgcata ctgcgtttgt 2820
gtaattgttt gctgtatctc cttccctct gagctgtatt gttctttaat ggctgtcttg 2880
cccttccaaa aaaaattgaa aaaaaaaaaa 2910

```

&lt;210&gt; 419

&lt;211&gt; 563

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 419

```

accacagtgg tgtccgagaa gtcaggcagc tagctcagcg gcggccgcgc cgcgtgcgtc 60
tgtgcctctg cgcgggtctc ctggtccttc tgccatcatg ccgatgttca tcgtaaacac 120
caacgtgccc cgcgcctccc tgccggacgc gttcctctcc gagctacccc agcagctggc 180
gcaggccacc ggcaagcccc ccagttacat cgcgggtgac gtggtcccgc accagctcat 240

```

149

```

ggccttcggc ggctccagcg agccgtgccc gctctgcagc ctgcacagca tcggcaagat 300
cgggcgccgc cagaaccgct cctacagcaa gctgctgtgc ggcctgctgg ccgagcgcc 360
cgccatcagc ccggacaggg tctacatcaa ctattacgac atgaacgcgg ccaatgtggg 420
ctggaacaac tccaccttcg cctaagagcc gcagggaccc acgctgtctg cgctggctcc 480
acccgggaac ccgcccagcg ctgtgttcta ggcccgcaca ccccaacctt ctggtgggga 540
gaaataaacg gtttagagac ttc
563

```

&lt;210&gt; 420

&lt;211&gt; 2690

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 420

```

cccggacaca cgcaagcagc cctccactta actcgcgccg ccgcggcagc tcgagtccac 60
cagcagcgcc gtcgcgttga ccgagatgct gggggcctgt cagttatcgg gtgtgaccgc 120
cgccgcccag agttgtctct gtgggaagtt tgtccctccg ccatcgagac catgccgcag 180
atactctact tcaggcagct ctgggttgac tactggcaaa attgctggag ctggcctttt 240
gtttgttggt ggaggtattg gtggcactat cctatatgcc aaatgggatt cccatttccg 300
ggaaagtgtg gagaaaacca taccttactc agacaaactc ttcgagatgg ttcttggtcc 360
tgcagcttat aatgttccat tgccaaagaa atcgattcag tcgggtccac taaaaatctc 420
tagtgtatca gaagtaatga aagaatctaa acagcctgcc tcacaactcc aaaaacaaaa 480
gggagatact ccagcttcag caacagcacc tacagaagcg gctcaaatta tttctgcagc 540
aggtgatacc ctgtcggtgc cagcccctgc agttcagcct gaggaatctt taaaaactga 600
tcacctgaa attggtgaag gaaaaccac acctgcactt tcagaagaag catcctcatc 660
ttctataagg gagcgaccac ctgaagaagt tgcagctcgc cttgcacaac aggaaaaaca 720
agaacaagtt aaaattgagt ctctagccaa gagcttagaa gatgctctga ggcaaaactgc 780
aagtgtcact ctgcaggcta ttgcagctca gaatgtctgc gtccaggctg tcaatgcaca 840
ctccaacata ttgaaagccg ccatggacaa ttctgagatt gcaggcgaga agaaatctgc 900
tcagtggcgc acagtggagg gtgcattgaa ggaacgcaga aaggcagtag atgaagctgc 960
cgatgcctct ctcaaagcca aagaagagtt agagaagatg aaaagtgtga ttgaaaatgc 1020
aaagaaaaaa gaggttgctg gggccaagcc tcatataact gctgcagagg gtaaaacttc 1080
caacatgata gttgatctgg ataagtgtgt caaaaaggct caagcagctc agtctgaggc 1140
taagtgtgta ttgagttgta atgagctggt cctccagctt aggtgtgctt tttaacgaga 1200
gctggacagt attactccag aagtcccttc tgggtggaaa ggaatgagtg tttcagactt 1260
agctgacaag ctctctactg atgatctgaa ctccctcatt gctcatgcac atcgtcgtat 1320
tgatcagctg aacagagagc tggcagaaca gaaggccacc gaaaagcagc acatcacgtt 1380
agccttggag aaacaaaaagc tggaaagaaa gggggcattt gactctgcag tagcaaaagc 1440
attagaacat cacagaagtg aaatacaggc tgaacaggac agaaagatag aagaagtcag 1500
agatgccatg gaaaatgaaa tgagaaccga gcttcgccga caggcagctg cccacactga 1560
tcacttgcca gatgtcctta gggatcaaga acaggaattg aagtctgaat ttgagcagaa 1620
cctgtctgag aaactctctg aacaagaatt acaatttcgt cgtctcagtc aagagcaagt 1680
tgacaacttt actctggata taaatactgc ctatgccaga ctgagaggaa tcgaacaggc 1740
tgttcagagc catgcagttg ctgaagagga agccagaaaa gccaccaac tctggctttc 1800
agtggaggca ttaaagtaca gcatgaagac ctcatctgca gaaacaccta ctatcccgct 1860
gggtagtgcg gttgaggcca tcaaagccaa ctgttctgat aatgaattca cccaagcttt 1920
aaccgcagct atccctccag agtccctgac ccgtgggggtg tacagtgaag agacccttag 1980
agcccgtttc tatgctgttc aaaaactggc ccgaagggtg gcaatgattg atgaaaccag 2040
aaatagcttg taccagtact tcctctccta cctacagtcg ctgtccttat tcccacctca 2100
gcaactgaag ccgccccagc agctctgccc tgaggatata aacacattta aattactgtc 2160
atatgcttcc tattgcattg agcatggtga tctggagcta gcagcaaaat ttgtcaatca 2220
gctgaagggg gaatccagac gagtggcaca ggactggctg aaggaagccc gaatgaccct 2280
agaaacgaaa catgagtgtg aaatcctgac agcatatgcc agcgccgtag gaataggaac 2340
cactcaggtg cagccagagt gaggtttagg aagattttca taaagtcata tttcatgtca 2400
aaggaaatca gcagtgatag atgaaggggt cgcagcgaga gtcccgact tgtctagaaa 2460
tgagcaggtt tacaagtact gttctaaatg ttaacacctg ttgcatttat attctttcca 2520
tttgctatca tgtcagtgaa cgccaggagt gctttctttg caacttgtgt aacattttct 2580
gttttttcag gttttactga tgaggcttgt gaggccaatc aaaataatgt ttgtgatctc 2640
tactactgtt gattttgccc tcggagcaaa ctgaataaag caacaagatg 2690

```



150

<210> 421  
<211> 3303  
<212> DNA  
<213> Homo sapiens

&lt;400&gt; 421

```
cgaccaaagc gcctgaggac cggcaacatg gtgcggctcg ggaataaggc agctgttgtg 60
ctgtgtatgg acgtgggctt taccatgagt aactccattc ctggtataga atccccattt 120
gaacaagcaa agaaggtgat aaccatgttt gtacagcgac aggtgtttgc tgagaacaag 180
gatgagattg ctttagtcct gtttgggtaca gatggcactg acaatcccct ttctgggtggg 240
gatcagtatc agaacatcac agtgcacaga catctgatgc taccagattt tgatttgctg 300
gaggacattg aaagcaaaat ccaaccagggt tctcaacagg ctgacttcct ggatgcacta 360
atcgtgagca tggatgtgat tcaacatgaa acaataggaa agaagtttga gaagaggcat 420
attgaaatat tcactgacct cagcagccga ttcagcaaaa gtcagctgga tattataatt 480
catagcttga agaaatgtga catctccctg caattcttct tgcctttctc acttggcaag 540
gaagatggaa gtggggacag aggagatggc ccttttcgct tagtgggcca tgggccttcc 600
tttccactaa aagggaattac cgaacagcaa aaagaaggtc ttgagatagt gaaaaagggtg 660
atgatatctt tagaagggtga agatgggttg gatgaaattt attcattcag tgagagtctg 720
agaaaaactgt gcgtcttcaa gaaaattgag aggcattcca ttcactggcc ctgcccactg 780
accattggct ccaatttgtc tataaggatt gcagcctata aatcgattct acaggagaga 840
gttaaaaaaga cttggacagt tgtggatgca aaaaccctaa aaaaagaaga tatacaaaaa 900
gaaacagttt attgcttaaa tgatgatgat gaaactgaag ttttaaaaga ggatattatt 960
caagggttcc gctatggaag tgatatagtt cctttctcta aagtggatga ggaacaaatg 1020
aaatataaat cggaggggaa gtgcttctct gttttgggat tttgtaaatc ttctcaggtt 1080
cagagaagat tcttcattgg aaatcaagtt ctaaaggctt ttgcagcaag agatgatgag 1140
gcagctgcag ttgcactttc ctccctgatt catgctttgg atgacttaga catggtggcc 1200
atagttcgat atgcttatga caaaagagct aatcctcaag tcggcgtggc ttttctctat 1260
atcaagcata actatgagtg tttagtgtat gtgcagctgc ctttcattga agacttgccg 1320
caatacatgt tttcatcctt gaaaaacagt aagaaatatg ctcccaccga ggcacagttg 1380
aatgctgttg atgctttgat tgactccatg agcttggcaa agaaagatga gaagacagac 1440
acccttgaag acttgtttcc aaccacaaa atcccaaatc ctcgatttca gagattattt 1500
cagtgtctgc tgcacagagc tttacatccc cgggagcctc taccoccaat tcagcagcat 1560
aaataaaaga ccttttttcc tctgattgaa gccaagaaaa aggatcaagt gactgctcag 1620
gaaattttcc aagacaacca tgaagatgga cctacagcta aaaaattaaa gactgagcaa 1740
gggggagccc acttcagcgt ctccagctctg gctgaaggca gtgtcacctc tgttgggaag 1800
gtgaatcctg ctgaaaactt ccgtgttcta gtgaaacaga agaaggccag ctttgaggaa 1860
gcgagtaacc agctcataaa tcacatcgaa cagtttttgg atactaatga aacaccgtat 1920
tttatgaaga gcatagactg catccgagcc ttccgggaag aagccattaa gttttcagaa 1980
gagcagcgct ttaacaactt cctgaaagcc cttcaagaga aagtggaaat taaacaatta 2040
aatcatttct gggaaattgt tgtccaggat ggaattactc tgatcaccaa agaggaagcc 2100
tctggaagtt ctgtcacagc tgaggaagcc aaaaagtttc tggcccccac agacaaacca 2160
agtggagaca cagcagctgt atttgaagaa ggtgggtgat tggacgattt attggacatg 2220
atataggtcg tggatgtatg gggaaatctaa gagagctgcc atcgctgtga tgctgggagt 2280
tctaacaaaa caagttggat cgggccattc aaggggagcc aaaaatctca gaaattccca 2340
gdaggttacc tggaggcgga tcatctaatt ctctgtggaa tgaatacaca catatatatt 2400
acaagggata atttagacc catacaagtt tataaagagt cattgttatt ttctggttgg 2460
tgtattattt tttctgtggt cttactgata tttgtatatt acatacatgc tttgaagttt 2520
ctggaagata gatcttttct tgacctagta tatcagtgc agttgcagcc cttgtgatgt 2580
gattagtgtc tcatgtggaa ccatggcatg gttattgatg agtttcttaa ccctttccag 2640
agtcctcctt tgcctgatcc tccaacagct gtcacaaact gtgttagaca agcagtagca 2700
tttcttctct cccaacaagc agctgggtta ggaaaccat gggtaaggac ggactcactt 2760
ctcttttttag ttgaggcctt ctagttacca cattactctg cctctgtata taggtggttt 2820
tctttaagtg gggtggaag gggagcaciaa tttcccttca tactcctttt aagcagtga 2880
ttatgggtgt ggtctcatga agaaaagacc ttttggccca atctctgcca tatcagtga 2940
ccttttagaaa ctcaaaaact gagaaattta cttcagtagt tagaattata tcacttca 3000
gttctctact tgcaagcctc aaagagagaa agtttcgtta tattaaaaca cttaggtaac 3060
ttttcggctc ttccatttc tacctaagtc agctttcctc tttgtggatg gtgtctcctt 3120
tactaaataa gaaaataaca aagcccttat tctctttttt tcttgcctc attcttgcct 3180
```

151

tgagttccag ttcctctttg gtgtacagac ttcttggtac ccagtcacct ctgtcttcag 3240  
 caccctcata agtcgtcact aatacacagt tttgtacatg taacattaaa ggcataaatg 3300  
 act 3303

<210> 422  
 <211> 1315  
 <212> DNA  
 <213> Homo sapiens

<400> 422  
 ttcccgcccg cggatagagg ggcggggccg gggctgctgt gggagagttc tgttctgctg 60  
 gcggggcctg cacgttgact gtgggaaact cggaacaag ctcacatctt cctgtgggaa 120  
 accttctagc aacaggatga gtctgcagtg gactgcagtt gccaccttc tctatgcgga 180  
 ggtctttgtt gtgttgcttc tctgcattcc cttcatttct cctaaaagat ggcagaagat 240  
 tttcaagtcc cggctggtgg agttgttagt gtctatggc aacaccttct ttgtggttct 300  
 cattgtcatc cttgtgctgt tgggtcatga tgcctgctgc gaaattcgga agtatgatga 360  
 tgtgacggaa aaggtgaacc tccagaacaa tccccgggccc atggagcact tccacatgaa 420  
 gcttttccgt gccagagga atctctacat tgcctggcttt tccttgctgc tgtccttcc 480  
 gcttagacgc ctggtgactc tcatttcgca gcaggccacg ctgctggcct ccaatgaagc 540  
 ctttaaaaag caggcggaga gtgctagtga ggcggccaag aagtacatgg aggagaatga 600  
 ccagctcaag aaggagctg ctgttgacgg aggcgaagtg gatgtcggga atgtgaggt 660  
 gaagtggag gaagagaaca ggagcctgaa ggctgacctg cagaagctaa aggacgagct 720  
 ggccagcact aagcaaaaac tagagaaagc tgaaaaccag gttctggcca tgcggaagca 780  
 gtctgagggc ctaccaagg agtacgaccg cttgctggag gagcacgcaa agctgcaggc 840  
 tgcagtagat ggtcccatgg acaagaagga agagtaaggg cctccttcc cccctgcctg 900  
 cagctggctt ccacctggca cgtgcctgct gcttcttgag agcccgccct ctccctccag 960  
 taactctgtt tgtgcccttc tgcctcccc attcccttc acagctcata gctcgtcatc 1020  
 tcggcccttg tccacactct ccaagcacat tacaggggac ctgattgcta cacttcaga 1080  
 atgcgtttgc tgtcatcctg cttggcctgg ccaggcctgg cacagcctt gcttccacgc 1140  
 ctgagcgtgg agagcacgag ttagtttag tccggcttg ggtgggctg acttctgtt 1200  
 ggtttgagcc cctttttgtt ttgccctctg ggtgtttct ttggtccgc agggaggtg 1260  
 gtggagcagg tggactggag tttctcttga gggcaataaa agttgtcatg gtgtg 1315

<210> 423  
 <211> 2294  
 <212> DNA  
 <213> Homo sapiens

<400> 423  
 gggcgtcgcg cctggggcc ggggcccggc ggcaccgcgg tgcgcaagcg caaccgtcgg 60  
 tgggtcgggg atcggtcgcc tgagaggtat cacctcttct gggctcaaga tggacaacaa 120  
 gaagcgcctg gcctacgcca tcatccagtt cctgcatgac cagctccggc acgggggcct 180  
 ctgctccgat gctcaggaga gcttgaagt cgcctccag tgcctggaga ctgctttgg 240  
 ggtgacggtg gaagacagt accttgcgct cctcagact ctgcccggaga tatttgaagc 300  
 ggctgccacg ggcaaggaga tgccgcagga cctgaggagc cccgcgcgaa ccccgccctc 360  
 cgaggaggac tcagcagagg cagagcgctt caaaaccgaa ggaacgagc agatgaaagt 420  
 ggaaaacttt gaagctgccg tgcatttcta cggaaaagcc atcgagctca acccagccaa 480  
 cgccgtctat tctgcaaca gagccgcagc ctacagcaaa ctgcgcaact acgcaggcgc 540  
 ggtgcaggac tgtgagcggg ccatctgcat tgaccgggcc tacagcaagg cctacggcag 600  
 gatgggcctg gcctctcca gcctcaacaa gcacgtggag gccgtggctt actacaagaa 660  
 ggctctggag ctggacccc acaacgagac atacaagtcc aacctcaaga tagcggagct 720  
 gaagctcgcg agggccccc gccccacggg aggcgtgggc agcttcgaca tgcgggcct 780  
 gctgaacaac cctggcttca tgagcatggc ttcaaaccta atgaacaatc cccagattca 840  
 gcagctcatg tccggcatga tttcgggtgg caacaacccc ttgggaactc ccggcaccag 900  
 cccctcgcat aacgacctg ccagcctcat ccaggcgggc cagcagttt cccagcagat 960  
 gcagcagcag aaccagagt tgatagagc gctcaggagc cagatccgga gtcggacgc 1020  
 cagcgccagc aacgacgacc agcaggagt acgctgctg ctccgggtgt gaccgcgtcc 1080  
 ttccctggcc gaccgaagg aagccttctg gttgtctgcc acttctctct gttggactgc 1140  
 ctgagagagg ggaagagaga gacctcgac ctgcatgtca agatggattt tccccttta 1200

tctctgcect	cctccactcc	ctttttgtaa	ctcccttaca	gccccagac	ccttcttgaa	1260
acgagagcca	gcaagctgag	cacagaccag	cagcgacctc	ccttccagcc	cccagaaagc	1320
tcggtcactt	gagtggtttc	tagaatcctg	gggtgctccc	gggcccctct	cagagaagtg	1380
gcaggtttca	cgttcagccg	tgtggcggat	cgtgtggctt	ccaaagcctt	ttacagcccc	1440
cgcccccat	cccggtggtc	gtctgcagga	actctcccgt	ctgtgagaag	cctctttccg	1500
agtcgacctc	ccggccaccc	cggccctgtg	cctgctcgga	agagctcact	gccagctgcg	1560
gcctgggac	cgcgggccat	gtgtgtttgc	atgaggaaact	cttttagtggc	agacacctaa	1620
gagacggctg	cggtcacccc	acgcctccgc	ggctcaggag	ccgtcctggg	tgcataggac	1680
cagtttctgt	gactttttctc	cagttgggca	tgttgacaga	catgtttccc	ctcctccac	1740
cctcattttc	tggctcctcg	gactgagagc	caggggcgac	atcatgacct	tctgtcccgg	1800
ccgccttagc	cccgggcaca	gggaaggcag	ctgggcccgtt	tctgtctgtg	tcccatcctg	1860
ctgtccttct	gtcctggatg	tttcatgggc	ccggggcccc	ccagggaagc	ttacccctcc	1920
tgtgtcgggt	ggaggccacg	ggacacctca	ggtgccaccc	accttgcccc	taaaacagcc	1980
accaggaaag	cagccggaga	gccggacagc	aggcagcctg	tctgggttcc	tgaggcctgg	2040
gggtggcaga	cgagcccacg	gcgcggtggt	cccagcagca	gggttgcag	tcggagcattc	2100
ctggggctcc	ctggctcctg	gccgtctgtg	aggtaggcgc	agtaccgtgt	atcgtaggta	2160
gcagtaggaa	cggggggccg	cgcgccctg	cagccgctca	tggcggtgag	gtgtgtgcca	2220
agccaccccg	gggtgcaggg	cgtgacgtgt	ggggaataaa	taggcgttgt	gacctctaaa	2280
aaaaaaaaaa	aaaa					2294

&lt;210&gt; 424

&lt;211&gt; 3075

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 424

gaattcggca	cgagcagccc	tcggctgagc	cgcgccgcac	catgcccgcc	gtggacaagc	60
tectgctaga	ggaggcggtg	caggacagcc	cccagactcg	ctctttactg	agcgtgtttg	120
aagaagatgc	tggcacccctc	acagactata	ccaaccagct	gctccaggca	atgcagcgcg	180
tctatggagc	ccagaatgag	atgtgcctgg	ccacacaaca	gctttctaag	caactgctgg	240
catatgaaaa	acagaacttt	gctcttggca	aagggtatga	agaagtaatt	tcaactctcc	300
actatttttc	caaagtgggtg	gatgagctta	atcttctcca	tacagagctg	gctaaacagt	360
tggcagagac	gctggttctc	cctatgntac	aattccgaga	aaaggatctc	aaagaagta	420
gcactltaaa	ggatctattt	ggactcgcta	gcaatgagca	tgacctctca	atggcaaaat	480
acagcaggct	gcctaagaaa	aaggagaatg	agaagggtgaa	gaccgaagtc	ggaaaagagg	540
tggccgcggc	ccggcggaag	cagcacctct	cctcccttca	gtactactgt	gccctcaacg	600
cgctgcagta	cagaaaagcaa	atggccatga	tggagcccat	gataggcttt	gccccatggac	660
agattaactt	ttttaagaag	ggagcagaga	tgttttccaa	acgtatggac	agctttttat	720
cctccggttg	agacatgggt	caaagcattc	aggtagaact	ggaagccgag	gcggaaaaga	780
tgcgggtgtc	ccagcaagaa	ttactttctg	ttgatgaatc	tgtttacact	ccagactctg	840
atgtggccgc	accacagatc	aacagggaacc	tcatccagaa	ggctggttac	cttaatctta	900
gaaacaaaac	agggtcgtgc	accaccacct	gggagaggct	ttatttcttc	acccaaggcg	960
ggaatctcat	gtgtcagccc	aggggagccg	tggctggagg	tttgatccag	gacctggaca	1020
actgtctcagt	gatggccgtg	gattgcgaag	accggcgcta	ctgcttccag	atcaccacgc	1080
ccaatggaaa	atcgggaata	atcctccagg	ctgagagcag	aaaggaaaat	gaagagtggg	1140
tatgtgcaat	aaacaacacc	tccagacaga	tctacctgac	cgacaaccct	gaggccgtcg	1200
cgatcaagtt	gaatcagacc	gctctgcaag	cagtgactcc	cattacaagt	tttggaaaaa	1260
aacaagaaag	ctcatgcccc	agccagaacc	tgaaaaattc	agagatggaa	aatgaaaatg	1320
acaagattgt	tcccaaagca	acagccagtc	tacctgaagc	agaggagctg	atcgcgctcg	1380
gaacgccgat	tcaattcgat	attgtgcttc	ctgctacaga	attccttgat	cagaacagag	1440
ggagcaggcg	taccaaccct	tttggtgaaa	ctgaggatga	atcatttcca	gaagcagaag	1500
attctctttt	gcagcagatg	tttatagttc	ggtttttggg	atcaatggca	gttaaaacag	1560
acagcactac	ttgaagtgt	ttatgaagcg	atgagacaag	tattggctgc	tcgggctatt	1620
cataacatct	tccgcatgac	agaatcccat	ctgatggtca	ccagtcaatc	tttgagggtt	1680
atagatccac	agactcaagt	atcaagggcc	aattttgaac	ttaccagtgt	cacacaattt	1740
gctgctcatc	aagaaaacaa	gagactgggt	ggttttgtca	tccgtgttcc	tgaatccact	1800
ggagaagaat	ctctgagtac	atacattttt	gaaagcaact	cagaaggcga	aaagatatgt	1860
tatgttatta	atttgggaaa	agaaattatt	gaggttcaga	aggatccaga	agcactggct	1920
caattaatgc	tgtccatacc	actaaccaat	gatggaaaat	atgtactgtt	aaacgatcaa	1980

153

```

ccagatgacg atgatggaaa tccaaatgaa catagaggcg cagaatccga agcataactc 2040
acttgccgct gtgggggaag agcaaacagg aaggagagct acctcctaag ggttttaacg 2100
tctctgacat acaggcacac tgacctgatt tccgaaggct gacaatcgtt tgtggaatgt 2160
aatcttgatg ccttgatact gagacttggg agggaaacta agaaatggtt gacagcgttc 2220
ccaccatctc acaatgttat tttagggtgct ttgtggttaag tcttttttct tagattgcgc 2280
taaaatttct tagattgttc agcgctcaga acaaaagttt gaaaaatgca ttgttcatat 2340
gaatgtcatc tcttttcagt ttccagtatc ctttttaaaa aatggcaaaa gcctagattt 2400
acaatttgat gaacactaaa tatttcttat taatataatc tatttttgta ttttacttaa 2460
tgagctttta gtgcctgtcg ttctgaaaat tgtgtattta taattcagct tatctcacia 2520
ttggacctaa tagcatttct ttgtgcagtt aggtgacgag cactgctttg aggcccaagc 2580
actagtagag atgcgcgata caggcttagt ttccgtaact gttccagaca tcaagcaata 2640
aaaaaatgaa taccacaaaa gatgtttgat tttacagtgg agccttactg aaccagcatt 2700
cagaagttaa aggtctctct aggtatgagt atttttagta gtggatcact gtggacaggg 2760
tgagctctta ccagttcctg tttcttctga gccagaccct cttcagggaa gggaccaatt 2820
aattttaaaa ctcaactgaa gcacagctgg tcatggggct tggataaaag ttcctatttc 2880
caccctgata cttccaattc ctggaacccc agccactcc cccatccctc ctccctatca 2940
aactagtata atgattttga atcggtacag tgtgtttaac tgtaactaag ttcaacagac 3000
tattattatc tttgtaataa attaacctag caataaaaat tattctgttt caaaaaaaaa 3060
aaaaaacaac tcgag                                     3075

```

&lt;210&gt; 425

&lt;211&gt; 819

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 425

```

Gly Asp Phe Gly Gly Gly Ser Ser Leu Ala Ala Gly Met Ala Gly Thr
                    5              10              15
Val Val Leu Asp Asp Val Glu Leu Arg Glu Ala Gln Arg Asp Tyr Leu
                    20              25              30
Asp Phe Leu Asp Asp Glu Glu Asp Gln Gly Ile Tyr Gln Ser Lys Val
                    35              40              45
Arg Glu Leu Ile Ser Asp Asn Gln Tyr Arg Leu Ile Val Asn Val Asp
                    50              55              60
Asp Leu Arg Arg Lys Asn Glu Lys Arg Ala Asn Arg Leu Leu Asn Asn
                    65              70              75              80
Ala Phe Glu Glu Leu Val Ala Phe Gln Arg Ala Leu Lys Asp Phe Val
                    85              90              95
Ala Ser Ile Asp Ala Thr Tyr Ala Lys Gln Tyr Glu Glu Phe Tyr Val
                    100             105             110
Gly Leu Glu Gly Ser Phe Gly Ser Lys His Val Ser Pro Arg Thr Leu
                    115             120             125
Thr Ser Cys Phe Leu Ser Cys Val Val Cys Val Glu Gly Ile Val Lys
                    130             135             140
Cys Ser Leu Val Arg Pro Lys Val Val Arg Ser Val His Tyr Cys Pro
                    145             150             155             160
Ala Thr Lys Lys Thr Ile Glu Arg Arg Tyr Ser Asp Leu Thr Thr Leu
                    165             170             175
Val Ala Phe Pro Ser Ser Ser Val Tyr Pro Thr Lys Asp Glu Glu Asn
                    180             185             190
Asn Pro Leu Glu Thr Glu Tyr Gly Leu Ser Val Tyr Lys Asp His Gln
                    195             200             205
Thr Ile Thr Ile Gln Glu Met Pro Glu Lys Ala Pro Ala Gly Gln Leu
                    210             215             220
Pro Arg Ser Val Asp Val Ile Leu Asp Asp Asp Leu Val Asp Lys Ala
                    225             230             235             240
Lys Pro Gly Asp Arg Val Gln Val Val Gly Thr Tyr Arg Cys Leu Pro
                    245             250             255
Gly Lys Lys Gly Gly Tyr Thr Ser Gly Thr Phe Arg Thr Val Leu Ile

```

154

260	265	270
Ala Cys Asn Val Lys Gln Met Ser Lys Asp Ala Gln Pro Ser Phe Ser		
275	280	285
Ala Glu Asp Ile Ala Lys Ile Lys Lys Phe Ser Lys Thr Arg Ser Lys		
290	295	300
Asp Ile Phe Asp Gln Leu Ala Lys Ser Leu Ala Pro Ser Ile His Gly		
305	310	315
His Asp Tyr Val Lys Lys Ala Ile Leu Cys Leu Leu Gly Gly Val		
325	330	335
Glu Arg Asp Leu Glu Asn Gly Ser His Ile Arg Gly Asp Ile Asn Ile		
340	345	350
Leu Leu Ile Gly Asp Pro Ser Val Ala Lys Ser Gln Leu Leu Arg Tyr		
355	360	365
Val Leu Cys Thr Ala Pro Arg Ala Ile Pro Thr Thr Gly Arg Gly Ser		
370	375	380
Ser Gly Val Gly Leu Thr Ala Ala Val Thr Thr Asp Gln Glu Thr Gly		
385	390	395
Glu Arg Arg Leu Glu Ala Gly Ala Met Val Leu Ala Asp Arg Gly Val		
405	410	415
Val Cys Ile Asp Glu Phe Asp Lys Met Ser Asp Met Asp Arg Thr Ala		
420	425	430
Ile His Glu Val Met Glu Gln Gly Arg Val Thr Ile Ala Lys Ala Gly		
435	440	445
Ile His Ala Arg Leu Asn Ala Arg Cys Ser Val Leu Ala Ala Ala Asn		
450	455	460
Pro Val Tyr Gly Arg Tyr Asp Gln Tyr Lys Thr Pro Met Glu Asn Ile		
465	470	475
Gly Leu Gln Asp Ser Leu Leu Ser Arg Phe Asp Leu Leu Phe Ile Met		
485	490	495
Leu Asp Gln Met Asp Pro Glu Gln Asp Arg Glu Ile Ser Asp His Val		
500	505	510
Leu Arg Met His Arg Tyr Arg Ala Pro Gly Glu Gln Asp Gly Asp Ala		
515	520	525
Met Pro Leu Gly Ser Ala Val Asp Ile Leu Ala Thr Asp Asp Pro Asn		
530	535	540
Phe Ser Gln Glu Asp Gln Gln Asp Thr Gln Ile Tyr Glu Lys His Asp		
545	550	555
Asn Leu Leu His Gly Thr Lys Lys Lys Lys Glu Lys Met Val Ser Ala		
565	570	575
Ala Phe Met Lys Lys Tyr Ile His Val Ala Lys Ile Ile Lys Pro Val		
580	585	590
Leu Thr Gln Glu Ser Ala Thr Tyr Ile Ala Glu Glu Tyr Ser Arg Leu		
595	600	605
Arg Ser Gln Asp Ser Met Ser Ser Asp Thr Ala Arg Thr Ser Pro Val		
610	615	620
Thr Ala Arg Thr Leu Glu Thr Leu Ile Arg Leu Ala Thr Ala His Ala		
625	630	635
Lys Ala Arg Met Ser Lys Thr Val Asp Leu Gln Asp Ala Glu Glu Ala		
645	650	655
Val Glu Leu Val Gln Tyr Ala Tyr Phe Lys Lys Val Leu Glu Lys Glu		
660	665	670
Lys Lys Arg Lys Lys Arg Ser Glu Asp Glu Ser Glu Thr Glu Asp Glu		
675	680	685
Glu Glu Lys Ser Gln Glu Asp Gln Glu Gln Lys Arg Lys Arg Arg Lys		
690	695	700
Thr Arg Gln Pro Asp Ala Lys Asp Gly Asp Ser Tyr Asp Pro Tyr Asp		
705	710	715
Phe Ser Asp Thr Glu Glu Met Pro Gln Val His Thr Pro Lys Thr		
725	730	735

155

Ala Asp Ser Gln Glu Thr Lys Glu Ser Gln Lys Val Glu Leu Ser Glu  
 740 745 750  
 Ser Arg Leu Lys Ala Phe Lys Val Ala Leu Leu Asp Val Phe Arg Glu  
 755 760 765  
 Ala His Ala Gln Ser Ile Gly Met Asn Arg Leu Thr Glu Ser Ile Asn  
 770 775 780  
 Arg Asp Ser Glu Glu Pro Phe Ser Ser Val Glu Ile Gln Ala Ala Leu  
 785 790 795 800  
 Ser Lys Met Gln Asp Asp Asn Gln Val Met Val Ser Glu Gly Ile Ile  
 805 810 815  
 Phe Leu Ile

<210> 426  
 <211> 178  
 <212> PRT  
 <213> Homo sapiens

<400> 426  
 Glu Pro Arg Gly Ser Arg Ala Arg Phe Gly Cys Trp Arg Leu Gln Pro  
 5 10 15  
 Glu Phe Lys Pro Lys Gln Leu Glu Gly Thr Met Ala Asn Cys Glu Arg  
 20 25 30  
 Thr Phe Ile Ala Ile Lys Pro Asp Gly Val Gln Arg Gly Leu Val Gly  
 35 40 45  
 Glu Ile Ile Lys Arg Phe Glu Gln Lys Gly Phe Arg Leu Val Gly Leu  
 50 55 60  
 Lys Phe Met Gln Ala Ser Glu Asp Leu Leu Lys Glu His Tyr Val Asp  
 65 70 75 80  
 Leu Lys Asp Arg Pro Phe Phe Ala Gly Leu Val Lys Tyr Met His Ser  
 85 90 95  
 Gly Pro Val Val Ala Met Val Trp Glu Gly Leu Asn Val Val Lys Thr  
 100 105 110  
 Gly Arg Val Met Leu Gly Glu Thr Asn Pro Ala Asp Ser Lys Pro Gly  
 115 120 125  
 Thr Ile Arg Gly Asp Phe Cys Ile Gln Val Gly Arg Asn Ile Ile His  
 130 135 140  
 Gly Ser Asp Ser Val Glu Ser Ala Glu Lys Glu Ile Gly Leu Trp Phe  
 145 150 155 160  
 His Pro Glu Glu Leu Val Asp Tyr Thr Ser Cys Ala Gln Asn Trp Ile  
 165 170 175  
 Tyr Glu

<210> 427  
 <211> 570  
 <212> PRT  
 <213> Homo sapiens

<400> 427  
 Thr Glu Arg Ser Ala Leu Asp Val Lys Leu Lys His Ala Arg Asn Gln  
 5 10 15  
 Val Asp Val Glu Ile Lys Arg Arg Gln Arg Ala Glu Ala Asp Cys Glu  
 20 25 30  
 Lys Leu Glu Arg Gln Ile Gln Leu Ile Arg Glu Met Leu Met Cys Asp  
 35 40 45  
 Thr Ser Gly Ser Ile Gln Leu Ser Glu Glu Gln Lys Ser Ala Leu Ala  
 50 55 60  
 Phe Leu Asn Arg Gly Gln Pro Ser Ser Ser Asn Ala Gly Asn Lys Arg

156

65					70					75				80	
Leu	Ser	Thr	Ile	Asp	Glu	Ser	Gly	Ser	Ile	Leu	Ser	Asp	Ile	Ser	Phe
				85					90					95	
Asp	Lys	Thr	Asp	Glu	Ser	Leu	Asp	Trp	Asp	Ser	Ser	Leu	Val	Lys	Thr
			100					105					110		
Phe	Lys	Leu	Lys	Lys	Arg	Glu	Lys	Arg	Arg	Ser	Thr	Ser	Arg	Gln	Phe
		115					120					125			
Val	Asp	Gly	Pro	Pro	Gly	Pro	Val	Lys	Lys	Thr	Arg	Ser	Ile	Gly	Ser
	130					135					140				
Ala	Val	Asp	Gln	Gly	Asn	Glu	Ser	Ile	Val	Ala	Lys	Thr	Thr	Val	Thr
145					150					155					160
Val	Pro	Asn	Asp	Gly	Gly	Pro	Ile	Glu	Ala	Val	Ser	Thr	Ile	Glu	Thr
			165						170					175	
Val	Pro	Tyr	Trp	Thr	Arg	Ser	Arg	Arg	Lys	Thr	Gly	Thr	Leu	Gln	Pro
		180						185					190		
Trp	Asn	Ser	Asp	Ser	Thr	Leu	Asn	Ser	Arg	Gln	Leu	Glu	Pro	Arg	Thr
	195						200					205			
Glu	Thr	Asp	Ser	Val	Gly	Thr	Pro	Gln	Ser	Asn	Gly	Gly	Met	Arg	Leu
	210					215					220				
His	Asp	Phe	Val	Ser	Lys	Thr	Val	Ile	Lys	Pro	Glu	Ser	Cys	Val	Pro
225					230					235					240
Cys	Gly	Lys	Arg	Ile	Lys	Phe	Gly	Lys	Leu	Ser	Leu	Lys	Cys	Arg	Asp
			245						250					255	
Cys	Arg	Val	Val	Ser	His	Pro	Glu	Cys	Arg	Asp	Arg	Cys	Pro	Leu	Pro
		260						265					270		
Cys	Ile	Pro	Thr	Leu	Ile	Gly	Thr	Pro	Val	Lys	Ile	Gly	Glu	Gly	Met
	275						280					285			
Leu	Ala	Asp	Phe	Val	Ser	Gln	Thr	Ser	Pro	Met	Ile	Pro	Ser	Ile	Val
	290					295					300				
Val	His	Cys	Val	Asn	Glu	Ile	Glu	Gln	Arg	Gly	Leu	Thr	Glu	Thr	Gly
305				310						315					320
Leu	Tyr	Arg	Ile	Ser	Gly	Cys	Asp	Arg	Thr	Val	Lys	Glu	Leu	Lys	Glu
			325						330					335	
Lys	Phe	Leu	Arg	Val	Lys	Thr	Val	Pro	Leu	Leu	Ser	Lys	Val	Asp	Asp
		340						345					350		
Ile	His	Ala	Ile	Cys	Ser	Leu	Leu	Lys	Asp	Phe	Leu	Arg	Asn	Leu	Lys
	355						360					365			
Glu	Pro	Leu	Leu	Thr	Phe	Arg	Leu	Asn	Arg	Ala	Phe	Met	Glu	Ala	Ala
	370					375					380				
Glu	Ile	Thr	Asp	Glu	Asp	Asn	Ser	Ile	Ala	Ala	Met	Tyr	Gln	Ala	Val
385					390					395					400
Gly	Glu	Leu	Pro	Gln	Ala	Asn	Arg	Asp	Thr	Leu	Ala	Phe	Leu	Met	Ile
			405						410					415	
His	Leu	Gln	Arg	Val	Ala	Gln	Ser	Pro	His	Thr	Lys	Met	Asp	Val	Ala
		420						425					430		
Asn	Leu	Ala	Lys	Val	Phe	Gly	Pro	Thr	Ile	Val	Ala	His	Ala	Val	Pro
	435						440					445			
Asn	Pro	Asp	Pro	Val	Thr	Met	Leu	Gln	Asp	Ile	Lys	Arg	Gln	Pro	Lys
	450					455					460				
Val	Val	Glu	Arg	Leu	Leu	Ser	Leu	Pro	Leu	Glu	Tyr	Trp	Ser	Gln	Phe
465					470					475					480
Met	Met	Val	Glu	Gln	Glu	Asn	Ile	Asp	Pro	Leu	His	Val	Ile	Glu	Asn
			485						490					495	
Ser	Asn	Ala	Phe	Ser	Thr	Pro	Gln	Thr	Pro	Asp	Ile	Lys	Val	Ser	Leu
		500						505					510		
Leu	Gly	Pro	Val	Thr	Thr	Pro	Glu	His	Gln	Leu	Leu	Lys	Thr	Pro	Ser
	515						520					525			
Ser	Ser	Ser	Leu	Ser	Gln	Arg	Val	Arg	Ser	Thr	Leu	Thr	Lys	Asn	Thr
	530					535					540				

157

Pro Arg Phe Gly Ser Lys Ser Lys Ser Ala Thr Asn Leu Gly Arg Gln  
 545 550 555 560  
 Gly Asn Phe Phe Ala Ser Pro Met Leu Lys  
 565 570

<210> 428  
 <211> 532  
 <212> PRT  
 <213> Homo sapiens

<400> 428  
 Leu Leu Asp Ala Gly Pro Gln Phe Pro Ala Ile Gly Val Gly Ser Phe  
 5 10 15  
 Ala Arg His His His Ser Ala Ala Ala Ala Ala Ala  
 20 25 30  
 Glu Met Gln Asp Arg Glu Leu Ser Leu Ala Ala Ala Gln Asn Gly Phe  
 35 40 45  
 Val Asp Ser Ala Ala Ala His Met Gly Ala Phe Lys Leu Asn Pro Gly  
 50 55 60  
 Ala His Glu Leu Ser Pro Gly Gln Ser Ser Ala Phe Thr Ser Gln Gly  
 65 70 75 80  
 Pro Gly Ala Tyr Pro Gly Ser Ala Ala Ala Ala Ala Ala Ala  
 85 90 95  
 Leu Gly Pro His Ala Ala His Val Gly Ser Tyr Ser Gly Pro Pro Phe  
 100 105 110  
 Asn Ser Thr Arg Asp Phe Leu Phe Arg Ser Ala Arg Leu Pro Gly Thr  
 115 120 125  
 Ser Ala Pro Gly Gly Gly Gln His Gly Leu Phe Gly Pro Gly Ala Gly  
 130 135 140  
 Gly Leu His His Ala His Ser Asp Ala Gln Gly His Leu Leu Phe Pro  
 145 150 155 160  
 Gly Leu Pro Glu Gln His Gly Pro His Gly Ser Gln Asn Val Leu Asn  
 165 170 175  
 Gly Glu Met Arg Leu Gly Leu Pro Gly Glu Val Phe Gly Arg Ser Glu  
 180 185 190  
 Gln Tyr Arg Gln Val Ala Ser Pro Arg Thr Asp Pro Tyr Ser Ala Ala  
 195 200 205  
 Gln Leu His Asn Gln Tyr Gly Pro Met Asn Met Asn Met Gly Met Asn  
 210 215 220  
 Met Ala Ala Ala Ala Ala His His His His His His His His Pro  
 225 230 235 240  
 Gly Ala Phe Phe Arg Tyr Met Arg Gln Gln Cys Ile Lys Gln Glu Leu  
 245 250 255  
 Ile Cys Lys Trp Ile Asp Pro Glu Gln Leu Ser Asn Pro Lys Lys Ser  
 260 265 270  
 Cys Asn Lys Thr Phe Ser Thr Met His Glu Leu Val Thr His Val Ser  
 275 280 285  
 Val Glu His Val Gly Gly Pro Glu Gln Ser Asn His Val Cys Phe Trp  
 290 295 300  
 Glu Glu Cys Pro Arg Glu Gly Lys Pro Phe Lys Ala Lys Tyr Lys Leu  
 305 310 315 320  
 Val Asn His Ile Arg Val His Thr Gly Glu Lys Pro Phe Pro Cys Pro  
 325 330 335  
 Phe Pro Gly Cys Gly Lys Val Phe Ala Arg Ser Glu Asn Leu Lys Ile  
 340 345 350  
 His Lys Arg Thr His Thr Gly Glu Lys Pro Phe Gln Cys Glu Phe Glu  
 355 360 365  
 Gly Cys Asp Arg Arg Phe Ala Asn Ser Ser Asp Arg Lys Lys His Met  
 370 375 380



158

His Val His Thr Ser Asp Lys Pro Tyr Leu Cys Lys Met Cys Asp Lys  
 385 390 395 400  
 Ser Tyr Thr His Pro Ser Ser Leu Arg Lys His Met Lys Val His Glu  
 405 410 415  
 Ser Ser Pro Gln Gly Ser Glu Ser Ser Pro Ala Ala Ser Ser Gly Tyr  
 420 425 430  
 Glu Ser Ser Thr Pro Pro Gly Leu Val Ser Pro Ser Ala Glu Pro Gln  
 435 440 445  
 Ser Ser Ser Asn Leu Ser Pro Ala Ala Ala Ala Ala Ala Ala Ala  
 450 455 460  
 Ala Ala Ala Ala Ala Val Ser Ala Val His Arg Gly Gly Gly Ser  
 465 470 475 480  
 Gly Ser Gly Gly Ala Gly Gly Gly Ser Gly Gly Ser Gly Ser Gly  
 485 490 495  
 Gly Gly Gly Gly Gly Ala Gly Gly Gly Gly Gly Ser Ser Gly Gly  
 500 505 510  
 Gly Ser Gly Thr Ala Gly Gly His Ser Gly Leu Ser Ser Asn Phe Asn  
 515 520 525  
 Glu Trp Tyr Val  
 530

&lt;210&gt; 429

&lt;211&gt; 629

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 429

Gly Gly Ala Pro Ala Ser Phe Pro Gly Arg Ala Pro Arg Ser Leu Ala  
 5 10 15  
 Ser Gln Pro Ala Ala Arg Ala Ala Ala Pro Ala Met Pro Ser Ala  
 20 25 30  
 Lys Gln Arg Gly Ser Lys Gly Gly His Gly Ala Ala Ser Pro Ser Glu  
 35 40 45  
 Lys Gly Ala His Pro Ser Gly Gly Ala Asp Asp Val Ala Lys Lys Pro  
 50 55 60  
 Pro Pro Ala Pro Gln Gln Pro Pro Pro Pro Ala Pro His Pro Gln  
 65 70 75 80  
 Gln His Pro Gln Gln His Pro Gln Asn Gln Ala His Gly Lys Gly Gly  
 85 90 95  
 His Arg Gly Gly Gly Gly Gly Gly Gly Lys Ser Ser Ser Ser Ser Ser  
 100 105 110  
 Ala Ser Ala Ala Ala Ala Ala Ala Ala Ser Ser Ser Ala Ser Cys  
 115 120 125  
 Ser Arg Arg Leu Gly Arg Ala Leu Asn Phe Leu Phe Tyr Leu Ala Leu  
 130 135 140  
 Val Ala Ala Ala Ala Phe Ser Gly Trp Cys Val His His Val Leu Glu  
 145 150 155 160  
 Glu Val Gln Gln Val Arg Arg Ser His Gln Asp Phe Ser Arg Gln Arg  
 165 170 175  
 Glu Glu Leu Gly Gln Gly Leu Gln Gly Val Glu Gln Lys Val Gln Ser  
 180 185 190  
 Leu Gln Ala Thr Phe Gly Thr Phe Glu Ser Ile Leu Arg Ser Ser Gln  
 195 200 205  
 His Lys Gln Asp Leu Thr Glu Lys Ala Val Lys Gln Gly Glu Ser Glu  
 210 215 220  
 Val Ser Arg Ile Ser Glu Val Leu Gln Lys Leu Gln Asn Glu Ile Leu  
 225 230 235 240  
 Lys Asp Leu Ser Asp Gly Ile His Val Val Lys Asp Ala Arg Glu Arg

159

					245											255
Asp	Phe	Thr	Ser	Leu	Glu	Asn	Thr	Val	Glu	Glu	Arg	Leu	Thr	Glu	Leu	
			260					265					270			
Thr	Lys	Ser	Ile	Asn	Asp	Asn	Ile	Ala	Ile	Phe	Thr	Glu	Val	Gln	Lys	
			275				280					285				
Arg	Ser	Gln	Lys	Glu	Ile	Asn	Asp	Met	Lys	Ala	Lys	Val	Ala	Ser	Leu	
			290			295					300					
Glu	Glu	Ser	Glu	Gly	Asn	Lys	Gln	Asp	Leu	Lys	Ala	Leu	Lys	Glu	Ala	
305				310						315					320	
Val	Lys	Glu	Ile	Gln	Thr	Ser	Ala	Lys	Ser	Arg	Glu	Trp	Asp	Met	Glu	
			325					330						335		
Ala	Leu	Arg	Ser	Thr	Leu	Gln	Thr	Met	Glu	Ser	Asp	Ile	Tyr	Thr	Glu	
			340					345					350			
Val	Arg	Glu	Leu	Val	Ser	Leu	Lys	Gln	Glu	Gln	Gln	Ala	Phe	Lys	Glu	
			355				360					365				
Ala	Ala	Asp	Thr	Glu	Arg	Leu	Ala	Leu	Gln	Ala	Leu	Thr	Glu	Lys	Leu	
			370			375					380					
Leu	Arg	Ser	Glu	Glu	Ser	Val	Ser	Arg	Leu	Pro	Glu	Glu	Ile	Arg	Arg	
385				390						395					400	
Leu	Glu	Glu	Glu	Leu	Arg	Gln	Leu	Lys	Ser	Asp	Ser	His	Gly	Pro	Lys	
			405					410					415			
Glu	Asp	Gly	Gly	Phe	Arg	His	Ser	Glu	Ala	Phe	Glu	Ala	Leu	Gln	Gln	
			420					425					430			
Lys	Ser	Gln	Gly	Leu	Asp	Ser	Arg	Leu	Gln	His	Val	Glu	Asp	Gly	Val	
			435				440					445				
Leu	Ser	Met	Gln	Val	Ala	Ser	Ala	Arg	Gln	Thr	Glu	Ser	Leu	Glu	Ser	
			450			455					460					
Leu	Leu	Ser	Lys	Ser	Gln	Glu	His	Glu	Gln	Arg	Leu	Ala	Pro	Ala	Gly	
465				470						475					480	
Ala	Leu	Glu	Gly	Leu	Gly	Ser	Ser	Glu	Ala	Asp	Gln	Asp	Gly	Leu	Ala	
			485					490					495			
Ser	Thr	Val	Arg	Ser	Leu	Gly	Glu	Thr	Gln	Leu	Val	Leu	Tyr	Gly	Asp	
			500					505				510				
Val	Glu	Glu	Leu	Lys	Arg	Ser	Val	Gly	Glu	Leu	Pro	Ser	Thr	Val	Glu	
			515				520					525				
Ser	Leu	Gln	Lys	Val	Gln	Glu	Gln	Val	His	Thr	Leu	Leu	Ser	Gln	Asp	
			530			535					540					
Gln	Ala	Gln	Ala	Ala	Arg	Leu	Pro	Pro	Gln	Asp	Phe	Leu	Asp	Arg	Leu	
545				550						555					560	
Ser	Ser	Leu	Asp	Asn	Leu	Lys	Ala	Ser	Val	Ser	Gln	Val	Glu	Ala	Asp	
			565					570						575		
Leu	Lys	Met	Leu	Arg	Thr	Ala	Val	Asp	Ser	Leu	Val	Ala	Tyr	Ser		

**<210> 430**

<211> 147

<212> PRT

<213> Homo sapiens

**<400> 430**

Pro Gln Trp Cys Pro Arg Ser Gln Ala Arg Ser Ser Ala Ala Ala Ala

5 10 15

160

Ala Arg Ala Ser Val Pro Leu Arg Gly Ser Pro Gly Pro Ser Ala Ile  
 20 25 30  
 Met Pro Met Phe Ile Val Asn Thr Asn Val Pro Arg Ala Ser Val Pro  
 35 40 45  
 Asp Gly Phe Leu Ser Glu Leu Thr Gln Gln Leu Ala Gln Ala Thr Gly  
 50 55 60  
 Lys Pro Pro Gln Tyr Ile Ala Val His Val Val Pro Asp Gln Leu Met  
 65 70 75 80  
 Ala Phe Gly Gly Ser Ser Glu Pro Cys Ala Leu Cys Ser Leu His Ser  
 85 90 95  
 Ile Gly Lys Ile Gly Gly Ala Gln Asn Arg Ser Tyr Ser Lys Leu Leu  
 100 105 110  
 Cys Gly Leu Leu Ala Glu Arg Leu Arg Ile Ser Pro Asp Arg Val Tyr  
 115 120 125  
 Ile Asn Tyr Tyr Asp Met Asn Ala Ala Asn Val Gly Trp Asn Asn Ser  
 130 135 140  
 Thr Phe Ala  
 145

&lt;210&gt; 431

&lt;211&gt; 775

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 431

Leu Ala Pro Pro Arg Gln Leu Glu Ser Thr Ser Ser Ala Val Arg Leu  
 5 10 15  
 Thr Glu Met Leu Arg Ala Cys Gln Leu Ser Gly Val Thr Ala Ala Ala  
 20 25 30  
 Gln Ser Cys Leu Cys Gly Lys Phe Val Leu Arg Pro Leu Arg Pro Cys  
 35 40 45  
 Arg Arg Tyr Ser Thr Ser Gly Ser Ser Gly Leu Thr Thr Gly Lys Ile  
 50 55 60  
 Ala Gly Ala Gly Leu Leu Phe Val Gly Gly Gly Ile Gly Gly Thr Ile  
 65 70 75 80  
 Leu Tyr Ala Lys Trp Asp Ser His Phe Arg Glu Ser Val Glu Lys Thr  
 85 90 95  
 Ile Pro Tyr Ser Asp Lys Leu Phe Glu Met Val Leu Gly Pro Ala Ala  
 100 105 110  
 Tyr Asn Val Pro Leu Pro Lys Lys Ser Ile Gln Ser Gly Pro Leu Lys  
 115 120 125  
 Ile Ser Ser Val Ser Glu Val Met Lys Glu Ser Lys Gln Pro Ala Ser  
 130 135 140  
 Gln Leu Gln Lys Gln Lys Gly Asp Thr Pro Ala Ser Ala Thr Ala Pro  
 145 150 155 160  
 Thr Glu Ala Ala Gln Ile Ile Ser Ala Ala Gly Asp Thr Leu Ser Val  
 165 170 175  
 Pro Ala Pro Ala Val Gln Pro Glu Glu Ser Leu Lys Thr Asp His Pro  
 180 185 190  
 Glu Ile Gly Glu Gly Lys Pro Thr Pro Ala Leu Ser Glu Glu Ala Ser  
 195 200 205  
 Ser Ser Ser Ile Arg Glu Arg Pro Pro Glu Glu Val Ala Ala Arg Leu  
 210 215 220  
 Ala Gln Gln Glu Lys Gln Glu Gln Val Lys Ile Glu Ser Leu Ala Lys  
 225 230 235 240  
 Ser Leu Glu Asp Ala Leu Arg Gln Thr Ala Ser Val Thr Leu Gln Ala  
 245 250 255  
 Ile Ala Ala Gln Asn Ala Ala Val Gln Ala Val Asn Ala His Ser Asn

## 161

260	265	270
Ile Leu Lys Ala Ala Met Asp Asn Ser Glu Ile Ala Gly Glu Lys Lys		
275	280	285
Ser Ala Gln Trp Arg Thr Val Glu Gly Ala Leu Lys Glu Arg Arg Lys		
290	295	300
Ala Val Asp Glu Ala Ala Asp Ala Leu Leu Lys Ala Lys Glu Glu Leu		
305	310	315
Glu Lys Met Lys Ser Val Ile Glu Asn Ala Lys Lys Lys Glu Val Ala		
	325	330
Gly Ala Lys Pro His Ile Thr Ala Ala Glu Gly Lys Leu His Asn Met		
340	345	350
Ile Val Asp Leu Asp Asn Val Val Lys Lys Val Gln Ala Ala Gln Ser		
355	360	365
Glu Ala Lys Val Val Ser Gln Tyr His Glu Leu Val Val Gln Ala Arg		
370	375	380
Asp Asp Phe Lys Arg Glu Leu Asp Ser Ile Thr Pro Glu Val Leu Pro		
385	390	395
Gly Trp Lys Gly Met Ser Val Ser Asp Leu Ala Asp Lys Leu Ser Thr		
	405	410
Asp Asp Leu Asn Ser Leu Ile Ala His Ala His Arg Arg Ile Asp Gln		
420	425	430
Leu Asn Arg Glu Leu Ala Glu Gln Lys Ala Thr Glu Lys Gln His Ile		
435	440	445
Thr Leu Ala Leu Glu Lys Gln Lys Leu Glu Glu Lys Arg Ala Phe Asp		
450	455	460
Ser Ala Val Ala Lys Ala Leu Glu His His Arg Ser Glu Ile Gln Ala		
465	470	475
Glu Gln Asp Arg Lys Ile Glu Glu Val Arg Asp Ala Met Glu Asn Glu		
	485	490
Met Arg Thr Gln Leu Arg Arg Gln Ala Ala Ala His Thr Asp His Leu		
500	505	510
Arg Asp Val Leu Arg Val Gln Glu Glu Leu Lys Ser Glu Phe Glu		
515	520	525
Gln Asn Leu Ser Glu Lys Leu Ser Glu Gln Glu Leu Gln Phe Arg Arg		
530	535	540
Leu Ser Gln Glu Gln Val Asp Asn Phe Thr Leu Asp Ile Asn Thr Ala		
545	550	555
Tyr Ala Arg Leu Arg Gly Ile Glu Gln Ala Val Gln Ser His Ala Val		
	565	570
Ala Glu Glu Glu Ala Arg Lys Ala His Gln Leu Trp Leu Ser Val Glu		
580	585	590
Ala Leu Lys Tyr Ser Met Lys Thr Ser Ser Ala Glu Thr Pro Thr Ile		
595	600	605
Pro Leu Gly Ser Ala Val Glu Ala Ile Lys Ala Asn Cys Ser Asp Asn		
610	615	620
Glu Phe Thr Gln Ala Leu Thr Ala Ala Ile Pro Pro Glu Ser Leu Thr		
625	630	635
Arg Gly Val Tyr Ser Glu Glu Thr Leu Arg Ala Arg Phe Tyr Ala Val		
	645	650
Gln Lys Leu Ala Arg Arg Val Ala Met Ile Asp Glu Thr Arg Asn Ser		
660	665	670
Leu Tyr Gln Tyr Phe Leu Ser Tyr Leu Gln Ser Leu Leu Phe Pro		
675	680	685
Pro Gln Gln Leu Lys Pro Pro Pro Glu Leu Cys Pro Glu Asp Ile Asn		
690	695	700
Thr Phe Lys Leu Leu Ser Tyr Ala Ser Tyr Cys Ile Glu His Gly Asp		
705	710	715
Leu Glu Leu Ala Ala Lys Phe Val Asn Gln Leu Lys Gly Glu Ser Arg		
	725	730
		735

## 162

Arg Val Ala Gln Asp Trp Leu Lys Glu Ala Arg Met Thr Leu Glu Thr  
                   740                  745                  750  
 Lys Gln Ile Val Glu Ile Leu Thr Ala Tyr Ala Ser Ala Val Gly Ile  
                   755                  760                  765  
 Gly Thr Thr Gln Val Gln Pro  
                   770                  775

&lt;210&gt; 432

&lt;211&gt; 741

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 432

Arg Pro Lys Arg Leu Arg Thr Gly Asn Met Val Arg Ser Gly Asn Lys  
                   5                  10                  15  
 Ala Ala Val Val Leu Cys Met Asp Val Gly Phe Thr Met Ser Asn Ser  
                   20                  25                  30  
 Ile Pro Gly Ile Glu Ser Pro Phe Glu Gln Ala Lys Lys Val Ile Thr  
                   35                  40                  45  
 Met Phe Val Gln Arg Gln Val Phe Ala Glu Asn Lys Asp Glu Ile Ala  
                   50                  55                  60  
 Leu Val Leu Phe Gly Thr Asp Gly Thr Asp Asn Pro Leu Ser Gly Gly  
                   65                  70                  75                  80  
 Asp Gln Tyr Gln Asn Ile Thr Val His Arg His Leu Met Leu Pro Asp  
                   85                  90                  95  
 Phe Asp Leu Leu Glu Asp Ile Glu Ser Lys Ile Gln Pro Gly Ser Gln  
                   100                  105                  110  
 Gln Ala Asp Phe Leu Asp Ala Leu Ile Val Ser Met Asp Val Ile Gln  
                   115                  120                  125  
 His Glu Thr Ile Gly Lys Lys Phe Glu Lys Arg His Ile Glu Ile Phe  
                   130                  135                  140  
 Thr Asp Leu Ser Ser Arg Phe Ser Lys Ser Gln Leu Asp Ile Ile Ile  
                   145                  150                  155                  160  
 His Ser Leu Lys Lys Cys Asp Ile Ser Leu Gln Phe Phe Leu Pro Phe  
                   165                  170                  175  
 Ser Leu Gly Lys Glu Asp Gly Ser Gly Asp Arg Gly Asp Gly Pro Phe  
                   180                  185                  190  
 Arg Leu Gly Gly His Gly Pro Ser Phe Pro Leu Lys Gly Ile Thr Glu  
                   195                  200                  205  
 Gln Gln Lys Glu Gly Leu Glu Ile Val Lys Met Val Met Ile Ser Leu  
                   210                  215                  220  
 Glu Gly Glu Asp Gly Leu Asp Glu Ile Tyr Ser Phe Ser Glu Ser Leu  
                   225                  230                  235                  240  
 Arg Lys Leu Cys Val Phe Lys Lys Ile Glu Arg His Ser Ile His Trp  
                   245                  250                  255  
 Pro Cys Arg Leu Thr Ile Gly Ser Asn Leu Ser Ile Arg Ile Ala Ala  
                   260                  265                  270  
 Tyr Lys Ser Ile Leu Gln Glu Arg Val Lys Lys Thr Trp Thr Val Val  
                   275                  280                  285  
 Asp Ala Lys Thr Leu Lys Lys Glu Asp Ile Gln Lys Glu Thr Val Tyr  
                   290                  295                  300  
 Cys Leu Asn Asp Asp Asp Glu Thr Glu Val Leu Lys Glu Asp Ile Ile  
                   305                  310                  315                  320  
 Gln Gly Phe Arg Tyr Gly Ser Asp Ile Val Pro Phe Ser Lys Val Asp  
                   325                  330                  335  
 Glu Glu Gln Met Lys Tyr Lys Ser Glu Gly Lys Cys Phe Ser Val Leu  
                   340                  345                  350  
 Gly Phe Cys Lys Ser Ser Gln Val Gln Arg Arg Phe Phe Met Gly Asn

163

355 360 365  
 Gln Val Leu Lys Val Phe Ala Ala Arg Asp Asp Glu Ala Ala Ala Val  
 370 375 380  
 Ala Leu Ser Ser Leu Ile His Ala Leu Asp Asp Leu Asp Met Val Ala  
 385 390 395 400  
 Ile Val Arg Tyr Ala Tyr Asp Lys Arg Ala Asn Pro Gln Val Gly Val  
 405 410 415  
 Ala Phe Pro His Ile Lys His Asn Tyr Glu Cys Leu Val Tyr Val Gln  
 420 425 430  
 Leu Pro Phe Met Glu Asp Leu Arg Gln Tyr Met Phe Ser Ser Leu Lys  
 435 440 445  
 Asn Ser Lys Lys Tyr Ala Pro Thr Glu Ala Gln Leu Asn Ala Val Asp  
 450 455 460  
 Ala Leu Ile Asp Ser Met Ser Leu Ala Lys Lys Asp Glu Lys Thr Asp  
 465 470 475 480  
 Thr Leu Glu Asp Leu Phe Pro Thr Thr Lys Ile Pro Asn Pro Arg Phe  
 485 490 495  
 Gln Arg Leu Phe Gln Cys Leu Leu His Arg Ala Leu His Pro Arg Glu  
 500 505 510  
 Pro Leu Pro Pro Ile Gln Gln His Ile Trp Asn Met Leu Asn Pro Pro  
 515 520 525  
 Ala Glu Val Thr Thr Lys Ser Gln Ile Pro Leu Ser Lys Ile Lys Thr  
 530 535 540  
 Leu Phe Pro Leu Ile Glu Ala Lys Lys Lys Asp Gln Val Thr Ala Gln  
 545 550 555 560  
 Glu Ile Phe Gln Asp Asn His Glu Asp Gly Pro Thr Ala Lys Lys Leu  
 565 570 575  
 Lys Thr Glu Gln Gly Gly Ala His Phe Ser Val Ser Ser Leu Ala Glu  
 580 585 590  
 Gly Ser Val Thr Ser Val Gly Ser Val Asn Pro Ala Glu Asn Phe Arg  
 595 600 605  
 Val Leu Val Lys Gln Lys Lys Ala Ser Phe Glu Glu Ala Ser Asn Gln  
 610 615 620  
 Leu Ile Asn His Ile Glu Gln Phe Leu Asp Thr Asn Glu Thr Pro Tyr  
 625 630 635 640  
 Phe Met Lys Ser Ile Asp Cys Ile Arg Ala Phe Arg Glu Glu Ala Ile  
 645 650 655  
 Lys Phe Ser Glu Gln Arg Phe Asn Asn Phe Leu Lys Ala Leu Gln  
 660 665 670  
 Glu Lys Val Glu Ile Lys Gln Leu Asn His Phe Trp Glu Ile Val Val  
 675 680 685  
 Gln Asp Gly Ile Thr Leu Ile Thr Lys Glu Glu Ala Ser Gly Ser Ser  
 690 695 700  
 Val Thr Ala Glu Glu Ala Lys Lys Phe Leu Ala Pro Lys Asp Lys Pro  
 705 710 715 720  
 Ser Gly Asp Thr Ala Ala Val Phe Glu Glu Gly Gly Asp Val Asp Asp  
 725 730 735  
 Leu Leu Asp Met Ile  
 740

&lt;210&gt; 433

&lt;211&gt; 291

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 433

Phe Arg Pro Arg Tyr Glu Gly Arg Gly Arg Gly Cys Cys Gly Arg Val  
 5 10 15

164

Leu Leu Leu Arg Arg Gly Leu His Val Asp Cys Gly Lys Leu Gly Asn  
                   20                  25                  30  
 Lys Leu Thr Ser Ser Cys Gly Lys Pro Ser Ser Asn Arg Met Ser Leu  
                   35                  40                  45  
 Gln Trp Thr Ala Val Ala Thr Phe Leu Tyr Ala Glu Val Phe Val Val  
                   50                  55                  60  
 Leu Leu Leu Cys Ile Pro Phe Ile Ser Pro Lys Arg Trp Gln Lys Ile  
                   65                  70                  75                  80  
 Phe Lys Ser Arg Leu Val Glu Leu Leu Val Ser Tyr Gly Asn Thr Phe  
                   85                  90                  95  
 Phe Val Val Leu Ile Val Ile Leu Val Leu Leu Val Ile Asp Ala Val  
                   100                  105                  110  
 Arg Glu Ile Arg Lys Tyr Asp Asp Val Thr Glu Lys Val Asn Leu Gln  
                   115                  120                  125  
 Asn Asn Pro Gly Ala Met Glu His Phe His Met Lys Leu Phe Arg Ala  
                   130                  135                  140  
 Gln Arg Asn Leu Tyr Ile Ala Gly Phe Ser Leu Leu Leu Ser Phe Leu  
                   145                  150                  155                  160  
 Leu Arg Arg Leu Val Thr Leu Ile Ser Gln Gln Ala Thr Leu Leu Ala  
                   165                  170                  175  
 Ser Asn Glu Ala Phe Lys Lys Gln Ala Glu Ser Ala Ser Glu Ala Ala  
                   180                  185                  190  
 Lys Lys Tyr Met Glu Glu Asn Asp Gln Leu Lys Lys Gly Ala Ala Val  
                   195                  200                  205  
 Asp Gly Gly Lys Leu Asp Val Gly Asn Ala Glu Val Lys Leu Glu Glu  
                   210                  215                  220  
 Glu Asn Arg Ser Leu Lys Ala Asp Leu Gln Lys Leu Lys Asp Glu Leu  
                   225                  230                  235                  240  
 Ala Ser Thr Lys Gln Lys Leu Glu Lys Ala Glu Asn Gln Val Leu Ala  
                   245                  250                  255  
 Met Arg Lys Gln Ser Glu Gly Leu Thr Lys Glu Tyr Asp Arg Leu Leu  
                   260                  265                  270  
 Glu Gln His Ala Lys Leu Gln Ala Ala Val Asp Gly Pro Met Asp Lys  
                   275                  280                  285  
 Lys Glu Glu  
                   290

&lt;210&gt; 434

&lt;211&gt; 349

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 434

Gly Val Ala Pro Trp Gly Arg Gly Arg Ala Ala Pro Arg Cys Ala Ser  
                   5                  10                  15  
 Ala Thr Val Gly Gly Ser Gly Ile Gly Arg Leu Arg Gly Ile Thr Ser  
                   20                  25                  30  
 Ser Gly Leu Lys Met Asp Asn Lys Lys Arg Leu Ala Tyr Ala Ile Ile  
                   35                  40                  45  
 Gln Phe Leu His Asp Gln Leu Arg His Gly Gly Leu Ser Ser Asp Ala  
                   50                  55                  60  
 Gln Glu Ser Leu Glu Val Ala Ile Gln Cys Leu Glu Thr Ala Phe Gly  
                   65                  70                  75                  80  
 Val Thr Val Glu Asp Ser Asp Leu Ala Leu Pro Gln Thr Leu Pro Glu  
                   85                  90                  95  
 Ile Phe Glu Ala Ala Ala Thr Gly Lys Glu Met Pro Gln Asp Leu Arg  
                   100                  105                  110  
 Ser Pro Ala Arg Thr Pro Pro Ser Glu Glu Asp Ser Ala Glu Ala Glu

165

115	120	125
Arg Leu Lys Thr Glu Gly Asn Glu Gln Met Lys Val Glu Asn Phe Glu		
130	135	140
Ala Ala Val His Phe Tyr Gly Lys Ala Ile Glu Leu Asn Pro Ala Asn		
145	150	155
Ala Val Tyr Phe Cys Asn Arg Ala Ala Ala Tyr Ser Lys Leu Gly Asn		160
	165	170
Tyr Ala Gly Ala Val Gln Asp Cys Glu Arg Ala Ile Cys Ile Asp Pro		175
	180	185
Ala Tyr Ser Lys Ala Tyr Gly Arg Met Gly Leu Ala Leu Ser Ser Leu		190
	195	200
Asn Lys His Val Glu Ala Val Ala Tyr Tyr Lys Lys Ala Leu Glu Leu		205
	210	215
Asp Pro Asp Asn Glu Thr Tyr Lys Ser Asn Leu Lys Ile Ala Glu Leu		220
225	230	235
Lys Leu Arg Glu Ala Pro Ser Pro Thr Gly Gly Val Gly Ser Phe Asp		240
	245	250
Ile Ala Gly Leu Leu Asn Asn Pro Gly Phe Met Ser Met Ala Ser Asn		255
	260	265
Leu Met Asn Asn Pro Gln Ile Gln Gln Leu Met Ser Gly Met Ile Ser		270
	275	280
Gly Gly Asn Asn Pro Leu Gly Thr Pro Gly Thr Ser Pro Ser Gln Asn		285
	290	295
Asp Leu Ala Ser Leu Ile Gln Ala Gly Gln Gln Phe Ala Gln Gln Met		300
305	310	315
Gln Gln Gln Asn Pro Glu Leu Ile Glu Gln Leu Arg Ser Gln Ile Arg		320
	325	330
Ser Arg Thr Pro Ser Ala Ser Asn Asp Asp Gln Gln Glu		335
	340	345

&lt;210&gt; 435

&lt;211&gt; 519

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 435

Gln Pro Ser Ala Glu Pro Arg Arg Thr Met Pro Ala Val Asp Lys Leu		
	5	10
Leu Leu Glu Glu Ala Leu Gln Asp Ser Pro Gln Thr Arg Ser Leu Leu		15
	20	25
Ser Val Phe Glu Glu Asp Ala Gly Thr Leu Thr Asp Tyr Thr Asn Gln		30
	35	40
Leu Leu Gln Ala Met Gln Arg Val Tyr Gly Ala Gln Asn Glu Met Cys		45
	50	55
Leu Ala Thr Gln Gln Leu Ser Lys Gln Leu Leu Ala Tyr Glu Lys Gln		60
	65	70
Asn Phe Ala Leu Gly Lys Gly Asp Glu Glu Val Ile Ser Thr Leu His		75
	85	90
Tyr Phe Ser Lys Val Val Asp Glu Leu Asn Leu Leu His Thr Glu Leu		95
	100	105
Ala Lys Gln Leu Ala Asp Thr Met Val Leu Pro Ile Ile Gln Phe Arg		110
	115	120
Glu Lys Asp Leu Thr Glu Val Ser Thr Leu Lys Asp Leu Phe Gly Leu		125
	130	135
Ala Ser Asn Glu His Asp Leu Ser Met Ala Lys Tyr Ser Arg Leu Pro		140
	145	150
Lys Lys Lys Glu Asn Glu Lys Val Lys Thr Glu Val Gly Lys Glu Val		155
	165	170
		175



166

Ala Ala Ala Arg Arg Lys Gln His Leu Ser Ser Leu Gln Tyr Tyr Cys  
 180 185 190  
 Ala Leu Asn Ala Leu Gln Tyr Arg Lys Gln Met Ala Met Met Glu Pro  
 195 200 205  
 Met Ile Gly Phe Ala His Gly Gln Ile Asn Phe Phe Lys Lys Gly Ala  
 210 215 220  
 Glu Met Phe Ser Lys Arg Met Asp Ser Phe Leu Ser Ser Val Ala Asp  
 225 230 235 240  
 Met Val Gln Ser Ile Gln Val Glu Leu Glu Ala Glu Lys Met  
 245 250 255  
 Arg Val Ser Gln Gln Glu Leu Leu Ser Val Asp Glu Ser Val Tyr Thr  
 260 265 270  
 Pro Asp Ser Asp Val Ala Ala Pro Gln Ile Asn Arg Asn Leu Ile Gln  
 275 280 285  
 Lys Ala Gly Tyr Leu Asn Leu Arg Asn Lys Thr Gly Leu Val Thr Thr  
 290 295 300  
 Thr Trp Glu Arg Leu Tyr Phe Phe Thr Gln Gly Gly Asn Leu Met Cys  
 305 310 315 320  
 Gln Pro Arg Gly Ala Val Ala Gly Gly Leu Ile Gln Asp Leu Asp Asn  
 325 330 335  
 Cys Ser Val Met Ala Val Asp Cys Glu Asp Arg Arg Tyr Cys Phe Gln  
 340 345 350  
 Ile Thr Thr Pro Asn Gly Lys Ser Gly Ile Ile Leu Gln Ala Glu Ser  
 355 360 365  
 Arg Lys Glu Asn Glu Glu Trp Ile Cys Ala Ile Asn Asn Thr Ser Arg  
 370 375 380  
 Gln Ile Tyr Leu Thr Asp Asn Pro Glu Ala Val Ala Ile Lys Leu Asn  
 385 390 395 400  
 Gln Thr Ala Leu Gln Ala Val Thr Pro Ile Thr Ser Phe Gly Lys Lys  
 405 410 415  
 Gln Glu Ser Ser Cys Pro Ser Gln Asn Leu Lys Asn Ser Glu Met Glu  
 420 425 430  
 Asn Gln Asn Asp Lys Ile Val Pro Lys Ala Thr Ala Ser Leu Pro Glu  
 435 440 445  
 Ala Glu Glu Leu Ile Ala Pro Gly Thr Pro Ile Gln Phe Asp Ile Val  
 450 455 460  
 Leu Pro Ala Thr Glu Phe Leu Asp Gln Asn Arg Gly Ser Arg Arg Thr  
 465 470 475 480  
 Asn Pro Phe Gly Glu Thr Glu Asp Glu Ser Phe Pro Glu Ala Glu Asp  
 485 490 495  
 Ser Leu Leu Gln Met Phe Ile Val Arg Phe Leu Gly Ser Met Ala  
 500 505 510  
 Val Lys Thr Asp Ser Thr Thr  
 515

&lt;210&gt; 436

&lt;211&gt; 357

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 436

Met Leu Gln Ile His Leu Pro Gly Arg His Thr Leu Phe Val Arg Ala  
 5 10 15  
 Met Ile Asp Ser Gly Ala Ser Gly Asn Phe Ile Asp His Glu Tyr Val  
 20 25 30  
 Ala Gln Asn Gly Ile Pro Leu Arg Ile Lys Asp Trp Pro Ile Leu Val  
 35 40 45  
 Glu Ala Ile Asp Gly Arg Pro Ile Ala Ser Gly Pro Val Val His Glu

167

50 55 60  
 Thr His Asp Leu Ile Val Asp Leu Gly Asp His Arg Glu Val Leu Ser  
 65 70 75 80  
 Phe Asp Val Thr Gln Ser Pro Phe Phe Pro Val Val Leu Gly Val Arg  
 85 90 95  
 Trp Leu Ser Thr His Asp Pro Asn Ile Thr Trp Ser Thr Arg Ser Ile  
 100 105 110  
 Val Phe Asp Ser Glu Tyr Cys Arg Tyr His Cys Arg Met Tyr Ser Pro  
 115 120 125  
 Ile Pro Pro Ser Leu Pro Pro Pro Ala Pro Gln Pro Pro Leu Tyr Tyr  
 130 135 140  
 Pro Val Asp Gly Tyr Arg Val Tyr Gln Pro Val Arg Tyr Tyr Tyr Val  
 145 150 155 160  
 Gln Asn Val Tyr Thr Pro Val Asp Glu His Val Tyr Pro Asp His Arg  
 165 170 175  
 Leu Val Asp Pro His Ile Glu Met Ile Pro Gly Ala His Ser Ile Pro  
 180 185 190  
 Ser Gly His Val Tyr Ser Leu Ser Glu Pro Glu Met Ala Ala Leu Arg  
 195 200 205  
 Asp Phe Val Ala Arg Asn Val Lys Asp Gly Leu Ile Thr Pro Thr Ile  
 210 215 220  
 Ala Pro Asn Gly Ala Gln Val Leu Gln Val Lys Arg Gly Trp Lys Leu  
 225 230 235 240  
 Gln Val Ser Tyr Asp Cys Arg Ala Pro Asn Asn Phe Thr Ile Gln Asn  
 245 250 255  
 Gln Tyr Pro Arg Leu Ser Ile Pro Asn Leu Glu Asp Gln Ala His Leu  
 260 265 270  
 Ala Thr Tyr Thr Glu Phe Val Pro Gln Ile Pro Gly Tyr Gln Thr Tyr  
 275 280 285  
 Pro Thr Tyr Ala Ala Tyr Pro Thr Tyr Pro Val Gly Phe Ala Trp Tyr  
 290 295 300  
 Pro Val Gly Arg Asp Gly Gln Gly Arg Ser Leu Tyr Val Pro Val Met  
 305 310 315 320  
 Ile Thr Trp Asn Pro His Trp Tyr Arg Gln Pro Pro Val Pro Gln Tyr  
 325 330 335  
 Pro Pro Pro Gln Pro Pro Pro Pro Pro Pro Pro Pro Pro Pro Pro  
 340 345 350  
 Ser Tyr Ser Thr Leu  
 355

&lt;210&gt; 437

&lt;211&gt; 501

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(501)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 437

cgcaccagct ctctgctctc ccagcgcagc gccgcgcgcc ggcccctcca gcttcccgga 60  
 ccatggccaa cctggagcgc accttcacgc ccatcaagcc ggacggcgtg cagcgcggcc 120  
 tgggtggcga gatcatcaag cgcttcgagc agaagggatt ccgcctcgtg gccatgaagt 180  
 tcctccgggc ctctgaagaa cacctgaagc agcactacat tgacctgaaa gaccgaccat 240  
 tcttcctcgtg gctggtgaag tacatgaact cagggccggt tgtggccatg gtctgggagg 300  
 ggctgaacgt ggtgaagaca ggccgagtga tgcttgggga gaccaatcca gcagattcaa 360

168

agccaggcac	cattcgtggg	gacttctgca	ttcaggttgg	caggaacatc	attcatggca	420
gtgattcagt	aaaaagtgt	gaaaaagaaa	tcancctatg	gtttaagcct	gaanaactgg	480
ttgactacaa	gtcttgtgct	c				501

&lt;210&gt; 438

&lt;211&gt; 501

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 438

tgaaatactg	gagctgttgt	agaagaaaaa	cttctgattt	taatacattc	ttagcccaag	60
agggctgtac	aaaagggaaa	cacatgtgga	ctaaaaaaga	tgctgggaaa	aaagttgttc	120
catgtagaca	tgactggcat	cagactggag	ggtgaaagt	ccatttcagt	atatgctaaa	180
aactcacttc	cagaacttag	ccgagtagaa	gcaaatagca	cattgttaaa	tgtgcatatt	240
gtatttgaag	gagagaagga	atttgatcaa	aatgtgaaat	tatgggtgt	gattgatgta	300
aagcgaagtt	atgtaactat	gactgcaaca	aagattgaaa	tcactatgag	aaaagctgaa	360
ccgatgcagt	gggcaagcct	tgaactgcct	gcagctaaaa	agcaggaaaa	acaaaaagat	420
gacacaacag	attgagtggg	agatggaagg	aaggctatta	cattatttcc	gaatttttaa	480
tactgtgtga	agtgtgtggc	t				501

&lt;210&gt; 439

&lt;211&gt; 501

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 439

taaaacaagc	acttgataaa	cttaaaactgt	catcaggga	tgaagaaaat	aagaagaag	60
aagacaatga	tgaaattaag	attgggacct	catgtaagaa	tggagggtgt	tcaaagacat	120
accagggtct	agagagtcta	gaagaagtct	gtgtatatca	ttctggagta	cctattttcc	180
atgaggggat	gaaatactgg	agctgttgta	gaagaaaaac	ttctgatttt	aatacattct	240
tagcccaaga	gggctgtaca	aaagggaaa	acatgtggac	taaaaaagat	gctgggaaaa	300
aagttgttcc	atgtagacat	gactggcatc	agactggagg	tgaagttacc	atttcagtat	360
atgtgaaa	ctgaattcca	gaacttagcc	ggagttagag	caaatagcac	attgttga	420
gtgcatattg	tatttgaagg	agagaaggaa	tttgatcaaa	atgtgaaatt	atgggggtgt	480
attgatgtaa	agcgaattat	t				501

&lt;210&gt; 440

&lt;211&gt; 481

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;221&gt; misc\_feature

&lt;222&gt; (1)...(481)

&lt;223&gt; n = A,T,C or G

&lt;400&gt; 440

tgatccctat	tgttttgtgg	agtttcatga	gcacgtcat	gcagctgcag	cattagctgc	60
tatgaatgga	cggaagataa	tggttaagga	agtcaaagt	aattgggcaa	caaccctag	120
cagtcaaaag	aaagatacaa	gcaatcattt	ccatgtcttt	gttggatgac	tcagcccaga	180
aattacaact	gaagatataa	aaagtgcctt	tgcaccattt	ggaagaatat	cagatgcccg	240
agtggtaaaa	gacatggcaa	caggaaagtc	taagggatat	ggctttgtct	cctttttcaa	300
caaatgggat	gctgaaaacg	ccattcaaca	gatgggtggc	cagtggcttg	gtggaagaca	360
aatcagaact	aactgggcaa	cccgaagcc	tcccgtcca	aagagtacat	atgagtcaaa	420
taccaaacag	ctatcatatg	atganggtgt	aatcagtcct	aatccaagca	actgtctgta	480
t						481

**This Page is Inserted by IFW Indexing and Scanning  
Operations and is not part of the Official Record**

**BEST AVAILABLE IMAGES**

Defective images within this document are accurate representations of the original documents submitted by the applicant:

Defects in the images include but are not limited to the items checked:

- ☐ **BLACK BORDERS**
- ☐ **IMAGE CUT OFF AT TOP, BOTTOM OR SIDES**
- ☐ **FADED TEXT OR DRAWING**
- ☐ **BLURRED OR ILLEGIBLE TEXT OR DRAWING**
- ☐ **SKEWED/SLANTED IMAGES**
- ☐ **COLOR OR BLACK AND WHITE PHOTOGRAPHS**
- ☐ **GRAY SCALE DOCUMENTS**
- ☒ **LINES OR MARKS ON ORIGINAL DOCUMENT**
- ☐ **REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY**
- ☐ **OTHER:** \_\_\_\_\_

**IMAGES ARE BEST AVAILABLE COPY.**

**As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.**